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OM protein - protein search, using sw model

August 29, 2002, 07:54:53 ; Search time 69.02 Seconds (without alignments) 793.551 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-701-586B-2 2998 1 MAARRRSTGGGRARALNES......PNQVRMRYLLKVQENFLQLW

570

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	NAD+ ADP-ribosyltr	probable NAD+ ADP-	NAD+ ADP-ribosyltr	-	NAD+ ADP-ribosyltr	probable poly (ADP	NAD+ ADP-ribosyltr	NAD+ ADP-ribosyltr	hypothetical prote	NAD+ ADP-ribosyltr	hypothetical prote	NAD+ ADP-ribosyltr	protein ZK1005.1 [NAD+ ADP-ribosyltr	hypothetical prote		hypothetical prote	conserved hypothet	myosin X - human	lmpl protein - Myc	lmpl protein - Myc	rhoptry protein -	kinesin heavy chai	hyaluronan recepto					
SUMMARIES	OI (I	T01311	T03656	JH0581	S04200	A29725	JS0428	S26057	S31735	A47474	T51353	C84719	S42208	T03657	T18600	T08713	T20414	PN0494	D88948	T03058	A72287	S48411	A64465	F75103	A59267	T18351	T30822	T28676	^	JC4298
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dР	Query	39.2	38.3	34.1	33.9	33.8	33.7	33.6	32.8	32.7	32.2	32.2	32.2	32.1	22.9	22.5	17.5	11.1	5.5	4.7	4.5	4.4	4.4	4.2	4.2	4.2	4.2	4.1	4.1	4.0
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Page]	hypothetical prote	giantin - human	hypothetical prote	hypothetical prote	male-enhanced anti	myosin heavy chain	hypothetical prote	kinesin heavy chai	hyaluronan recepto	conserved hypothet	hypothetical prote.	hypothetical prote	transcription fact	hypothetical prote	paraflagellar rod
toor 1482	T22615 (02 C)	A56539	T29145	T17272	T42722	A29320	71870	A41919	JC5016	н69378	r16270	S28298	140984	838085	33658
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	120.5	120	119	119	118.5	117.5	117.5	117	116.5	116.5	116.5	116	116	115.5	115.5
-2.rpr	30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 TO1311 NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - Arabidopsis thaliana NA)+ ADP-ribosyltransferase (EC 2.4.2.30) - Arabidopsis thaliana NA)+ ALEGRATE names: poly(ADP-ribose) polymerase; protein T14P8.19 C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 21-Jul-2000 C; Accession: T01311; S65662 R; Kallscht, J.; Elliott, G.; Cloud, J. Submitted to the EMBL Data Library, May 1998 A; Description: The sequence of A. thaliana T14P8. A; Reference number: 214290 A; Accession: T01311 A; Status: translated from GB/EMBL/DDBJ	A.Molecule type: DNA A.Molecule type: DNA A.Residues: 1.635 cKaLA A.FResidues: 1.635 cKaLA A.FResidues: 1.635 cKaLA A.Cross-references: EMBL:AF069298; NID:g3193282; PID:g3193299 A.Experimental source: cultivar Columbia R.Expiniaco L.; Babiychuk, E.; Kushnir, S.; Van Montagu, M.; Inze, D. FBBS Lett. 364, 103-108, 1995 A.Title: Characterization of an Arabidopsis thaliana cDNA homologue to animal poly(AD A.Reference number: S65662; MUID:95269779 A.Reference number: S65662; MUID:95269779 A.Status: nucleic acid sequence not shown A.Molecule type: mRNA A.Residues: 1-115, GT', 116-635 cLEP> A.Cross-references: EMBL:248243; NID:g853721; PIDN:CAA88288.1; PID:g853722	A,Gene: PARP A,Gene: PARP A,Gene: PARP A,Gene: PARP A,Gene: PARP A,Introns: 28/3; 116/1; 162/3; 190/1; 268/3; 312/1; 330/3; 355/2; 371/1; 387/3; 408/3 A,Introns: 28/3; 116/1; 162/3; 190/1; 268/3; 312/1; 330/3; 355/2; 371/1; 387/3; 408/3 A,Mote: T14PB.19 C,Keywords: DNA binding; glycosyltransferase; NAD; pentosyltransferase; zinc finger C,Keywords: DNA binding; glycosyltransferase; NAD; pentosyltransferase; zinc finger Query Match Best Local Similarity 43.9%; Pred. No. 9.9e-67; Matches 254; Conservative 98; Mismatches 187; Indels 40; Gaps 11;	QY 2 AARRRSTGGGRARALNESKRVNNGNTAPEDSSPAKKTRRCORQESKKMPVAGGKA 57 1 1 1 1 1 1 1 1 1	OY 58 NKDRTEDKQDESVKALLLKGKAPVDPECTAKV-GKAHYYCEGNDYYDVMLNOTNLOF 113 119 EDDNNGFEBEKKEEKIVTATKKGAAVLDQMIPDEIKSQYHVLQRGDDVYDAILNOTNVRD 178	Oy 114 NNNKYLLQLLEDDAQRNFSVWARWGRVGKMGQHSLVACSGNLNKAKEIFQKKFLDKTKN 173
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174 NWEDREKFEKVPGKYDMLQMDYATNTQDEEETKKEESLKSPLKPP-SQLDLRVQELIKLI 232 179 NNNKFFVLQVLESDSKKTYMVYTRWGRVGVKGQSKLDGPYDSWDRAIEIFTNKFNDKTKN 238 g δλ

2

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Cyaccession: JH0581
R:Ittel, M.E.; Garnier, J.M.; Jeltsch, J.M.; Niedergang, C.P.
Gene 102, 157-164, 1991
R:Ittel, M.E.; Garnier, J.M.; Jeltsch, J.M.; Niedergang, C.P.
Gene 102, 157-164, 1991
A; Title: Chicken poly(ADP-ribose) synthetase: complete deduced amino acid sequence an A; Reference number: JH0581; MUID:91340148
A; Reference number: JH0581; MUID:91340148
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-1011 

A; Coss. references: EMBL:X52690; NID:963742; PIDN:CAA36917.1; PID:963743
C; Comment: This protein is a chromatin-bound enzyme.
C; Comment: This enzyme catalyzes DNA-dependent post-translational modifications of va C; Superfamiliy: NAD-ADP-ribosyltransferase
C; Superfamiliy: NAD-ADP-ribosyltransferase; NAD; nucleus; pentosyltransferase; zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N;Alternate names: poly(ADP-ribose) synthase
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
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                                                                                                                                                   LWHGSRMSNWVGILSHGLRIAPPEAPITGYMFGKGIYFADMSSKSANYCFASRLKNTGLL
                                                     355 ALRPLDHESYEFKVISQYLQSTHAPTHSDYTMTLLDLFEVEKDGEKEAFRE--DLHNRML
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Best Local Similarity 40.6%; Pred. No. 1e-56;
Matches 217; Conservative 110; Mismatches 187; Indels
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NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - chicken
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[Species: Zea mays (maize)
[Species: Cottrill, P.; Storozhenko, S.; Fuangthong, M.; O'Farrell, M.; Van Monta submitted to the EMBL Data Library, November 1997
[Species Titled to the EMBL Data Library, November 1997
[Species Titled to the EMBL Data Library, November 1997
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[Species Titled to the EMBL AJ222588; NID:e1264090; PIDN:CAA10888.1; PID:e1264091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 LIQLLEDDAQRNFSVWMRWGRVGKMGQHSLVACSGNLNKAKEIFQKKFLDKTKNNWEDRE 179
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                                                                                                                                                           YTRIPHDFGLR--TPPLIRTQKELSEKIQLLEALGDIEIAIKLVKTELQSPEHPLDQHYR
                                                                                                                                                                                                                                                              NLHCALRPLDHESYEFKVISQYLQSTHAPTHSDYTMTLLDLFEVEKDGEKEAFRE--DLH
                                                                                                                                                                                                                                                                                           NRMLLWHGSRMSNWVGILSHGLRIAPPEAPITGYMFGKGIYFADMSSKSANYCFASRLKN
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                                                                                CNVQAMEEMMMEMKYNTKKAPLGKLTVAQIKAGYQSLKKIEDCIRAGQHGRALMEACNEF
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Nacession: A29725; MUID:88076933

Night apprints of the poly (ADP-ribose) polymerase: poly (ADP-ribose) synthetase; poly (ADP-ribose) polymerase; poly (ADP-ribose) polymerase; poly (ADP-ribose) synthetase; poly (ADP-ribose) polymerase; poly (ADP-ribose) and 
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A; Residues: 1-69, 70', 71-1014 <UCH>
A; Residues: 1-69, 60', 71-1014 <UCH>
A; Residues: 1-69, 60', 71-1014 <UCH>
B; Ricrosaki, T.; Ushiro, H.; Mitsuuchi, Y.; Suzuki, S.; Matsuda, M.; Matsuda, Y.; Katu
J. Biol. Chem. 262, 15990-15997, 1987
A; Title: Primary structure of human poly (ADP-ribose) synthetase as deduced from CDNA
A; Reference number: A28498; MUID:88058958
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A;Residues: 12-26,'T',28-66;116-166 <GRA>
R;Schneider, R.; Auer, B.; Kuehne, C.; Herzog, H.; Klocker, H.; Burtscher, H.J.; Hirs
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C;Keywords: DNA binding; glycosyltransferase; NAD; nucleus; pentosyltransferase; zinc
                                                                                                                                                                                                                                                                                                                                                                                             C; Species: Mus musculus (house mouse)
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
C; Accession: S04200
R; Huppl, K.; Bhatia, K.; Siwarski, D.; Klinman, D.; Cherney, B.; Smulson, M.
Nucleic Acids Res. 17, 3387-3401, 1989
A; Fitle: Sequence and organization of the mouse poly (ADP-ribose) polymerase gene. A; Reference number: S04200; MUID: 89263780
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A;Residues: 1-1013 <HUP>
A;Cross references: EMBL:X14206; NID:g49893; PIDN:CAA32421.1; PID:g49894
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151 ACSGNLNKAKEIFQKKFLDKTKNNWEDREKFEKVPGKYDMLQMDYATNTQDEEFTKKEES
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                                                                                                                                               36;
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                                                                                                     518 LNGSTVPLGPASDTGILNPDGYTLNYNEYIVYNPNQVRMRYLLKVQFNF-LQLW
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A; Reference number: JS0428
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                                                                                                                                                                                                                                                                                                  A;Cross-references: GDB:119508; OMIM:173870
A;Map position: 1q41-1q42
C;Superfamily: NAD+ ADP-ribosyltransferase
C;Keywords: DNA binding; DNA repair; glycosyltransferase; NAD; nucleus; pentosyltransfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - bovine
                                                                                                     K.; Ushiro, H.; Terashi
                   for human NAD (+): protein ADP-ribosyltransferase
                                                              A; Molecule type: mRNA
A; Residues: 381-420; 682-710 <SCH>
A; Residues: 381-420; 682-710 <SCH>
R; Yokoyama, Y.; Kawamoto, T.; Mitsuuchi, Y.; Kurosaki, T.; Toda, K.; Ushiro, H.;
Eur. J. Biochem. 194, 521-526, 1990
A; Title: Human poly(ADP-ribose) polymerase gene. Cloning of the promoter region.
A; Reference number: S14010; MUID:91099327
A; Accession: S14010
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
                                                                                                                                                                                                                              A;Cross-references: EMBL:X56140; NID:g35286; PIDN:CAA39606.1; PID:g825702
C;Comment: This protein can ADP-ribosylate itself as well as other proteins.
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  || | ::|:| || || ::|:| GKTTPDPSANISLDGVDVPLGTGISSGV---NDTSLLYNEYIVYDIAQVNLKYLLKIKFN 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -LIVNPGTKSKLPKPVQDLIKMIFDVESMKKAMVEYEIDLQKMPLGKLSKRQIQAAYSI 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKKIEDCIRAGQHGRALMEACNEFYTRIPHDFGLRTPPLIRTQKELSEKIQLLEALGDIE 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKMAPSSAHFVTLNGSTVPLGPASDTGILNPDGYTLNYNEYIVYNPNQVRMRYLLKVQFN 565
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APEDSSPAKKTRRCQRQESKKMPVAGGKANKDRTEDKQDESVKALLLKGKAPVDPECTAK 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IAIKLVK-TELQSPEHPLDQHYRNLHCALRPLDHESYEFKVISQYLQSTHAPTHSDYTMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VGKAHVYCEGNDVYDVMLNQTNLQFNNNKYYLIQLLEDDAQRNFSVWMRWGRVGKMGQHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 LVACSGNLNKAKEIFQKKFLDKTKNNWEDREKFEKVPGKYDMLQMDYATNTQDEEETKKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESLKSPLKPESQLDLRVQELIKLICNVQAMEEMMMEMKYNTKKAPLGKLTVAQIKAGYQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLDLFEVEXDGEXEAFR - - EDLHNRMLLWHGSRMSNWVGILSHGLRIAPPEAPITGYMFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLEQMPSKEDAIEHFMKLYEEKTGNAWHSK-NFTKYPKKFYPLEIDYG---QDEEAVKK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KGIYFADMSSKSANYCFASRLKNTGLLLLSEVALGQCNELLEANPKAEGLLQGKHSTKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                        29;
                                                                                                                                                                                                                                                                                                                                                                                                      Length 1014;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 33.8%; Score 1012.5; DB 1;
Best Local Similarity 40.5%; Pred. No. 4.1e-56;
Matches 221; Conservative 111; Mismatches 185;
                 Title: Isolation of a cDNA clone for hur
Reference number: A61559; MUID:88082900
Accession: A61559
Cell Biol. 44, 302-307, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APRGKSGAALSKKSKGOV-----
                                                                                                                                                                                                                                                                                      A; Gene: GDB: ADPRT; PPOL
                                                                                                                                                                                                      Molecule type: DNA
Residues: 1-95 <YOK>
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A; Molecule type: mRNA
A; Readdues: 1-1016 <53.17
A; Experimental source: thywus
R; Taniguchi, T.; Yamauchi, K.; Yamamoto, T.; Toyoshima, K.; Harada, N.; Tanaka, H.; T
Eur. J. Blochem. 171, 571, 198
Bur. J. Blochem. 171, 575, 198
A; Title: Depression in gene expression for poly(ADP-ribose) synthetase during the int
A; Reference number: $00328; MUID:88151954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleotide binding; nucleus; P-loo
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C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001
C;Accession: JS0428; S00328; A30458
S;Salto, I.
submitted to JIPID, February 1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 GNTAPEDSSPAKKTRRCQRQESKKMPVAGGKANKDRTEDKQDESVKALLLKGKAPVDPEC 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAKVGKAHVYCEGNDVYDVMLNQTNLQFNNNKYYLIQLLEDDAQRNFSVWMRWGRVGKMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGLEHNAHVLEKGGKVFSATLGLVDIVKGTNSYYKLQLLEDDKESRYWIFRSWGRVGTVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146 QHSLVACSGNLNKAKEIFQKKFLDKTKNNWEDREKFEKVPGKYDMLQMDYATNTQDEEET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKEESLKSPLKPESQLDLRVQELIKLICNVQAMEEMMMEMKYNTKKAPLGKLTVAQIKAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;128-165/Region: zinc finger
F;200-220/Region: helix-turn-helix motif
F;204-231/Region: nuclear location signal
F;250-270/Region: helix-turn-helix motif
F;494-501/Region: nucleotide-binding motif A (P-loop)
F;890-903/Region: nucleotide binding #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 658-685;899-696;893-901 <TA2>
C;Superfamily: NAD+ ADP-ribosyltransferase
C;Keywords: DNA binding; 91ycosyltransferase;
F;21-51/Region: zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                               <TAN>
                                                                                                                                                                                                                                                                                                                                                                                                A,Accession: S00328
A;Molecule type: mRNA
A;Residues: 648-714,838-904 <TAN
A;Cross-references: EMBL:X06986
A;Accession: A30458
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pento

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A. Molecule type: MRNA
A. Residues: 1-998 < SAUD
A. Molecule type: MRNA
A. Residues: 1-998 < SAUD
B. Cawa, Y.; Uchida, M.; Ami, Y.; Kushida, S.; Okada, N.; Miwa, M.
B. Cawa, Y.; Uchida, K.; Uchida, M.; Ami, Y.; Kushida, S.; Okada, N.; Miwa, M.
Biochem. Blophys. Res. Commun. 193, 119-125, 1993
A. Title: Isolation of cDNAs encoding the catalytic domain of poly(ADP-ribose)polymera
A. Reference number: PNO494; MUID:93277538
A. Reference number: PNO495
A. Molecule type: MRNO95
A. Molecule type: MRNO95
A. Residues: 742-745, E., 747-876 < COZA
C. Comment: This zinc-finger protein plays a role in DNA repair, cell growth, and diff
C. Superfamily: NADP-ribosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Keywords: DNA binding; glycosyltransferase; hexosyltransferase; NAD; nucleus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A47474
NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - fruit fly (Drosophila melanogaster)
  N;Alternate names: poly ADP-ribose polymerase
C;Species: Xenopus laevis (African clawed frog)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
C;Accession: S31735; PN0495
R;Saulier-le Drean, B.M.
submitted to the EMBL Data Library, May 1992
A;Reference number: S31735
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 AQRNFSVWMRWGRVGK-MGQHSLVACSGNLNKAKEIFQKKFLDKTKNNWEDREKFEKVPG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 YNTKKAPLGKLTVAQIKAGYQSLKKIEDCIRAGQHGRALMEACNEFYTRIPHDFGLRTPP 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIRTOKELSEKIQLLEALGDIEIAIKLVKTELQSPE-HPLDQHYRNLHCALRPLDHESYE 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 KRVNNGNTAPE-----BSSPAKKTRRCQRQESKKMPVAG------GKANKDRTEDKQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESVKALLLKGKAPVDPECTAKVGKAHVYCEGNDVYDVMLNQTNLQFNNNKYYLIQLLEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 KYDMLQMDYATNTQDEEETKKEESLKSPLKPESQLDLRVQELIKLICNVQAMEEMMMEMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         794 SRIICDYVKNTHADTHNAYDLEVLEIFKIDREGEYQRYKPFKQLHNRQLLWHGSRTTNFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        484 ELLEANPKAEGLLQGKHSTKGLGKMAPSSAHFVTLNGSTVPLGPA-----SDTGILNPDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .4e-54;
es 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 32.8%; Score 984.5; Best Local Similarity 39.1%; Pred. No. 2.4e Matches 222; Conservative 109; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----YNEYIVYDIAQVNLKYLLKKKFNY 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         539 YTLNYNEYIVYNPNQVRMRYLLKVQFNF 566
                                                                                                                                                                          A; Accession: S31735
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                                                                                                                                    NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 18-Jun-1999
C;Accession: 826657; 878453; 152331
R;Thibodeau, J.; Gradwohl, G.; Dumas, C.; Clairoux-Moreau, S.; Brunet, G.; Penning, C.;
Biochem. Cell Biol. 67, 653-660, 1989
A;Title: Cloning of rodent cDNA encoding the poly(ADP-ribose) polymerase catalytic domains. R;Accession: 826057.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEDDAQRNFSVWMRWGRVGKMGQHSLVACSGNLNKAKEIFQKKFLDKTKNNWEDREKFEK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302 LRTPPLIRTQKELSEKIQLLEALGDIEIAIKLVK-TELQSPEHPLDQHYRNLHCALRPLD 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HESYEFKVISQYLQSTHAPTHSDYTMTLLDLFEVEKDGEKEAFR--EDLHNRMLLWHGSR 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MSNWVGILSHGLRIAPPEAPITGYMFGKGIYFADMSSKSANYCFASRLKNTGLLLLSEVA 478
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NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - African clawed frog (fragment)
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A;Residues: 1-500 <THI>
A;Cross-references: EMBL:X65497; NID:956849; PIDN:CAA46478.1; PID:956850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MMEMKYNTKKAPLGKLTVAQIKAGYQSLKKIEDCIRAGQHGRALMEACNEFYTRIPHDFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.6%; Score 1006.5; DB 2; ilarity 42.6%; Pred. No. 3.7e-56; Conservative 101; Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VNDTCLLYNEYIVYDIAQVNLKYLLKKKFNFKTSLW 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Potvin, F. submitted to the EMBL Data Library, March 1992 NReference number: S78453 A;Accession: S78453
KENEKTSLW 1016
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Best Local 9
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Gaps

70;

151;

Score 966; DB 2; Pred. No. 3.4e-53; 5; Mismatches 151;

Length 983; Indels

pentosyltransferase

NAD;

PIDN:CAA10482.1

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KSPLKPESQLDLRVQELIKLICNVQAMEEMMMEMKYNTKKAPLGKLTVAQIKAGYQSLKK 271
                                                                                                                                                                                                                                                                                                                                                             QESKKMPVAGGKANKDRTEDKQDESVKALLLKGKAPVDPECTAKVGKAHVYCEGNDVYDV 104
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                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule: 1-983 <br/>
A;Residues: 1-983 <br/>
A;Cross-references: EMBL:AJ131705; PIDN:CAA10482.1<br/>
A;Experimental source: cultivar landsberg erecta<br/>
A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: C;Function: A;Genetion: App-ribose polymer synthesis<br/>
C;Superfamily: NAD+ ADP-ribosyltransferase<br/>
C;Keywords: DNA binding; glycosyltransferase; NAD;
                    translated from GB/EMBL/DDBJ
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Best Local Similarity 38.8%; Pre
Matches 213; Conservative 115;
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971 LQFLLKVRF 979
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A; Accession: T51353
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              Fuchida, K.; Hanal, S.; Ishikawa, K.; Ozawa, Y.; Uchida, M.; Sugimura, T.; Miwa, M. Proc. Natl. Acad. Sci. U.S.A. 90, 3481-3485, 1993
A.Title: Cloning of CDNA encoding Drosophila poly(ADP-ribose) polymerase: leucine zipper A; Reference number: A47474; MUID:93234521
A; Reference number: A47474
A; Accession: A47474
A; Astatus: preliminary
A; Astatus: preliminary
A; Residues: 1-994 < CUCH>
A; Residues: 1-994 < CUCH>
A; Cross-references: GB:D13806; GB:D13808; NID:9303545; PIDN:BAA02964.1; PID:94
A; Cross-references: GB:D13806; Dackbone (NCBIN:129703, NCBIP:129704)
C; Genetics:
A; Cross-references: FlyBase:FBgn0010247
C; Superfamily: NAD+ ADP-ribosyltransferase
C; Keywords: DNA binding; glycosyltransferase; NAD; nucleus; pentosyltransferase
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    Arabidopsis thaliana

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                                                                                                                                                                                                                                                                                                                                                        Length 994;
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YIVYDVAQVNIQYLFRMEFKY
  Accession: A47474
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384

441

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probable poly (ADP-ribose) polymerase [imported] - Arabidopsis thaliana Cispecies: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Daccession: C84719
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.M.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Ka.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Accession: C84719
496
                                                                                   914
                                                                                                                                                                                                        YMFGKGIYFADMSSKSANYCFASRLKNTGLLLLSEVALGQCNELLEAN-----PKAEGLL
                                             QGKHSTKGLGKMAPSSAHFVTLNGS-TVPLGPASDTGILNPDGYTLNYNEYIVYNPNQVR
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C; Species: Sarcophaga peregrina
C; Species: Sarcophaga peregrina
C; Accession: $42208; $71496
R; Masutani, M.; Nozaki, T.; Hitomi, Y.; Ikejima, M.; Nagasaki, K.; de Prati, A.C.; Kurat
Bur. J. Blochem. 220, 607-614, 1994
A; Title: Cloning and functional expression of poly(ADP-ribose) polymerase cDNA from Sard
A; Reference number: $42208; MUID:94170813
                                                                                                                                                                 17;
A;Molecule type: DNA
A;Residues: 1-1009 <STO>
A;Cross-references: GB:AE002093; NID:g4432827; PIDN:AAD20677.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g31320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - flesh fly (Sarcophaga peregrina)
                                                                                                                                                                                                              |: ::| | ||::|:::| : |: :||||| |:|
551 TLSMSDLSTGINSYYILQIIQEDKGSDCYVFRKWGRVGNEKIGG------NKVEEM 600
                                                                                                                                                                                                                                                      MINQINIQFNNNKYYLIQLLEDDAQRNFSVWMRWGRVG--KMGQHSLVACSGNLNKAKEI 162
                                                                                                                                                                                                                                                                                                                                                                                          825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       385 TMTLLDLFEVEKDGEKEAF---REDLHNRMLLWHGSRMSNWVGILSHGLRIAPPEAPITG 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QGKHSTKGLGKMAPSSAHFVTLNGS-TVPLGPASDTGILNPDGYTLNYNEYIVYNPNQVR 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:D16482; NID:g473742; PIDN:BAA03943.1; PID:g538248 A;Accession: S71496 A;Molecule type: protein A;Molecule type: protein A;Residues: 170-188;721-736;813-819;879-885 <MAX> C;Superfamily: NAD+ ADP-ribosyltransferase
                                                                                                                                                                                                                                                                                                                -----FQKKFLDKTKNNWEDREK---FEKVPGKYDMLQMDYAINTQDEEETKKEESL 211
                                                                                                                                                                                                                                                                                                                                                                           KSPLKPESQLDLRVQELIKLICNVQAMEEMMMEMKYNTKKAPLGKLTVAQIKAGYQSLKK 271
                                                                                                                                                                                                                                                                                                                                                                                                                                    IEDCI-----RAGQHGRALMEACNEFYTRIP--HDFGLRTPPLIRTQKELSEKIQLLEAL 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDIEIAIKLVKTELQSPEHPLDQHYRNLHCALRPLDHESYEFKVISQYLQSTHAPTHSDY 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YMFGKGIYFADMSSKSANYCFASRLKNTGLLLSEVALGQCNELLEAN-----PKAEGLL 496
                                                                                                                                                                                           QESKKMPVAGGKANKDRTEDKQDESVKALLLKGKAPVDPECTAKVGKAHVYCEGNDVYDV 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                       Length 1009;
                                                                                                                                  Query Match 32.2%; Score 966; DB 2; Length 10
Best Local Similarity 38.8%; Pred. No. 3.5e-53;
Matches 213; Conservative 115; Mismatches 151; Indels
                                                                        ;Map position: 2
;Superfamily: NAD+ ADP-ribosyltransferase
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LQFLLKVRF 1005
                                                                                                                                Query Match
Best Local Similarity
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A; Residues: 1-996 <MAS>
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C; Keywords: DNA binding; glycosyltransferase; NAD; pentosyltransferase; zinc finger F;1-59/Domain: DNA binding #status predicted <DNA> F:370-507/Domain: auto-modification #status predicted <AMO> F;508-996/Domain: NAD binding #status predicted <AMD>
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C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 20-Jun-2000
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 20-Jun-2000
C;Accession: T03657
R;Babiychuk, E.; Cottrill, P.; Storozhenko, S.; Fuangthong, M.; O'Farrell, M.; Van Nsubmitted to the EMBL Data Library, November 1997
A;Description: Higher plants possess two poly(ADP-ribose) polymerases.
A;Reference number: 214992
A;Reference number: 214992
A;Reference number: preliminary; translated from GB/EMBL/DDBJ
A;Reference review mRNA
A;Residues: 1-969 < RAB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : :| |:| | ||::|||: :| :| :| || : || ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: |
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760 YSLLQTEDSKADINPIDKHYEQLKTKLEPLDKNSEEYILLQKYVKNTHAETHKLYDLEVV
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C;Superfamily: NAD+ ADP-ribosyltransferase
C;Keywords: DNA binding; glycosyltransferase; NAD; pentosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 ACSGNLNKAKEIFQKKFLDKTKNNWEDREKFEKVPGKYDMLQMDYATNTQDEEETKKEES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32;
                                                                                                                                                                                                                                                                                                                                                                            Length 996;
                                                                                                                                                                                                                                                                                                                                                                      Query Match 32.2%; Score 964; DB 1; Length 99 Best Local Similarity 39.9%; Pred. No. 4.7e-53; Matches 216; Conservative 116; Mismatches 177; Indels
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C;Genetics:
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80

Score 961.5;

32.1%;

---VGKAHVYCEGNDVYDVMLNQTNLQFNNNKYYLIQLLED 126

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Best Local Similarity 39.3%; Pred. No. 6.5e-53; Matches 223; Conservative 104; Mismatches 179; Indels 61; Gaps 18;	Qy 32 DSSPAKKTRRCQRQESKKMPVAGGKANKDRTEDKQDESVKALLL 75 ::::	Qy 76 KGKAPVDPECTAKVGKAHVYCEGNDVYDVMLNQTNLQFNNNKYYLIQLLEDDAQRNFSVW 135	Qy 136 MRWGRVGKMGOHSLVACSGNLNKAKEIFQKKFLDKTKNNWEDREKFEKVPGKYDM 190 	QY 191 LQMDYATNTQDEEETKKEESLKSPLKPESQLDLRVQELIKLICNVQAMEEMMEMYNTK 250 19 19 19 19 19 19 19 1	Qy 251 KAPLGKLTVAQIKAGYQSLKKIEDCIR-AGQHGRALMEACNEFYTRIPHDFGL 302 	QY 303 RTPPLIRTQKELSEKIQLLEALGDIEIAIKLVKTELQSPEHPLDQHYRNLHCALRPLDHE 362 : :	Qy 363 SYEFKVISQYLQSTHAPTHSDYTMTLLDLFEVEKDGEKEAFREDLHNRMLLWHGSRM 419 :: : :: ::	Qy 420 SNWVGILSHGLRIAPPEAPIJGYMFGKGIYFADMSSKSANYCFASRLKNTGLLLLSEVAL 479 	QY 480 GQCNELLEANPKAEGLLQGKHSTKGLGKMAPSSAHFVTLNGS-TVPLGPASDTGILNPDG 538 : : :	Qy 539 YTLNYNEYIVYNPNOVRMRYLLKVQFN 565 	RESULT 14 T18600 hypothetical protein ACB.1 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: L15-oct-1999 #text_change 15-oct-1999 C; Accession: T18600 R; McMurray, A. Submitted to the EMBL Data Library, November 1996 A; Reference number: Z18996 A; Reference number: Z18996 A; Reference number: T18600 A; Accession: T18600	A;Gene: CESP:AC8.1 A;Map position: 5 A;Introns: 31/3; 271/3; 312/3; 348/1; 466/3; 545/3; 617/3; 702/2	Query Match 22.9%; Score 685.5; DB 2; Length 727; Best Local Similarity 31.1%; Pred. No. 1.2e-35; Matches 178; Conservative 110; Mismatches 220; Indels 65; Gaps 16;

ESKRVNNGNTAPEDSSPAKKTRRCQRQESKKMPVAGGKANKDRTEDKQDESVKALLLKGK 78

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C; Accession: T08713
R; Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
Submitted to the Protein Sequence Database, May 1999
A; Reference number: 216472
A; Reference number: 216472
A; Recession: T08713
A; Molecule type: mRNA
A; Residues: 1-459
A; Cross-references: EMBL:AL050034
A; Experimental source: fetal kidney; clone DKF2p566G0224
C; Genetics: Cspecies: Cspecies (Cspecies)
C; Superfamily: NAD+ ADP-ribosyltransferase
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                                                                299 NEQD------IPEGHDRTAQDVFH----EKTKNDMIYRKHFRKMPG 334
                                                                                                                                                                                                                     304 TPPLIRTQKELSEKIQLLEALGDIEIAIKLV-----KTELQSPEHPLDQHYRNLHCAL 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            477 VALGQCNELLEA-NPKAEGLLQGKHSTKGLGKMAPSS-AHFVTLNGSTVPLGPA--SDTG 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 VQELIKLICNVQAMEEMMMEMKYNTKKAPLGKLTVAQIKAGYQSLKKIEDCIRA-GQHGR 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 GNPDENDFAKKRRMKKEARLMEVQKKRMKKQSDLLWEYRQIFERMPYTDN----ISILRE 298
                                                                                                                                                        335 MFSYVETDYSEFVGTNNGHKKKITPGSKITPGSKTLLPKSVKEVVMSIFDVENMKSALKS 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 LQFNNNKYYLIQLLEDDAQRNFSVWMRWGRVGKMGQHSLVACSGNLNKAKEIFQKKFLDK 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 284 ALMEACNEFYTRIPHDFGLRTPPLIRTQKELSEKIQLLEALGDIEI--AIKLVKTELQSP 341
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                                                                                                                                                                                                 245 MKYNTKKAPLGKLTVAQIKAGYQSLKKIED-CIRAGQHGRALMEACNEFYTRIPHDFGLR
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ALIGNMENTS

RESULT 1
T08713
NAD+ ADP-ribosyltransferase homolog DKFZp566G0224.1 - human (fragment)
C;Species: Homo saplens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 03-Nov-2000
C;Accession: T08713
R;Ansorge, W; Wirkner, U; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16472
A;Accession: T08713
A;Accession: T08713
A;Accession: T08713
A;Accession: T08713 C;Genetics:
A;Note: DKFZp566G0224.1
C;Superfamily: NAD+ ADP-ribosyltransferase A;Molecule type: mRNA A;Restidues: 1-459 <ANS: A;Cross-references: EMBL:AL050034 A;Experimental source: fetal kidney; clone DKFZp566G0224 502 SHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIELAQALQAVSEQEKTVEEVPHP NIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALEEALKGPTDGGQSLEELS PQGQPVPCPEFSSSTFSQSEYLIYQESQCRLRYLLEVHL 540 HVGYMFLGEVALGREHHINTDNPSLKSPPPGFDSVIARGHTEPDPTQDTELELDGQQVVV KLGNRKLLWHGTNMAVVAAILTSGLRIMPHSGGRVGKGIYFASENSKSAGYVIGMKCGAH LDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQTGSNHRCPTLQHIWKVNQEGEEDRFQAHS LDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQTGSNHRCPTLQHIWKVNQEGEEDRFQAHS KLGNRKLLWHGTNMAVVAAILTSGLRIMPHSGGRVGEGIYFASENSKSAGYVIGMKCGAH Conservative 99.8%; Score 2419; DB 2; Pred. No. 1.4e-161; 1; Mismatches 0; Length 459 Indels 0; Gaps 501 441 321 180 261 120 201 360 300 381 240 0

628

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FEBS Lett. 364, 103-108, 1995

A:Title: Characterization of an Arabidopsis the A:Reference number: S65662; MUID:95269779

A:Accession: S65662

A;Status: nucleic acid sequence not shown A:Molecule type: mRNA

A;Residues: 1-115, 'GT', 116-635 < LEP>
A;Cross-references: EMBL:Z48243; NID:9853721; if C:Genetics: A:Gene: PARP

A:Map position: 4
A:Introns: 28/3; 116/1; 162/3; 190/1; 268/3; 3:A:Note: T14P8.19

C:Keywords: DNA binding: glycosyltransferase; if the A:Mote: T14P8.19

C:Keywords: DNA binding: glycosyltransferase; if the A:Mote: T14P8.19
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NAD+ ADP-ribose) poly(ADP-ribose) polymerase; protein T14P8.19
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 21-Jul-2000
C;Accession: T01311; S65662
R;Ralicki, J.; Ellictt, G.; Cloud, J.
submitted to the EMBL Data Library, May 1998
A;Description: The sequence of A. thaliana T14P8.
A;Reference number: Z14290
A;Accession: T01311
A;Status: translated from GB/EMBL/DDBJ
A;Residues: 1-635 <KALD
A;Residue
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A;Experimental source: cultivar Columbia
R;Lepiniec, L.; Babiychuk, E.; Kushnir, S.; Van Montagu, M.;
FEBS Lett. 364, 103-108, 1995
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  VYFADMFSKSANYCYA-NTGAND-GVLLLCEVALGDMNELLYSDYNADNLPPGKLSTKGV
                                                        TYFASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSLKSPPPGFDSVIAR 479
                                                                                                                                                                       HIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPH----SGGRVGKG 419
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                                                                                                                 QLFRASRAVEADRFQQFSSSKNRMLLWHGSRLTNWAGILSQGLRIAPPEAPVTGYMFGKG
                                                                                                                                                                                                                                   SVDPGLQ-----DDPLYYHYQQLNCGLTPVGNDSEEFSMVANYMENTHAKTHSGYTVEIA 456
                                                                                                                                                                                                                                                                                                                                                 -DRYDRTRLEELSGEFYTVIPHDFGFKKMSQFVIDTPQKLKQKIEMVEALGEIELATKLL
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A; Residues: 658-685; 689-696; 893-901 <TA2>
C; Superfamily: NAD+ ADP-ribosyltransferase
C; Keywords: DNA binding; glycosyltransferase
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A; Residues: 648-714; 838-904 <TAN>
A; Cross-references: EMBL: X06986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: JS0428; R; Saito, I.
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                     VLADIELAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNPGTQVYED----YNCTLNQTNIENNNNKFYIIQLLQDSNRF-FTCWNRWGRVGEV-GQ 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVGPKGKSGAAPSKKSKGPVKEEG--TNKSEKRMKLTLKGGAA-----
NLLDIEVAYSLLRGGSDDSSKD----
                                                                                                                 AYSILSEVQQALSQGSSD--SHILDLSNRFYTLIPHDFGMKKPPLLNNANSVQAKVEMLD
                                                                                                                                                                                                                                TVNP-GTKSKLPKP-----VQNLIKMIFDVESMKKAMVEYEIDLQKMPLGKLSKRQIQA
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                                                                                                                                                                       GFEALEALEEAL-KGPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLL
                                                                                                                                                                                                                                                                                   DRGPVRTVTKRVQPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIAR
                                                                                                                                                                                                                                                                                                                                                 NKLEQMPSKEDAIEHFMKLYEEKTGNAWHSK-NFTKHPKKFYPLEIDYGQDE---EAVKKL
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Pred. No. 1.8e-39;
PIDVNYEKLKTDIKVVDKDSEEAEIIRKYVKNTH
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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 170-188; 721-736; 813-819; 879-885 < MAX>
C; Superfamily: NAD+ ADP-ribosyltransferase; NAD; pentosyltransferase; C; Keywords: DNA binding; glycosyltransferase; NAD; pentosyltransferase; F; 1-369/Domain: DNA binding #status predicted < CNA>
F; 370-507/Domain: auto-modification #status predicted < AMO>
F; 508-996/Domain: NAD binding #status predicted < NAD>
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A; Residues: 1-996 < MAS>
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nes 179; Conserv
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                                                                                                                                           E--ELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIELAQALQAVSEQEKTV
                                                                                                                                                                                          IENNNUKEYIIQLLQD--SNRFFTCWNRWGRVG-EVGQSKINHFTRLEDAKKDFEKKFRE
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                                                                                       EEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT-GSNHRCPTLQ--HIWKVNQEG
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                                                     NPIDKHYEQLKTKLEPLDKNSEEYILLQKYVKNTHAETHKLYDLEVVDIFKVARQG
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Pred. No. 5.1e-39;
N4; Mismatches 195
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A;Reference number: Z14991
A;Accession: T03656
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-653 < BAB>
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                                                                     VYFADMFSKSANYCYASE--ACRSGVLLLCEVALGDMNELLNADYDANNLPKGKLRSKGV
                                                                                                                                         QIFKVSRHGETERFQKFASTRNRMLLWHGSRLSNWAGILSQGLRIAPPEAPVTGYMFGKG
                                                                                                                                                                         HIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPH----SGGRVGKG 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDYNCTLNQTNIENNNNKFYIIQLLQ-DSNRFFTCWNRWGRVGEVGQSKINHFTRLED-A 128
GQTAPNMV-ESKVADDG--VVVPLGEPKQEPS-KRGGLLYNEYIVYNVDQIRMRYVLHVN
                                  GHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYLIYQESQCRLRYLLEVH
                                                                                                                                                                                                                                                                                     --KADRRHLEQLTGEFYTVIPHDFGFRKMREFIIDTPQKLKAKLEMVEALGEIEIATKL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGPVRTVTKRVQ 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EIYDATLNQTNVGDNNNKFYIIQVLESDAGGSFMVYNRWGRVGVRGQDKLHGPSPTRDQA 247
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                                                                                                      IYFASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSLKSPPPGFDSVIAR
                                                                                                                                                                                                             ----LEDDSSDQDDPLYARYKQLHCDFTPLEADSDEYSMIKSYLRNTHGKTHSGYTVDIV
                                                                                                                                                                                                                                              AVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT-GSNHRCPTLQ--
                                                                                                                                                                                                                                                                                                                    GPTDGGQSLEELSSHFYTVIPHNFGHSQPPP--INSPELLQAKKDMLLVLADIELAQALQ 306
                                                                                                                                                                                                                                                                                                                                                         ETKLETRIAQFISLICNISMMKQRMVEIGYNAEKLPLGKLRKATILKGYHVLKRISDVIS
                                                                                                                                                                                                                                                                                                                                                                                        PCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALEEALK 248
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Pred. No. 5.3e
93; Mismatches
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NAD+ ADP-ribosyltransferase (EC 2.4.2.30), nuclear - N;Alternate names: poly (ADP-ribose) polymerase; poly C;Species: Homo sapiens (man)

poly

(ADP-ribose)

synthetase;

poly(A

human

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A; residues: 1-69, 'Q', 71-1014 <UCH>
A; Residues: 1-69, 'Q', 71-1014 <UCH>
A; Cross-references: GB:M18112; NID:g190166; PIDN:AAA60137.1; PID:g190167
R; Kurosaki, T.; Ushiro, H.; Mitsuuchi, Y.; Suzuki, S.; Matsuda, M.; Matsuda,
J. Biol. Chem. 262, 15990-15997, 1987
A; Title: Primary structure of human poly (ADP-ribose) synthetase as deduced in A; Reference number: A28498; MUID:88058958
A; Maccession: A28498
A; Molecula **County **C
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A; Note: the sequence figure has an omission of forty res
R; Ogura, T.; Nyunoya, H.; Takahashi-Masutani, M.; Miwa,
Biochem. Biophys. Res. Commun. 167, 701-710, 1990
A; Title: Characterization of a putative promoter region
A; Reference number: I38096; MUID:90211250
A; Accession: I38096
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A; Molecule type: mRNA
A; Residues: 1.49, 'D',51-612,'Q',614-907,'Y',909-939,'R',941-979,'I',981-1014
A; Cross-references: GB:J03030
A; Note: the authors translated the codon ATA for residue 980 as Asn
R; Suzuki, H.; Uchida, K.; Shima, H.; Sato, T.; Okamoto, T.; Kimura, T.; Miwa,
Biochem. Biophys. Res. Commun. 146, 403-409, 1987
A; Title: Molecular cloning of cDNA for human poly(ADP-ribose) polymerase and
A; Reference number: A26901; MUID:87298455
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A.Residues: 1-16, E',18-211, 'K',213-236, 'R',238-366, 'H',369-1014
A.Residues: GB:J03473
A.Cross-references: GB:J03473
R;Cherney, B.W.; McBride, O.W.; Chen, D.; Alkhatib, H.; Bhatia, K.Proc. Natl. Acad. Sci. U.S.A. 84, 8370-8374, 1987
A.Title: cDNA sequence, protein structure, and chromosomal locatian and Reference number: A39976; MUID:88068596
A.Accession: A39976
                                                                                                                R;Schneider, R.; Auer, B.; Kuehne, C.
Eur. J. Cell Biol. 44, 302-307, 1987
A;Title: Isolation of a cDNA clone fo
                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 12-26, 'T', 28-66; 116-166 <GRA>
                                                                                                                                                                                                                                                                                                                                                               A;Note: these fragments represent a zinc finger-containing DNA-binding R;Gradwohl, G.; Menissler de Murcla, J.; Molinete, M.; Simonin, F.; Kok Proc. Natl. Acad. Sci. U.S.A. 87, 2990-2994, 1990 A;Title: The second zinc-finger domain of poly(ADP-ribose) polymerase cap;Reference number: A33635; MUID:90222155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M29544; GB:M22953
A;Note: the authors translated the codon GTG 1
A;Note: these fragments represent intron-exon
A;Accession: A33321
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                                              A; Reference number: A61559; MUID:88082900 A; Accession: A61559
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A;Accession: B33321
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DNA 8, 575-580, 1
                                                                                                                                                                                                                                                                                                                         A; Status: not compared with conceptual translation
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A; Residues: 16-66; 96; 121-159, 'D', 161-167 < AU2>
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A; Residues: 38-43;93-98;132-137;204-209;237-242;276-281;335-340;384-389;431-436;512-517
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        A; Molecule
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A; Residues: 1-40 < RES>
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R.; Schweiger, M.
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va, M.; Sugimura,
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C;Accession: JH0581
R;Ittel, M.E.; Garnier,
Gene 102, 157-164, 1991
                                                                                                        NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - chicken N;Alternate names: poly(ADP-ribose) synthase C;Species: Gallus gallus (chicken) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
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JH0581

Л.М.;

Jeltsch,

J.M.;

Niedergang, C.P

10-Sep-1999

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A; Reference number: S14010; MUID:9109327
A; Status. N. 194, 521-526, 1990
A; Title: Human poly(ADP-ribose) polymerase
A; Reference number: S14010; MUID:91099327
A; Accession: S14010
A; Status. N. 194, 521-526, 1990
A; Status. N. 1
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A; Residues: 1-95 < YOK>
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C; Keywords:
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C;Superfamily: NAD+ ADP-ribosyltransferase
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-references: GDB:119508;
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YDIAQVNLKYLLKL
                                                    YQESQCRLRYLLEV
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                                                                                                                                                                                                                                                                                          ----SGGRVGKGIYFASENSKSAGYVIGMKCGAHH----VGYMFLGEVALGREHHINTDNP
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Pred. No. 1.1e-38;
1; Mismatches 195;
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NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_chang
C:Accession: S26057; S78453; 152331
R:Thibodeau, J.; Gradwohl, G.; Dumas, C.; Clairoux-Moreau, S.;
Biochem. Cell Biol. 67, 653-660, 1989
A:Title: Cloning of rodent cDNA encoding the poly(ADP-ribose)
A;Reference number: 152331; MUID:90027702
A;Accession: S26057
A;Molecule type: mRNA
A;Residues: 1-500 cHILD
A;Cross-references: EMBL:X65497; NID:g56849; PIDN:CAA46478.1;
R:Potvin, F.
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A;Recession: JH0581
A;Rocession: H0581
A;Rocession: JH0581
A;Rocession: JH0581
A;Rocession: JH0581
A;Rocession: JH0581
C;Comment: This protein is a chromatin-bound enzyme.
C;Comment: This enzyme catalyzes DNA-dependent post-translational modifications C;Superfamily: NAD+ ADP-ribosyltransferase; NAD; nucleus; pentosyltransferase; C;Keywords: DNA binding; glycosyltransferase; NAD; nucleus; pentosyltransferase;
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                                                                                                                                                                                             NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - Af N,Alternate names: poly ADP-ribose polymerase C;Species: Xenopus laevis (African clawed froc c;Date: 22-Nov-1993 #sequence_revision 10-Nov C;Accession: S31735; PN0495
R;Saulier-le Drean, B.M.
submitted to the EMBL Data Library, May 1992
A;Reference number: S31735
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A;Accession: S78453
A;Molecule type: mRNA
A;Residues: 1-124,'H',126-127,'A',129-238,'D',
A;Cross-references: EMBL:X65497
C;Superfamily: NAD+ ADP-ribosyltransferase
C;Keywords: DNA binding; DNA repair; glycosylt
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Pred.
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10-Nov-1995
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No. 3
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.2e-38;
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A; Reference number: $31735
A; Accession: $31735
A; Accession: $31735
A; Molecule type: mRNA
A; Residues: 1-998 <SAU>
A; Cross-references: EMBL: Z12139; NID: g64967; PIDN: CAA78126.1; PID: g1334661
R; Ozawa, Y; Uchida, K; Uchida, M.; Ami, Y; Kushida, S.; Okada, N.; Miwa, Biochem. Biophys. Res. Commun. 193, 119-125, 1993
A; Title: Isolation of cDNAs encoding the catalytic domain of poly(ADP-ribos A; Reference number: PNO494; MUID: 93277538
A; Accession: PNO495
A; Accession: PNO495
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 742-745, 'E', 747-876 <OZA>
C; Comment: This zinc-finger protein plays a role in DNA repair, cell growth C; Superfamily: NAD+ ADP-ribosyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLILLGEVALGNMYELKHAS-HISKLPKGKHSVKGLGKTAPDPS--ASITLDG--VEVPL
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A; Map position: 1
C; Superfamily: NA:
C; Keywords: DNA b
                                                                                                                                       A;Cross-references: EMBL:X14206; NID:g49893; PIDN:CAA32421.1; PID:g49894 C;Genetics:
                                                                                                                                                                                            C;Accession: $04200
R;Huppi, K.; Bhatia, K.; Siwarski, D.; Kli
Nucleic Acids Res. 17, 3387-3401, 1989
A;Title: Sequence and organization of the
A;Reference number: $04200; MUID:89263780
A;Accession: $04200
                                                                                                                                                                                                                                                                           NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - mouse C;Species: Mus musculus (house mouse) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
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                                                                                                            NAD+ ADP-ribosyltransferase
                                                                                              binding; glycosyltransferase;
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32.3%;
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                         Score 653; DB
Pred. No. 1.7e
02; Mismatches
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Pred. No. 1.
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A;Cross-references: FlyBase:FBgn0010247
C;Superfamily: NAD+ ADP-ribosyltransferase
C;Keywords: DNA binding; glycosyltransferase;
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A;Title: Cloning of cDNA encoding Drosophila poly(ADP-ribose) polymerase: leucine A;Reference number: A47474; MUID:93234521
A;Sccession: A47474
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:D13806; GB:D13807; GB:D13808; NID:g303545; PIDN:BAA02964.1; A;Note: sequence extracted from NCBI backbone (NCBIN:129703, NCBIP:129704)
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A; Residues: 1-994 <UCH>
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LQ-DSNRFFTCWNRWGRVG-EVGQSKINHFTRLEDAKKDFEKKFREKTKNNWAERDHFVS 152

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NAD1 ADP-ribosyltransferase (EC 2.4.2.30) [imported] - Arabidopsis thaliana Nap1 App-ribosyltransferase C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000 C:Accession: T51353 R:Doucet-chabeaud, G.; Kazmaier, M. Submitted to the EMBL Data Library, December 1998 A:Reference number: 225379 A:Accession: T51353 A:Status: preliminary; translated from GB/EMBL/DDBJ A:Molecule type: mRNA A:Residues: 1-983 <DOUV A:Residues: 1-983 <DOUV A:Cross-references: EMBL:AJ131705; PIDN:CAA10482.1 A:Experimental source: cultivar landsberg erecta C:Genetics: A:Genetics: A:Genetics: A:Genetics: Dap1-1 C:Function: ADP-ribosyltransferase C:Superfamily: NAD+ ADP-ribosyltransferase; NAD; pentosyltransferase C:Keywords: DNA binding; glycosyltransferase; NAD; pentosyltransferase
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                                                                                                                                           TLNQTNIENNNNKFYIIQLLQDSNRFFTCW--NRWGRVG--EVGQSKINHFTRLEDAKKD
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                                                                                                                                                                                                                          KKGRQAGREEDPFRSTAEALKAIPAEKRIIRVDPTCPLSSNPGTQ----VYED----YNC
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                                                    FKRLFLEKTGNTWESWEQKTNFQKQPGKFLPLD------IDYGVNKQVAKK-E
                                                                                                                       TLSMSDLSTGINSYYILQIIQE-DKGSDCYVFRKWGRVGNEKIGGNKVEEMSK-SDAVHE
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                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                             21.0%; Score 598.5; DB 31.1%; Pred. No. 1e-33;
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A;Title: Sequence and analysis of chromosome 2 of the pla
A;Reference number: A84420; MUID:20083487
A;Accession: C84719
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1009 <STO>
A;Cross-references: GB:AE002093; NID:g4432827; PIDN:AAD20
C;Genetics:
A;Gene: At2g31320
A;Map position: 2
C;Superfamily: NAD+ ADP-ribosyltransferase
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                                                                                                                                                                                                                                             KKGRQAGREEDPFRSTAEALKAIPAEKRIIRVDPTCPLSSNPGTQ----VYED----YNC
RLLTESDPQPTMKESLLVDASNRFFTMIP----SIHPHIIRDEDDFKSKVKMLEALQDIE
                 EAL----KGPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIE
                                                                                                                        FEKKFREKTKN---NWAERDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGPVRTVTKRVQ
                                                                                                                                                              TLNQTNIENNNNKFYIIQLLQDSNRFFTCW--NRWGRVG--EVGQSKINHFTRLEDAKKD 131
                                                                                                                                                                                                                   KKQRKLPFDKYKIEDTSESLYTVKVKGR-----SAVHEASGLQEHCHILEDGNSIYNT
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                                                                             P----CSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALE
                                                                                                         FKRLFLEKTGNTWESWEQKTNFQKQPGKFLPLD------IDYGVNKQVAKK-E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFQTSSNLAPSLIELMKMLFDVETYRSAMMEFEINMSEMPLGKLSKHNIQKGFEALTEIQ
                                                                                                                                                                                                                                                                        Conservative 101;
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                                                                                                                                                                                                                                                                       21.0%; Score 598.5; DB: 31.1%; Pred. No. 1.1e-33 tive 101; Mismatches 199
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NAD+ ADP-ribosyltransferase (EC 2.4.2.30) 2 - maize C;Species: Zea mays (maize) C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 20-Jun-2000 C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 20-Jun-2000 C;Accession: T03657 R;Bablychuk, E.; Cottrill, P.; Storozhenko, S.; Fuangthong, M.; O'Farrell, M.; submitted to the EMBL Data Library, November 1997 A;Description: Higher plants possess two poly(ADP-ribose) polymerases. A;Reference number: Z14992 A;Accession: T03657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: PARP2
C;Superfamily: NAD+ ADP-ribosyltransferase
C;Keywords: DNA binding; glycosyltransferase;
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Best Local Similarity
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                    364 HIWKVNQEGEEDRFQAH-SKLGNRKLLWHGTNMAVVAAILTSGLRIMPH---
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                                                                                            QEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQTGSNHRCPT
                                                                                                                                                                                                                                    QKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALEEALKGPTDGGQS
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                                                                                                                                    VRESLIVAASNRFFTLIP----SIHPHIIRDEDDLMIKAKMLEALQDIEIASKIVGFDSD
                                                                                                                                                                        LEE-----LSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIELAQALQAV-SE
                                                                                                                                                                                                              LELMKMLFNVETYRAAMMEFEINMSEMPLGKLSKENIEKGFEALTEIQNLLKDTADQALA
                                                                                                                                                                                                                                                                                                                             TKNNWAE----RDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGPVRTVTKRVQPCSLDPAT
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                                                          SDES-----LDDKYMKLHCDITPLAHDSEDYKLIEQYL----LNTHAPTHKDWSLELE
                                                                                                                                                                                                                                                                                           TGNSWEAWECKTNFRKQPGRFYPLDVD-----YGVKKAPKRKDISEMK-SSLAPQL
                                                                                                                                                                                                                                                                                                                                                                                                         ENNNNKFYIIQLL-QDSNRFFTCWNRWGRVG--EVGQSKINHFTRLEDAKKDFEKKFREK
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  96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 578; DB 2;
Pred. No. 2.8e-32;
6; Mismatches 195
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A; Residues: 1-727 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted to the EMBL Data A; Reference number: Z18996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein AC8.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Decies: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T18600
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Best Local Similarity
Matches 162; Conser
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  KSPPPGFDSVIARG-----
                                      EAPVSGYMFGKGVYFADMFSKSFFY---CRANAKEEAYLLLCDVALGNVQQLMASKNVSR
                                                                        ----SGGRVGKGIYFASENSKSAGYVIGMKCGAHHVGYMFLGEVALGR-EHHINTDNPSL 466
                                                                                                                                                                                                                                                                         LAFEVLNDISDLLVKLPIDASKIL-DFSNKFYTIIPHNFGMRVPEPIDSFHKIKEKNNML
                                                                                                                                                                                                                                                                                                           RGFEALEALEEAL-KGPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDML 293
                                                                                                                                                                                                                                                                                                                                                   KKKITPGSKTTLPKSVKEVVMSIFDVENMKSALKSFEIDVNKMPLGRLSHNQIN 413
                                                                                                                                                                                                                                                                                                                                                                                     VRTVT--KRVQPCS---LDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKKDF-----EKKFREKTKNNWAERDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDGEGNPDENDFAKKRRMKKEARLMEVQKKRMKKQSDLLWEYRQIFERMPYTDNISILRE 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSTAEALKAIPAEKRIIRVDPTCPLSSNPGTQVYEDYNCTLNQTNIENNNNKFYIIQLLQ 96
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                                                                                                                  HGATHDLKVELIDILKVNRDNESSKFKRH--IGNRRLLWHGSGKMNFAGILGQGLRIAPP
                                                                                                                                                      -GSNHRCPT-LQHIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPH 411
                                                                                                                                                                                              {\tt NALLDIKFAYDQISGGDVPASTSLSIDPVDINYRKLKCIMEPLQQGCDDWNMIHQYLKNT}
                                                                                                                                                                                                                                                                                                                                                                                                                               NEQDIPEGHDRTAQDVFHEKTKNDWIYRKHFRKMPGMFSYVETDYSE-----FVGTNNGH
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28.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7%; Score 534; DB 2;
5%; Pred. No. 2.2e-29;
104; Mismatches 211
  ---HTEPD----PTQDTELELDGQQVVVPQGQPVPCPEFS
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Human brain PARP2 Human brain poly-A Human ORFX ORF2673

PARP-2 prote

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PARP; poly(ADP-ribose) polymerase; human; murine; detection; sepsis; diagnosis; therapy; necrosis; apoptosis; neurodegenerative illness; ischemic tissue damage; PARP1.
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AAU21687
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AAY68840
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AAB66301
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             AAY51174
AAB11480
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AAU21811
AAU21688
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WPI; 2000-087218/07.
N-PSDB; AAZ44290.
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RESULT
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Mouse PARP-2 prote
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474.226 Million cell updates/sec
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Murine PARP1 (shor
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                  polymerase (PARP) homologues, which are characterised by an amino acid sequence with a functional NAD^+-binding site and no zinc finger sequence motif, of general formula CX_2CX_2MKX_2C (I). The nucleic acid sequencemotif, of general formula CX_2CX_2MKX_2C (I). The nucleic acid detection of PARP homologues and antibodies are useful for analytic detection of PARP homologues and for identifying PARP effectors or binding partners, as well as for determining their effectiveness. PARP-binding partners are useful for the diagnosis or therapy of a disease condition, which is the result of a PARP protein, especially an energy deficiency, which may comprise tissue damage from cell death following necrosis or apoptosis. The disease condition may be chosen from a neurodegenerative illness, or sepsis or ischemic tissue damage, in particular neurotoxic disturbances, etc. This sequence represents the murine PARPI protein used in the method of the invention.
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                                                       invention describes novel human and murine poly(ADP-ribose)
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                                                                                                                                                                                                                                                                                                                     21; Length 533;
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                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                           Claim 4; Page 67-69; 96pp; German.
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Matches 533; Conserv
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polymerase (PARP) homologues, which are characterised by an amino acid sequence with a functional NAD^+-binding site and no zinc finger sequence motif, of general formula Cx_2Cx_ZHMX_C (1). The nucleic acid sequences, PARP homologues and antibodies are useful for analytic detection of PARP homologues and for identifying PARP effectors or binding partners, as well as for determining their effectiveness. PARP-binding partners are useful for the diagnosis or therapy of a disease condition, which is the result of a PARP protein, especially an energy deficiency, which may comprise tissue damage from cell death following necrosis or apoptosis. The disease condition may be chosen from a neurodegenerative illness, or sepsis or ischemic tissue damage, in particular neurotoxic disturbances, etc. This sequence represents the murine PARPI protein used in the method of the invention.
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PARP; poly(ADP-ribose) polymerase; human; murine; detection; sepsis; diagnosis; therapy; necrosis; apoptosis; neurodegenerative illness; ischemic tissue damage; PARP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 2776.5; DB 2:
Pred. No. 5.5e-240;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Otterbach B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 71-73; 96pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98.78;
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99DE-1008837.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kroeger
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MAPKRKASVQTEG - - SKKQRQGTEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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polymerase (PARP) homologues, which are characterised by an amino acid
sequence with a functional NAD++binding site and no zinc finger
sequence motif, of general formula CX_2CX_2MHX_2C (I). The nucleic acid
sequences, PARP homologues and antibodies are useful for analytic
detection of PARP homologues and for identifying PARP effectors or
binding partners, as well as for determining their effectiveness.
PARP-binding partners are useful for the diagnosis or therapy of a
disease condition, which hay comprise tissue damage from cell death
centry deficiency, which may comprise tissue damage from cell death
following necrosis or apoptosis. The disease condition may be chosen
from a neurodegenerative lilness, or sepsis or ischemic tissue damage,
in particular neurotoxic disturbances, etc. This sequence represents the
human PARP3 protein used in the method of the invention.
 VNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPHSGGRVGKGIYFASENS 420
               PARP; poly(ADP-ribose) polymerase; human; murine; detection; sepsis; diagnosis; therapy; necrosis; apoptosis; neurodegenerative illness; ischemic tissue damage; PARP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lemaire H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel genes and proteins, antibodies and binding partners useful in diagnosis and therapy of energy deficiency associated disease conditions -
                                                     KSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQTEPDPA
                                                                                                      Otterbach B, Lubisch W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 57-59; 96pp; German.
                                                                                                                                                                                                     AAY51175 standard; Protein; 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hoeger T, Kroeger B,
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99DE-1008837.
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                                                                                                                                                                                                                                                                                  Human brain PARP3 protein.
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01-MAR-1999;
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Gaps

Indels 12;

Length 533;

Query Match 79.7%; Score 2241; DB 21; Best Local Similarity 80.1%; Pred. No. 5.8e-192; Matches 432; Conservative 37; Mismatches 58;

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234
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                                   117
                                                                                   118 AKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKALSPQVDSGPVRT 177
                                                                                                                                                                                                                                                  414
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                                                                                                                                                                                                                                                                                                                                      415 FASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQ 474
475 TEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEIHL 533
                                                                                                                                                                                                                                                                                                                                                                                                    PARP; poly(ADP-ribose) polymerase; human; murine; detection; sepsis; diagnosis; therapy; necrosis; apoptosis; neurodegenerative illness; ischemic tissue damage; PARP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lemaire H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel genes and proteins, antibodies and binding partners useful in diagnosis and therapy of energy deficiency associated disease conditions -
                                    QVHEDYDCTLNQTNIGNNNNKFYIIQLLEEGSRFF-CWNRWGRVGEVGQSKMNHFTCLED
                                                                                                                                   V---VKPCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEA
                                                                                                                                                LRHVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPHSGGRVGKGIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY51176 standard; Protein; 540 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human uterus type 2 PARP3 protein.
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99DE-1008837.
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                                    polymerase (PARP) homologues, which are characterised by an amino acid sequence with a functional NAD<sup>+</sup>+binding site and no zinc finger sequence motif, of general formula CX_2CX_2MHX_2C (I). The nucleic acid sequences, PARP homologues and antibodies are useful for analytic detection of PARP homologues and for identifying PARP effectors or binding partners, as well as for determining their effectiveness. PARP-binding partners are useful, for the diagnosis or therapy of a disease condition, which is the result of a PARP protein, especially an energy deficiency, which may comprise tissue damage from cell death following necrosis or apoptosis. The disease condition may be chosen from a neurodegenerative illness, or sepsis or ischemic tissue damage, in particular neurotoxic disturbances, etc. This sequence represents the human PARP3 protein used in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; PARP; Poly (ADP-ribose) polymerase; antisense oligonucleotide;
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              540
                                                                                                                                                                                                                                                                  1 MAPKRKASVQTEG--SKKQRQGTEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGI 58
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                                                                                                                                                                                                                                                                             59 OVHEDYDCTLNOTNIGNNNNKFYIJOLLEEGSRFF-CWNRWGRVGEVGOSKMNHFTCLED
                                                                                                                                                                                                                                                                                                                       118 AKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKALSPQVDSGPVRT
                                                                                                                                                                                                                                                                                                                                                               178 V---VKPCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEA
                                                                                                                                                                                                                                                                                                                                                                                                       QTLQAAPGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQTGNSYRCPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEIHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention describes novel human and murine poly(ADP-ribose)
                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                        Length 540;
                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                       79.7%; Score 2241; DB 21;
80.1%; Pred. No. 6e-192;
iive 37; Mismatches 58;
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           German.
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         Page 62-64; 96pp;
                                                                                                                                                                                                                                   Best Local Similarity 80.1
Matches 432; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human PARP-3 protein.
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cytostatic; nootropic; neuroprotective; antiinflammatory; antidiabetic; immunosuppressant; hyperproliferative disorder; cancer; cellular injury; oxidative stress; neurological disorder; parkinsonism; apoptosis; meningitis-associated intracranial complication; ischaemia; inflammatory disorder; autoimmune disorder; arthritis; diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKALSPQVDSGPVRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense compound useful for treating hyperproliferative, neurological, inflammatory and autoimmune disorders and diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
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; Pred. No. 7e-191;
37; Mismatches 60; Indels
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Best Local Similarity 79.8'
Matches 430; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cowsert LM;
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N-PSDB; AAS45590.
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inhibits human PARP
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                                                                                                                                                                                                       Homo sapiens
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Sequence

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LRHVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPHSGGRVGKGIY 414
                                                                       FASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQ 474
                                                                                    qalqav-seqektveevphpldrdyqllkcqlqlldsgapeykviqtyleqtgsnhrcpt 354
                                                                                                                                TEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEIHL
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NAP; poly(ADP-ribose) polymerase; PARP; poly(ADP-ribose) transferase; programmed cell death; apoptosis; growth rate; stress; cold; pathogen; pest; drought; heat; fungi; nematode; seed-shatter.
                                       A poly(ADP-ribose) polymerase NAP protein of Zea mays.
                                                                                   Location/Qualifiers
1..159
       Ź
     AAY68834 standard; Protein; 653
                           16-MAY-2000 (first entry)
                                                                                    key
Misc-difference j.
                 AAY68834;
                                                                         Zea mays.
AAY 68834
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/note- "these residues are specifically claimed in claim 18" WO200004173-A1 27-JAN-2000

99WO-EP04940 12-JUL-1999;

98US-0118276 17-JUL-1998; (PLBZ) PLANT GENETIC SYSTEMS NV.

Block De Kushnir S, Babiychuk E,

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WPI; 2000-182436/16. N-PSDB; AAZ60616.

The present sequence represents the NAP protein of Zea mays. This protein is a poly(ADP-ribose) polymerase (PARP) protein (also known as potein is a poly(ADP-ribose) polymerase (PARP) protein (also known as potein the parameters confident to apoptosis, and is a nuclear enzyme is involved in programmed cell death or apoptosis, and is a nuclear enzyme. The NAP polynucleotide sequences can be used for modulation of programmed cell death in cukaryotic cells. The method is used, specifically in plants, to induce, or protect against, programmed cell death, depending on the extent to which PARP activity is reduced. Reducing expression of endogenous NAP class PARP only is also used to modulate programmed cell death, to increase growth rate and to produce plant cells that are more tolerant of stress (cold, chemical treatments, pathogens, pests, drought, heat, etc., or during transformation). Particular applications are generation of plants that are resistant to fungi or nematodes; are male or female sterile; or have better seed-shatter properties. The methods are also used to improve growth of transformed plant cells (and derived calli or complete plants). Modulating cell death, growth and stress resistance in eukaryotes, specifically plants, used, e.g. to impart fungus or nematode resistance Claim 18; Page 92-95; 126pp; English.

(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

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                                                                  gakevikggdeevevkkekmvtatkkgaavldqhipdhikvnyhv-----lqvgdely 190
                                                                                       DCTLNQTNIGNNNNKFYIIQLLEE - - GSRFFCWNRWGRVGEVGQSKMNHFTCLED - AKKD 121
                                                                                                                                    FKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQ-GEAESQEAVVKALSPQVDSGPVRTVVK 180
                                                                                                                                                                                                                                                                                                                     411
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                                                                                                                                                                                                                                                                                                                                                                                                                           GSKKQRQGTEEEDSFRS----TAEALRAAPADNRV---IRVDPSCPFSRNPGIQVHED-Y 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PARP; DNA-binding domain; poly(ADP-ribose) polymerase; gene therapy;
tumour treatment; DNA repair; over-expression.
                                                                                                                                                                                181 PCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEAMK
                                                                                                                                                   241 NPTGDGQSLEELSSCFYTVIPHNFG--RSRPPPINSPDVLQAKKDMLLVLADIELAQTLQ
                                                                                                                                                                                                                                                                         AAPGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQT --- GNSYRCPNL
                                                                                                                                                                                                                                                                                       RHVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGK
                                                                                                                                                                                                                                                                                                                                  GIYFASENSKSAGYVTTMHCGCHQV---GYMFLGEVALGKEHHITIDDPSLKSPPPGFDS
                                                                                                                                                                                                                                                                                                                                                                                469 VIARGOTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYL
                       58;
 Length 653;
                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Poly(ADP-ribose) polymerase contg. DNA-binding domain.
25.5%; Score 717; DB 21; 1 at 194.9%; Pred. No. 3.7e-55; Conservative 91; Mismatches 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR99642 standard; Protein; 1013 AA.
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 Query Match
Best Local Similarity
Matches 190; Conserv
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(first entry)

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Mouse PARP-2 protein.
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                                                                                                                                                                                                                                                                                                                                      The present sequence is that of a poly(ADP-ribose) polymerase (PARP) contg. a DNA-binding domain (DBD). It is encoded by AAT13732, from which a fragment comprising nucleotides 67-1220 (-29 to +1127) encoding the DBD can be inserted into vectors which are used for gene therapy. Over-expression of the DBD inhibits the DNA repair function of PARP, so the vectors are useful for gene therapy or tumours, esp. in combination with conventional chemo- and/or radiotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :: | |:| :| |: |: |: |: |: |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: 
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                                                                                                                                                                      Vectors contg. insert encoding DNA-binding domain of poly(ADP-ribose) polymerase - useful for gene therapy, esp.
                           H
                           Hausen
                                                                                                                                                                                                                                                                                     Disclosure; Fig 1; 22pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative 101;
                           Zur
                        Buerkle A, Kuepper J,
                                                                           WPI; 1996-300654/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1013 AA;
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                                                                                                         N-PSDB; AAT13732
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1003 kl 1004
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Best Local S
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AAU29022 standard; Protein; 522 AA.

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AAU29022 RESULT

AAU29022;

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The invention relates to antisense oligonucleotides targeted to human PARP nucleic acid and inhibiting expression of human PARP. PARP (Poly (APP-Tibose) polymerase plays an important role in chromatin decondensation, DNA replication, DNA repair, gene expression, malignant transformation, cellular differentiation and apoptosis. The antisense oligonucleotide inhibitors are useful for inhibiting the expression of PARP in human cells or tissues. They are also useful for treating a human with a disease associated with PARP especially hyperproliferative disorders (e.g. cancer), cellular injury resulting from oxidative stress, neurological (e.g parkinsonism, meningitis-associated intracranial complications and ischaemia), inflammatory and autolimune disorders (e.g arthritis) and diabetes. The present sequence is a PARP protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19;
                        cytostatic; nootropic; neuroprotective; antiinflammatory; antidiabetic; immunosuppressant; hyperproliferative disorder; cancer; cellular injury; oxidative stress; neurological disorder; parkinsonism; apoptosis; meningitis-associated intracranial complication; ischaemia; inflammatory disorder; autoimmune disorder; arthritis; diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PATONLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQOIARGFEALEALEEAMKNPTGD 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNIGNNNNKFYIIQLLEEGSR--FFCWNRWGRVGEVGQSKMNHFTC---LEDAKKDFKKK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKALSPQVDSGPVRTVVKPCSLD 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antisense compound useful for treating hyperproliferative, neurological, inflammatory and autoimmune disorders and diabetes inhibits human PARP -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.0%; Score 702.5; DB 22; 34.4%; Pred. No. 5.3e-54; Live 89; Mismatches 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 13; Page 109-111; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001; 2001WO-US06572.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAR-2000; 2000US-0517467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 34.4
Matches 186; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Popoff I, Cowsert LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-602570/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 522 AA;
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                                                                                                                                                                                                                                                                                              WO200164955-A1.
                                                                                                                                                                                                                                Mus musculus.
PARP;
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Mon Sep

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This is the human poly (ADP-ribose) polymerase protein (PARP) sequence.

PARP is a 116kD DNA-binding protein that binds tightly to single-strand double-strand breaks. The PARP protein and Escherichia coli UvrA and UVIB proteins (see AAY58041-Y58442) are used in a method for the detection and quantitation of DNA base damage. The method involves quantifying at least one modification of interest in a nucleic acid sequence through the used of capillary electrophoresis, laser induced fluorescente and a fluorescently labeled polypeptide (e.g. fluorescently labeled polypeptide (e.g. fluorescently labeled anti-PARP antibody) that is specific for the modification. The new method is useful for quantifying nucleic acid modifications, especially a mutation (including deletions, insertions and substitutions), mismatch, DNA adduct, or strand break (single or double). The method is useful for identifying and detecting exposure to carcthogens, and in early risk assessment for cancer, and is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ADP-ribose) polymerase; DNA excision repair; DNA damage; PARP;
Inogen; cancer therapy; base modification; human; cancer; UvrB, UvrB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quantifying nucleic acid modifications useful for identifying and detecting exposure to carcinogens, in early risk assessment for cancer, and in monitoring cancer therapy -
                                                                                                                                            413
                                                                                        473
                                                                                                                                                                                                                                                                                                     : | || | |:| || || || 459 kmapspahf1--tlngs--tvplgpasdtgilnpegytlnynefivyspnqvrmryllki 514
246 -GOSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAAPGEE 304
                                                                      EEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQTGNSYRCP-----NLRH 357
                    358 VWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKGI
                                                                                                                                                                                                             YFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARG
                                                                                                                                                                                                                                                401 yfadmssksanycfasrl--kntgllllsevalgqcnelleanpkaggllrgkhstkgmg
                                                                                                                                                                                                                                                                                 474 QTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSF--SQSEYLIYKESQCRLRYLLEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human poly (ADP-ribose) polymerase protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                           AAY58043 standard; peptide; 1014 AA
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(WEIN/) WEINFELD M.
(XING/) XING J Z.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          carcinogen; cancer
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                                                                                                                                   493 vaprgksga---alskkskgqvkeeginksekrmkltlkggaavdpdsglehsahvlekg 549
                                                                                                                                                              HEDYDCTLNQTNIGNNNNKFYIIQLLEEG--SRFFCWNRWGRVGEV-GQSKMNHFTCLED 117
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                                                                                                                                                                                        gkvfsatlglvdivkgtnsyyklqlleddkenrywifrswgrvgtvigsnklegmpsked
                                                                                                                                                                                                                                    --HVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVG
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                                                                                                                                                                                                                                                                          VVKPCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEE
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                                                                               38;
                                                   Length 1014;
                                                                               Indels
                                                   24.9%; Score 700; DB 21; larity 33.6%; Pred. No. 2.5e-53; Conservative 102; Mismatches 219;
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                                                                  Similarity
           1014 AA
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            Sequence
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                                                                                                                                                                                            The invention relates to antisense oligonucleotides targeted to human PARP nucleic acid and inhibiting expression of human PARP. PARP (POLY (ADP-ribose) polymerase plays an important role in chromatin decondensation, DNA replication, DNA repair, gene expression, malignant transformation, cellular differentiation and apoptosis. The antisense oligonucleotide inhibitors are useful for inhibiting the expression of PARP in human cells or tissues. They are also useful for treating a human with a disease associated with PARP especially hyperproliferative disorders (e.g. cancer), cellular injury resulting from oxidative stress, meurological (e.g parkinsonism, meningitis-associated intracranial complications and ischaemia), inflammatory and autoimmune disorders (e.g arthritis) and diabetes. The present sequence is a PARP protein, the cdNA encoding which was used to design the antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 AMKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTL
                                                                                                              nurrsense compound useful for treating hyperproliferative, neurological, inflammatory and autoimmune disorders and diabetes inhibits human PARP
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         24.9%; Score 700; DB 22; 33.6%; Pred. No. 2.5e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 33.6%; Pred. No. 2.5e
Matches 182; Conservative 102; Mismatches
                                                                                                                                                                         Example 13; Page 97-101; 168pp; English.
          02-MAR-2000; 2000US-0517467
                                   (ISIS-) ISIS PHARM INC
                                                           Cowsert LM;
                                                                                    WPI; 2001-602570/68.
                                                                                                                                                                                                                                                                                                                                                                                      1014 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequence for thuman tankyrase2 protein. This is found in two different versions, designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has polyADP-ribosylation activity and is involved in the modification of TRF1, which is a telomere-specific binding protein. The regulation ctelomere length, in which TRF1 has a role, is linked to ageing and cancer. The sequences are useful in the treatment of cancers and inflammatory disorders.
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aleqfmklyeektgnawhskn-ftkypkkfypleid-ygqdeeavkkl---tvnpgtksk
                                                                                                                                                                                                                                                                                                                Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasm; aging;
inflammatory disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAPKRKASVQTEGSKKQRQCTEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New tankyrase2 polypeptides, useful for treating conditions poly(adenosine diphosphate-ribose) polymerase activity e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goldman PS, McElligott DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; DB 22;
2.5e-53;
                                                                                                                                                                                                                                                                          Human tankyrase2 related protein sequence SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.9%; Score 700; 33.6%; Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammatory and autoimmune disorders
                                                                                                                             AAB66296 standard; Protein; 1014 AA.
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Best Local Similarity 33.6%; Pr
Matches 182; Conservative 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Demaggio AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JUN-2000; 2000WO-US17827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0141582
                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                         05-APR-2001
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1005 1 1005
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WO200112645-A1
                                                                  Sequence
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                                                                                                    Query Match
                                                                                                              Best Local
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel vector (A), suitable for gene therapy, which contains a DNA insert (I) that encodes a practically complete poly(adenosine diphosphate-ribose) polymerase (PARP) which has antitumor activity. PARP is a nuclear DNA repair enzyme (activated by strand breakage), that allows recovery of proliferating cells from the toxic effects of DNA damage (caused by alkylating or oxidizing agents or radiation), and protects cells against such damage or other causes of genomic instability. (A) are used for treatment of cancer and for cancer prevention in subjects at high risk (e.g. those with tumor-associated genetic defects). Tumor cells treated with (A) show an increased tendency to die when treated with radiation or chemotherapeutic
                                                                                                                                                                                                                                                                                                                                                                                                            Gene therapy; poly(adenosine diphosphate-ribose) polymerase; treatment; PARP; antitumor; nuclear DNA repair; proliferating cell; DNA damage; protection; genomic instability; cancer; prevention; human.
                                                                                                                                                                                                      --HVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVG 410
                                                                                                                                             KGIYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVI 470
                                                                                                                                                           297
                   471 ARGQTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLE
                                                   298 QAAPGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQT-GNSYRCPNLR
                                                                                                             AMKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        poly(adenosine
treating or preventing tumors
                                                                                                                                                                                                                                                                                                                                                                                       Human poly(ADP-ribose)polymerase protein.
                                                                                                                                                                                                                                                                                                                  AAY33699 standard; Protein; 1014 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New gene therapy vector expressing diphosphate-ribose)-polymerase for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 2; 12pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98DE-1008889
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N-PSDB; AAZ23799.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QAAPGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQ----TGNSYRCP 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          354 NLRHVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRV 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         891
                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                9
agent, and in cells that survive this treatment they inhibit genomic instability, so should reduce the likelihood of further development both malignant cells and resistance to chemotherapy. This sequence represents the human poly(ADP-ribose) polymerase described in the
                                                                                                                                                                                                                                                                                                                1 MAPKRKASVQTEGSKKQRQGTEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIOV
                                                                                                                                                                                                                                                                                                                                           AKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKALSPQVDSGPVRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  665 lpkp-----vqdlikmifdvesmkkamveyeidlqkmplgklskrqiqaaysilsevqq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 HEDYDCTLNQTNIGNNNNKFYIIQLLEEG--SRFFCWNRWGRVGEV-GQSKMNHFTCLED
                                                                                                                                                                                                                                                                                                                                                                                                                                           178 VVKPCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : ::|: |||| |:: :| ||||||||: | | ||: |||| | :| evidifkleregecqrykpfkqlhnrrllwhgsrttnfagilsqglriappeapvtgymf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 470 IARGOTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ischaemic disorder; cerebral ischaemia; cardiac ischaemia; myocardial infarction; stroke; inflammation; autoimmune disease; diabetes; multiple sclerosis; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; chromosome localisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 AMKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKGIYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSV
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                                                                                                                                                                                                                    DB 20;
                                                                                                                                                                                                               24.8%; Score 699; DB 33.8%; Pred. No. 3.1e ive 99; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human poly(ADP-ribose) synthetase sbhPARS2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB60693 standard; Protein; 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                            1014 AA;
                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                   183;
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computes, sbhPARS2. The invention also relates to fragments, variants and sequences with intention also relates to fragments, variants and sequences with at least 95% identity to the sbhPARS2 conclections or nucleotide sequence; expression systems and host cells computising an sbhPARS2 nuclectic acid sequence; the recombinant expression of sbhPARS2; and an antibody specific for sbhPARS2. sbhPARS2 proteins compounds which inhibit or stimulate its activity or expression level. It such a mammal. The sbhPARS2 protein is useful for identifying compounds which inhibit or stimulate its activity or expression level. Such agonists and antagonists of sbhPARS2 are useful for treating human cardiac ischaemia, myocardial infarction, stroke), inflammantion, autoimmune disease (e.g. diabetes, multiple sclerosis) and neurodegenerative diseases (e.g., Parkinson's disease and Alzheimer's disease). sbhPARS2 nucleic acids are useful as diseases and Alzheimer's detecting mutations in the associated gene; as hybridisation probes to isolate full-length sbhPARS2 cDNAS and sbhPARS2 protein is also useful as an immunogen to produce antibodies for therapeutic use. sbhPARS2 consening methods for detecting the effect of added compounds on the production of mRNA and protein in cells.
                                                                                                                                                                                                                                                                                                    New human polypeptide of the polyADPribose synthetase family for use in diagnostic assays and for screening modulators used for preventing and treating inflammation, autoimmune disease and Alzheimers disease
                                                                                                                                                                                               Zhu Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence represents a novel human poly(ADP-ribose)
                                                                                                                                                                                               Li X, McQueney MS,
                                                                                                                                                                                             Kabnick KS,
                                                                                                                                                  (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 21; 30pp; English.
                                                               10-AUG-2000; 2000WO-US21775.
                                                                                                       99US-0373441
                                                                                                                                                                                             Barone F, Field J,
                                                                                                                                                                                                                                       WPI; 2001-211196/21.
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                                                                                                       12-AUG-1999;
                  22-FEB-2001
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NQTNIGNNNNKFYIIQLLEEGSR--FFCWNRWGRVGEVGQSKMNHFTC---LEDAKKDFK 123 Gaps 57 13 GSKKQRQGTEEEDSFRSTAEALRA-APADNRVIRVDPSCPFSRNPG---IQVHEDYDCTL 68 Indels 64; Length 521; 24.8%; Score 698; DB 22; 33.9%; Pred. No. 1.3e-53; tive 92; Mismatches 205; Best Local Similarity 33.9% Matches 185; Conservative Query Match 69 28 õ 셤 8 ò

521 AA;

Sequence

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KKFWEKTKNKWEERDRFVAQPNKYTLIEV-----QGEAESQEAVVKALSPQVDSGPV 175 | :::: ||||:|:|| |::| ||:|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |: 224 edcir--agqhgralmeacnefytriphdfglrtpplirtqkelsekiqllealgdieia 281 295 QTLQAAPGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQT---GNSYR 351 ||| :|||| ||::| | || || :::: kkfldktknnwedrekfekvpgkydmlqmdyatntqdeeetkkeeslksplkpe-----RTVVKPCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEAL 236 EEAMKNPTGD-GOSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELA 124 116 176 170

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RVGKGIYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFD 467 452 stkglgkmapssahfv--tlngs--tvplgpasdtgilnpdgytlnyneyivynpnqvrm 507 CPNLRHVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGG 407 PARP; poly(ADP-ribose) polymerase; human; murine; detection; sepsis; diagnosis; therapy; necrosis; apoptosis; neurodegenerative illness; Lemaire H; Novel genes and proteins, antibodies and binding partners useful in diagnosis and therapy of energy deficiency associated disease SVIARGQTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSF--SQSEYLIYKESQCRL 3 Lubisch Otterbach B, Ą. AAY51174 standard; Protein; 570 Kroeger B, 99WO-EP03889. 98DE-1025213. 99DE-1008837 (first entry) Human brain PARP2 protein. ischemic tissue damage. Kock M, Hoeger T, WPI; 2000-087218/07 N-PSDB; AAZ44287 (BADI) BASF AG RYLLEI 531 508 ryllkv 513 Homo sapiens 31-MAR-2000 W09964572-A2 04-JUN-1999; 05-JUN-1998; 01-MAR-1999; conditions -16-DEC-1999 AAY51174; RESULT 14 468 352 408 526 AAY51174 g q q 음 ò à δŽ

This invention describes novel human and murine poly(ADP-ribose) polymerase (PARP) homologues, which are characterised by an amino acid sequence with a functional NAD⁺+-binding site and no zinc finger sequence motif, of general formula CX_2CX_2MXX_2C (I). The nucleic acid detection of PARP homologues and antibodies are useful for analytic detection of PARP homologues and antibodies are useful for analytic binding partners, as well as for determining their effectiveness. PARP-binding partners are useful for the diagnosis or therapy of a disease condition, which is the result of a PARP protein, especially an energy deficiency, which may comprise tissue damage from cell death following necrosis or apoptosis. The disease condition may be chosen from a neurodegenerative illness, or sepsis or ischemic tissue damage, in particular neurotoxic disturbances, etc. This sequence represents the human PARP2 protein used in the method of the invention.

Claim 4; Page 52-54; 96pp; German.

570 AA; Sequence

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                                                                                  NOTNIGNNNNKFYIIQLLEEGSR -- FFCWNRWGRVGEVGQSKMNHFTC -- - LEDAKKDFK 123
                                                                                                                                       KKFWEKTKNKWEERDRFVAQPNKYTLIEV-----QGEAESQEAVVKALSPQVDSGPV 175
                                                                                                                                                                                                                                           RTVVKPCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEAL 235
                                                                                                                                                                                                                                                                        219 ----sqldlrvqeliklicnvqameemmmemkyntkkaplgkltvaqikagyqslkki 272
                                                                                                                                                                                                                                                                                                                                                                                                                     407
                                                                                                                                                                                                                                                                                                                                                                                                                                                  442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236 EEAMKNPTGD-GOSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELA 294
                                                                                                                                                                                                                                                                                                                                                           295 QTLQAAPGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQT---GNSYR 351
                                                                                                                                                                                                                                                                                                                                                                               RVGKGIYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFD 467
                                      Gaps
                                                                13 GSKKQRQGTEEEDSFRSTAEALRA-APADNRVIRVDPSCPFSRNPG---IQVHEDYDCTL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; poly ADP-ribose polymerase; PARP; neuroprotective; nootropic;
                                                                                                                                                                                                 ||| :|||| ||:||:|| || || ::::
165 kkfldktknnwedrekfekvpgkydmlqmdyatntqdeeetkkeeslksplkpe-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  468 SVIARGQTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSF--SQSEYLIYKESQCRL
                                                                                                                                                                                                                                                                                                                                                                                                                                      385 tmtlldlfevekdgekeafr--edlhnrmllwhgsrmsnwvgilshglriappeapitgy
                                                                                                                                                                                                                                                                                                                                                                                                                  352 CPNLRHVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGG
                                      64;
       Length 570;
                                    Indels
Human brain poly-ADP-ribose-polymerase protein.
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                                   Conservative
                      Similarity
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                     Best Local Sim
Matches 185;
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controlled trauma or massive bleeding, especially apoplexy or spinal-cranial trauma or massive bleeding, especially apoplexy or spinal-cranial trauma; or Alzheimer's disease, Huntington's disease or parkinson's disease, Treating or preventing ischemic damage after candidated sachemic damage after renal ischemia or during and after (specifically renal damage after renal ischemia or during and after kidney transplantation or heart damage after cardiac ischemia), treating epilepsy, specifically generalized epileptic attacks (e.g. petit mal and conjex partial epileptic attacks (e.g. petit mal and conjex partial attacks), treating microinfarction (e.g. during and after heart valve replacement, aneurysm resectioning and heart transplantation), revascularization of critically constricted coronary arteries (e.g. after PCTA or by-pass operations) or peripheral arteries (e.g. leg arteries), treating acute myocardial ischemia and damage during or after its mechanical or drug'induced lysis and treating tumors and cliesase (e.g. rheumatoid arthritis), and diabetes mellitus. Although (I) inhibit pare (i.e. the known form designated parel), they especially constituellar (I) have very strong PARP), they especially pare particular (I) have very strong PARP2 inhibitory aclivity (e.g. with K_i values of 1-20 nM) and highs electivity for PARP2 relative to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes novel 4-substituted 2H-phthalazin-1-one derivatives (I) which are used for the treatment or prophylaxis of diseases associated with elevated poly (ADP-Those)-polymerase (PARP: EC 2.4.2.30) activity. The products of the invention have nootropic, neuroprotective, cerebroprotective, antiparkinsonian, nephrotropic, cardiant, vasotropic, antionament, oytostatic, antibacterial, immunosuppressive, antinflammatory, antirheumatic, antiarthritic, antidiabetic. (I) are especially used for treating or preventing neurodegenerative disease or neuronal damage (specifically associated
                                                                                                                                                                                                                                                                                                                                                          Drugs for inhibiting PARP or especially homologous enzymes comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 ggkankdrtedkgdesvkalllkgkap-----vdpectakvgkahvycegndvydvml 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 NQTNIGNNNNKFYIIQLLEEGSR--FFCWNRWGRVGEVGQSKMNHFTC---LEDAKKDFK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 RIVVKPCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEAL
                                                                                                                                                                                                                                                                                                                                                                                                   4-substituted phthalazinone derivatives, useful e.g. for treating neurodegenerative disease, ischemic damage, tumors or diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 GSKKQRQCTEEEDSFRSTAEALRA-APADNRVIRVDPSCPFSRNPG---IQVHEDYDCTL
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                                                                                                                                                          ij
                                                                                                                                                              Hoeger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example A; Page 12-13; 14pp; German.
                                                                                                                                                          Kock M,
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                                                                                                                                                              Sadowski
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1 MAPKRKASVQTEGSKKQRQG......EYLIYKESQCRLRYLLEIHL 533
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	NAD+ ADP-ribosyltr		NAD+ ADP-ribosyltr	probable poly (ADP	NAD+ ADP-ribosyltr	NAD+ ADP-ribosyltr	hypothetical prote	hypothetical prote	NAD+ ADP-ribosyltr	protein ZK1005.1 [hypothetical prote	hemicentin precurs	NAD+ ADP-ribosyltr	protein F19P19.26	carbamoy1-phosphat	subunit A of ATP-d	hypothetical prote				•								
SUMMARIES	T08713	T03656	A29725	JS0428	S31735	JH0581	T01311	S04200	S26057	S42208	T51353	C84719	A47474	T03657	T18600	T20414	PN0494	D88948	T20992	T43290	T03058	E86174	T33717	D86625	E96806	T12540	T17345	D97781	C83503
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% Query Match	70.2	25.5	25.1	25.0	24.4	24.4	24.3	24.3	24.3	22.9	22.1	22.1	22.0	20.8	16.9	14.1	6.9	6.4	4.5	4.5	4.3	•	•	4.1	•		•	3.8	
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W	106.5	106.5	106	105.5	105	105	104.5	104.5	104	104	103.5	102.5	102	101.5	101	101	
	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

RESULT 1 T08713 T08713 T08713 C) Species: Homo sapiens (man) C) Species: Homo sapiens (man) C) Species: Homo sapiens (man) C) Date: 11Jun.1999 #sequence_revision 11-Jun.1999 #text_change 03-Nov-2000 C) Accession: T08713 R) Ansorge, W. Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. R) Rinsorge, W. Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. R) Reference number: 216472 A) Recession: T08713 A) Reference number: 216472 A) Residues: 1-649 cANS A) Residues: 1-649 cANS A) Residues: 1-649 cANS A) Cross-references: EMBL.AL050034 A) Experimental source: fetal kidney; clone DKFZp566G0224 C) Genetics: A) Note: DKFZp56GG0224.1 C) Superfamily: NAD+ ADP-ribosyltransferase	Ouery Match 10.2%; Score 1975; DB 2; Length 459; Best Local Similarity 81.5%; Pred. No. 2.3e-135; Matches 379; Conservative 32; Mismatches 44; Indels 10; Gaps 73 IGNNNMFYIIQLEEGGREF-CWNRWGRVGEVGOSKMNHFTCLEDAKKDFKKFWEKT 131 111111111111111111111111111111111	IENNNNKFYIIOLLODSNRFFTCWNRMGRVGEVGOSKINHFTRLEDAKKDFEKKFREKTK NKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKALSPQVDSGFVRTV VKPCSLDPAT		LEELSSCFYTVIPHNEGRSRPPINSPDVLQAKKDMLLVLADIELAQTLQAAPGEEEEKV 308 	EEVPHPLDRDYQLLRCQLQLLDSGESEYRAIQTYLKQTGNSYRCPNLRHVWRVNREGEGD 368	RFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPHSGGRVGKGIYFASENSKSAGYVTT 428 	MHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQTEPDPAQDIELELD 488
RESULT 1 1708713 C) Species: C) Date: 11- C; Accession R; Ansorge, submitted t A; Reference A; Accession A; Accession A; Accession A; Accession A; CCUS - Tef A; Experimen C; Genetics: A; Note: DKF C; Superfami	Query Match Best Local Matches 37 73 IGN	132	61 189 116	249	309	369	429
SECREPADE	O M X	QQ .	0y 0b	Qy Db	Qy Db	Oy Dp	Qy

489 GQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEIHL 533

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A; Residues: 1-69, 70, 71-1014 <UCH>
A; Crossarian (R.M. 112; NID:9190166; PIDN:AAA60137.1; PID:9190167
B; Curosaki, T.; Ushiro, H.; Mitsuuchi, Y.; Suzuki, S.; Matsuda, M.; Matsuda, Y.; Katu J. Biol. Chem. 262, 15990-15997, 1987
A; Title: Primary structure of human poly (ADP-ribose) synthetase as deduced from CDNA A; Reference number: A28498; MUID:88058958
A; Reference number: A28498
A; Molecule type: mRNA
A; Residues: 1-16, E'. 18-211, K', 213-236, 'R', 238-366, 'H', 369-1014 <KUR>
A; Cross-references: GB:J03473
B; Cherney, B.W.; McBride, O.W.; Chen, D.; Alkhatib, H.; Bhatia, K.; Hensley, P.; Smul Proc. Natl. Acad. Sci. U.S.A. 84, 8370-8374, 1987
A; Title: CDNA sequence, protein structure, and chromosomal location of the human gene A; Reference number: A39976; MUID:88068596
                         C,Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: A29725; A28498; A39976; A26901; I38096; B33321; A33321; A35635; A61559; R;Uchida, K.; Morita, T.; Sato, T.; Ogura, T.; Yamashita, R.; Noguchi, S.; Suzuki, H. Biochem. Biophys. Res. Commun. 148, 617-622, 1997 A;Title: Nucleotide sequence of a full-length cDNA for human fibroblast poly(ADP-ribo A;Reference number: A29725; MUID:88076933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 441-610, N',612-880;921-1014 <SUZ>
A; Note: the sequence figure has an omission of forty residues
A; Note: the sequence figure has an omission of forty residues
B; Oguta, T.; Nyunoya, H.; Takahashi-Masutani, M.; Miwa, M.; Sugimura, T.; Esumi, H.
B; Ochem. B; Dphys. Res. Commun. 167, 701-710, 1990
A; Title: Characterization of a putative promoter region of the human poly(ADP-ribose)
A; Accession: 138096
A; MulD:90211250
A; Accession: Is8096
A; MulD:90211250
A; Accession: Is8096
A; Residues: Lranslation not shown
A; Residues: 1-40 <RES>
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A; Residues: 38-43:93-98;132-137;204-209;237-242;276-281;335-340;384-389;431-436;512-5
A; Cross-references: GB:M29544; GB:M22953
A; Cross-references: GB:M29544; GB:M2295
A; Note: the authors translated the codon GTG for residue 54 as Glu
A; Note: these fragments represent intron-exon boundaries
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A; Residues: 12-26, "7.26-66;116-166 <GRA>
A; Residues: 12-26, "7. Auer, B.; Kuehne, C.; Herzog, H.; Klocker, H.; Burtscher, H.J.; Hirs
Eur. J. Cell Biol. 44, 302-307, 1987
A; Title: Isolation of a cDNA clone for human NAD (+): protein ADP-ribosyltransferase.
A; Reference number: A61559; MUID:88082900
A; Accession: A61559
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A;Accession: A35635
A;Status: not compared with conceptual translation
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A;Status: nucleic acid sequence not shown; not compared with conceptual translation
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A;Reference number: A33321; MUID:90091744
A;Accession: B33321
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A; Residues: 16-66;96;121-159,'D',161-167 <AUZ>
A; Note: these fragments represent a zinc finger-containing DNA-binding region
R; Gradwohl, G.; Menlssier de Murcia, J.; Molinete, M.; Simonin, F.; Koken, M.;
Proc. Natl. Acad. Sci. U.S.A. 87, 2990-2994, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: A39976
A; Molecule type: mRNA
A; Residues: 1-49, 'D',51-612,'Q',614-907,'Y',909-939,'R',941-979,'I',981-1014
A; Cross-references: GB:J03030
A; Note: the authors translated the codon ATA for residue 980 as Asn
B; Suzuki, H.; Uchida, K.; Shima, H.; SaCo, T.; Okamoto, T.; Kimura, T.; Miwa,
Biochem. Biophys. Res. Commun. 146, 403-409, 1987
A; Title: Molecular cloning of cDNA for human poly(ADP-ribose) polymerase and A; Reference number: A26901; MUID:87298455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X16674; NID:9510112; PIDN:CAA34663.1; PID:91017423 R;Auer, B.; Nagl, U.; Herzog, H.; Schneider, R.; Schweiger, M. DNA 9, 575-580, 1989
       Homo sapiens (man)
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N/Alternate names: poly (ADP-ribose) polymerase; poly (ADP-ribose) synthetase; poly(ADP)
                                                                                                                                                                                                                                                                                                                                                           S.; Fuangthong, M.; O'Farrell, M.; Van Monta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17;
                                                                                                                                                                                                                                                                                                           Cyaccession: T0366
R;Babyichuk, E.; Cottrill, P.; Storozhenko, S.; Fuangthong, M.; O'Farrell, M.;
Submitted to the EMBL Data Library, November 1997
A;Description: Higher plants possess two poly(ADP-ribose) polymerases.
A;Beference number: 214991
A;Accession: T03656
A;Accession: T03656
A;Residues: 1-653 < ABB>
A;Residues: 1-653 < ABB>
A;Coss-references: EMBL:AJ222588; NID:e1264090; PIDN:CAA10888.1; PID:e1264091
C;Genetics:
A;Gene: PARP
C;Keywords: DNA binding; glycosyltransferase; NAD; pentosyltransferase
                                                                                                                                                                                                           probable NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - maize
C;Species: Zea mays (maize)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 29-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 NPTGDGQSLEELSSCFYTVIPHNFG--RSRPPPINSPDVLQAKKDMLLVLADIELAQTLQ 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 K--ADRRHLEQLTGEFYTVIPHDFGFRKWREFIIDTPQKLKAKLEMVEALGEIEIATKLL 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 GAKEVIKGGDEEVEVKKEKMVTATKKGAAVLDQHIPDHIKVNYHV-----LQVGDEIY 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DCTLNQTNIGNNNNKFYIIQLLEE--GSRFFCWNRWGRVGEVGQSKMNHFTCLED-AKKD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQ-GEAESQEAVVKALSPQVDSGPVRTVVK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58;
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91; Mismatches 205;
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submitted to JIPID, February 1990
A; Reference number: JS0428
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Best Local Similarity 34.28
Matches 187; Conservative
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C;Superfamily: NAD+ ADP-ribosyltransferase
C;Keywords: DNA binding; DNA repair; glycosyltransferase; NAD; nucleus; pentosyltransfer
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              A: Residues: 381-420; 682-710 <SCH>
R:Yokoyama, Y.; Kawamoto, T.; Mitsuuchi, Y.; Kurosaki, T.; Toda, K.; Ushiro, H.; Terashi Buru J. Biochen. 194, 521-526, 1990
A:Title: Human poly(ADP-ribose) polymerase gene. Cloning of the promoter region.
A:Reference number: $14010, MUID:91099327
A:Reterence number: preliminary
A:Reterence number: $4010
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-95 <YOK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - bovine
N;Alternate names: ADP-ribosyltransferase (polymerizing); poly(adenosine diphosphate C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001
C;Accession: JS0428; S00328; A30458
                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                     A)Cross-references: EMBL:X56140; NID:g35286; PIDN:CAA39606.1; PID:g825702 C;Comment: This protein can ADP-ribosylate itself as well as other proteins. C;Genetics: GB:ADPRT; PPOL A;Gene: GDB:ADPRT; PPOL A;Cenes: GDB:ADPRT; GDB:119508; OMIM:173870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  493 VAPRGKSGA---ALSKKSKGQVKEEGINKSEKRMKLTLKGGAAVDPDSGLEHSAHVLEKG 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QAAPGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQ----TGNSYRCP 353
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAPKRKASVQTEGSKKQRQGTEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HEDYDCTLNQTNIGNNNNKFYIIQLLEEG - - SRFFCWNRWGRVGEV - GOSKMNHFTCLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 AKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKALSPQVDSGPVRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 VVKPCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 AMKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKGIYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    470 IARGOTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLL
                                                                                                                                                                                                                                                                                                                                                                                  40;
                                                                                                                                                                                                                                                                                                                                               Length 1014;
                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                               Query Match 25.1%; Score 705; DB 1; L
Best Local Similarity 33.8%; Pred. No. 8.1e-43;
Matches 183; Conservative 101; Mismatches 218;
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KL 1005
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A. Molecule type: mRNA
A. Residues: 648-714;888-904 <TAN>
A. Rocession: A30458
A. Accession: A30458
A. Molecule type: mBL: X06986
A. Molecule type: protein
A. Residues: 658-685;689-696;893-901 <TA2>
C. Superfamily: NAP- AP-ribosyltransferase
C. Reywords: DNA binding: glycosyltransferase; NAD; nucleotide binding; nucleus; P-loo
F:21-71/Region: zinc finger
F:200-220/Region: belix-turn-helix motif
F:250-270/Region: helix-turn-helix motif
F:250-270/Region: nucleotide-binding motif A (P-loop)
F:494-501/Region: nucleotide-binding #status predicted
A;Accession: JSG428
A;Molecule type: mRNA
A;Residues: 1-1016 <SALyw
A;Residues: 1-1016 <SALyw
A;Experimental source: thymus
R;Taniguchi, T.; Yamauchi, K.; Yamamoto, T.; Toyoshima, K.; Harada, N.; Tanaka, H.; T
Bur. J Blochem: 171, 571-575, 1988
A;Tille: Depression in gene expression for poly(ADP-ribose) synthetase during the int
A;Reference number: S00328; MUID:88151954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 TCLEDAKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKALSPQVDS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAPKRKASVQTEGSKKQRQGTEEDSFRSTAE---ALRAAPADNRVIRVDPSCPFSRNPG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                662 GTKSKLPKP-----VQNLIKMIFDVESMKKAMVEYEIDLQKMPLGKLSKRQIQAAYSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   607 PSKEDAIEHFMKLYEEKTGNAWHSKN-FTKHPKKFYPLEID-YGQDEEAVKKL---TVNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 GPVRTVVKPCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          405 SGGRVGKGIYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.0%; Score 702; DB 1; Length 1016; 34.2%; Pred. No. 1.3e-42;
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C.P.

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J.M.; Jeltsch, J.M.; Niedergang,
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                                                                                                                                                                                     A; Wolecule type: mRNA
A; Residues: 1-998 cSAD.
A; Cross-references: EMBL:212139; NID:964967; PIDN:CAA78126.1; PID:91334661
A; Cross-references: EMBL:212139; NID:964967; PIDN:CAA78126.1; PID:91334661
B; Ozawa, Y.; Uchida, K.; Uchida, M.; Ami, Y.; Kushida, S.; Okada, N.; Miwa, M.
Biochem. Biophys. Res. Commun. 193, 119-125, 1993
A; Title: Isolation of cDNAs encoding the catalytic domain of poly(ADP-ribose)polymerase
A; Reference number: PN0494; MUID:93277538
A; Reference number: PN0495
A; Molecule type: mRNA
B; Residues: 742-745, 'E', 747-876 cOZA>
C; Comment: This zinc-finger protein plays a role in DNA repair, cell growth, and differe
C; Superfamily: NAD+ ADP-ribosyltransferase
C; Superfamily: NAD+ ADP-ribosyltransferase; hexosyltransferase; NAD; nucleus; pentosyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19;
    NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - African clawed frog (fragment) N.Alternate names: poly ADP-ribose polymerase (Species: Xenopus laevis (African clawed frog) (C.Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000 C.Accession: S31735; PNA955 R.Saulier-le Drean, B.M. submitted to the EMBL Data Library, May 1992 A.Reference number: S31735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - chicken
N;Alternate names: poly(ADP-ribose) synthase
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 *sequence_revision 10-Sep-1999 *text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 KSSGKVKEEKGSNKSEKKMKLTVKGGAAIDPDS---ELEDSCHVLETGG----KIFSATL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 PATONLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEEAMKNPTGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --VQELIKLIFDVESMKKAMVEFEIDLQKMPLGKLSKRQIQSAYSILSQVQQAVSESLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 GQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAAPGEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKGIYFAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         418 ENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQTEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  883 MVSKSANYCHAM - - PGSPIGLILLGEVALGNMHELKAASQITKL - PKGKHSVKGLGRTAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKALSPQVDSGPVRTVVKPCSLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.4%; Score 686.5; DB 2; 34.1%; Pred. No. 1.7e-41; ive 95; Mismatches 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 24.4%;
Best Local Similarity 34.1%;
Matches 182; Conservative
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A; Molecule type: mRNA
A; Residues: 1-1011 <ITT>
A; Cross-references: ENBL:X52690; NID:963742; PIDN:CAA36917.1; PID:963743
C; Comment: This protein is a chromatin-bound enzyme.
C; Comment: This enzyme catalyzes DNA-dependent post-translational modifications of va
C; Superfamily: NAD+ ADP-ribosyltransferase
C; Superfamily: NAD+ ADP-ribosyltransferase; NAD; nucleus; pentosyltransferase; zinc
                                                                     complete deduced amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - Arabidopsis thaliana NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - Arabidopsis thaliana (NAD-ribose) polymerase; protein T14P8.19 C; Species: Arabidospis thaliana (Mouse-ear cress) C; Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 21-Jul-2000 C; Accession: T01311; S65662 C; Accession: T01311; S65662 C; Accession: T01311; S65662 C; Cloud, J. R; Alicki, J.; Ellibit, G.; Cloud, J. A; A; Description: The sequence of A; Thaliana T14P8.

A; Description: The sequence of A: thaliana T14P8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P----IQDLIKMIFDVESMKKAMVEFEIDLOKMPLGKLSKRQIQSAYSILNEVQQAVS 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 NPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 YDCTLNQTNIGNNNKFYIIQLLEEG--SRFFCWNRWGRVGEV-GQSKMNHFTCLEDAKK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSVIARGQTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLR 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 RKASVQTEGSKKQRQG-TEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQVHED 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     610 HFLNLYEEKTGNSWHSKN-FTKYPKKFYPLEID-YGQDEEAVRKL---TVSAGTKSKLAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 PGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQ----TGNSYRCPNLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DFKKKFWEKTKNKWEERDREVAQPNKYTLIEVQGEAESQEAVVKALSPQVDSGPVRTVVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCSLDPATONLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEAMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               357 HVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEH-----HITIDDPSLKSPPPGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   943 HSVKGLGKTAPDPT--ATTTLDG--VEVPLGNGIS-TGINDTCLLYNEYIVYDVAQVNLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.4%; Score 686.5; DB 1; 33.8%; Pred. No. 1.8e-41; tive 97; Mismatches 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rittel, M.E.; Garnier, J.M.; Jeltsch, J.M.; N
Gene 102, 157-164, 1991
A;Title: Chicken poly(ADP-ribose) synthetase:
A;Reference number: JH0581; MUID:91340148
A;Accession: JH0581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 33.89
Matches 184; Conservative
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b

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Nath App-ribosyltransferase (EC 2.4.2.30) - rat (fragment)
C;Species: Rattus norvegious (Norway rat)
C;Species: L1-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 18-Jun-1999
C;Baccession: S26057; S78453; I53331
R;Thibodeau, J.; Gradwohl, G.; Dumas, C.; Clairoux-Moreau, S.; Brunet, G.; Penning, C Biochem Cell Biol. 67, 653-660, 1989
A;Title: Cloning of rodent cDNA encoding the poly(ADP-ribose) polymerase catalytic do A;Reference number: I52331; MUID:90027702
                                                                                                                                                                                                                                                                                                                                                   NAD; nucleus; pentosyltransferase; zinc
                                                mouse poly (ADP-ribose) polymerase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RCPNLRHVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     829 DL-EVIDIFKIEREGESORYKPFROLHNRRLLWHGSRTTNFAGILSQGLRIAPPEAPVTG 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            945 HSVKGLGKTTPDDPSASITLE---GVEVPLGTGI--PSGGVNDTALLYNEYIVYDIAQVNL 998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  493 VAPRGKSAAPSKKSK----GCFKEEGVNKSEKRMKLTLKGGAAVDPDSGLEHSAHVLEKG 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HEDYDCTLNQTNIGNNNNKFYIIQLLEEG--SRFFCWNRWGRVGEV-GQSKMNHFTCLED 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAPKRKASVQTEGSKKQRQGTEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-500 <THI>
A;Cross-references: EMBL:X65497; NID:g56849; PIDN:CAA46478.1; PID:g56850
Nucleic Acids Res. 17, 3387-3401, 1989
A:Title: Sequence and organization of the mouse poly (ADP-ribose) polymenty Reference number: S04200
A:Accession: S04200
A:Molecule type: DNA
A:Residues: 1-1013 <- HUP>
A:Residues: 1-1013 <- HUP>
C:Genetics: EMBL:X14206; NID:g49893; PIDN:CAA32421.1; PID:g49894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :| :: | :: | | |:| 774 YSLLRGGSDDSSK-----DPIDVNYEKLKTDIKVVDRDSEEAEVIRKYVKNTHATTHNAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKALSPQVDSGPVRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 VVKP---CSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRVGKGIYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  467 DSVIARGQTEPDPAQDIELELDGQPVVVPQGPPVQCPS-FKSSSFSQSEYLIYKESQCRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               235 LEEAMKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 24.3%; Score 683.5; DB 1; Best Local Similarity 32.4%; Pred. No. 2.9e-41; Matches 177; Conservative 105; Mismatches 215;
                                                                                                                                                                                                                                                                         A; Map position: 1
C; Superfamily: NAD+ ADP-ribosyltransferase
C; Keywords: DNA binding; glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|||::
KYLLKL 1004
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                                                                                                                                                                                                          thaliana cDNA homologue to animal poly(ADP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Map position: 4
;Introns: 28/3; 116/1; 162/3; 190/1; 268/3; 312/1; 330/3; 355/2; 371/1; 387/3; 408/3;
;Note: T14P8.19
;Keywords: DNA binding; glycosyltransferase; NAD; pentosyltransferase; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
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                                                                                                                                                                                                                                                                                                         A;Status: nucleic acid sequence not shown
A;Moleccule type: mRNA
A;Residues: 1-115,'GT',116-635 <LEP>
A;Cross-references: EMBL:Z40243; NID:9853721; PIDN:CAA88288.1; PID:9853722
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 VHED-YDCTLNQTNIGNNNNKFYIIQLLEEGSR--FFCWNRWGRVGEVGQSKMN-HFTCL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EDAKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKALSPQVDSGPV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 RTVVKP--CSLDPATQNLITNIFSKEMFKNAMTLANLDVKKMPLGKLTKQQIARGFEALE 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APVKSSNDEAE----DDNNGFEEEKKEEKIVTATKKGAAVLDQWI-----PDEIKSOYHVLO 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NSYRCPNLRHVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH--- 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 APKRKASVQTEGSKKQRQGTEEDSFRS--TAEALRAAPADNRVIRVDPSCPFSRNPGIQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --EVKPEQSKLDTRVAKFISLICNVSMMAQHMMEIGYNANKLPLGKISKSTISKGYEVLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELATKLISVDPGLQDD-----PLYYHYQQLNCGLTPVGNDSEEFSWVANYMENTHAKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATEMET STATEMENT STATEME
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                                                                                                                                               Ö.
                                                                                                                                               M.; Inze,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 635;
A; Molecule type: DNA
A; Residues: 1-635 < KAL.>
A; Residues: 1-635 < KAL.>
A; Cross-references: EMBL. AF069298; NID:g3193282; PID:g3193299
A; Cross-references: cultivar Columbia
B; Lepiniec, L.; Babiychuk, E.; Kushnir, S.; Van Montagu, M.; I FRBS Lett. 364, 103-108, 1995
A; Title: Characterization of an Arabidopsis thaliana cDNA homc A; Reference number: $65662; MUID:95269779
A; Accession: $65662
A; Status: nucleic acid sequence not shown
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EQIKMRYVIQV 629
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9

18;

Gaps

53;

Length 996; Indels --SRNPGIQVHEDYDCTL 68

652

Mon

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NAD+ ADP-ribosyltransferase (EC 2.4.2.30) [imported] - Arabidopsis thaliana N; Alternate names: poly(ADP-ribose) polymerase C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000 C; Accession: T51353 R; Doucet-chabeaud, G.; Kazmaier, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                       PATONLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEAAKNPTGD 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQTEPD 478
                                                                                                                                                                                        || | :| : : : | : : | : | EESKSSKSKSKSIYTKSVPKSMTLKIKDGLAVDPDSGLEDVAHVIVSRN-----KEKYNVVL 543
                                                                                                                                                                                                                                                                               FWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKALSPQVDSGPVRTVVKPCSLD 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAAPGEEE 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQT-GNSYRCPNLR--HVWKVN 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKGIYFASE 418
                                                                                                                                                                                                                                                     NQTNIGNNNNKFYIIQLLEEG--SRFFCWNRWGRVG-EVGQSKMNHFTCLEDAKKDFKKK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKQRQGTEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQVH----ED----YDC 66
                                                                                                                                                                                                                                                                                                                                                                      604 YLEKSGNHFENRENFVKVAGRMYPIDIDYAEDS-----KIDLSAEHDIKSKLPL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            886 VSKSANYCCTSH--HNSTGLMLLSEVALGDMMECTAAKYVTKLPNDK-HSCFGRGRTMPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEIH 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 645.5; DB 1,
pred. No. 1.6e.38;
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Pred. No. 8.8e-37;
7; Mismatches 209;
  F;508-996/Domain: NAD binding #status predicted <NAD>
                                                                                                                                                            22 EEEDSFRSTAEALRAAPADNRV----IRVDPSCPF----
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A, Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Description: ADP-ribose polymer synthesis
C; Superfamily: NAD+ ADP-ribosyltransferase
C; Keywords: DNA binding; glycosyltransferase; NAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:AJ131705; PIDN:CAA10482.1
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                                                                 Query Match 22.9%; Score 645.5; Best Local Similarity 32.8%; Pred. No. 1.6e Matches 175; Conservative 101; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ,87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kiDoucet-chabeaud, G.; Kazmaier, M. submitted to the EMBL Data Library, A;Reference number: 225379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 22.1%;
Best Local Similarity 32.7%;
Matches 179; Conservative 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-983 <DOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: parp-1
C; Function:
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                A;Reference number: S78453
A;Accession: S78453
A;Accession: S78453
A;Bolecule type: mRNA
A;Residues: 1-124,'H',126-127,'A',129-238,'D',240-500 <POT>
A;Cross-references: EMBL:X65497
C;Superfamily: NAD+ ADP-ribosyltransferase
C;Keywords: DNA binding; DNA repair; glycosyltransferase; NAD; nucleus; pentosyltransfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Naternate names: poly(ADP-ribose) polymerase
N;Alternate names: poly(ADP-ribose) polymerase
C;Species: Sarcophaga peregrina
C;Species: Sarcophaga peregrina
C;Species: Sarcophaga peregrina
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: $44208; $71456
E;Masutani, M.; Nozaki, T.; Hitomi, Y.; Ikejima, M.; Nagasaki, K.; de Prati, A.C.; Kurat
E;Masutani, M.; Nozaki, T.; Hitomi, Y.; Ikejima, M.; Nagasaki, K.; de Prati, A.C.; Kurat
A;Title: Cloning and functional expression of poly(ADP-ribose) polymerase cDNA from Sarc
A;Reference number: $42208; MUID:94170813
A;Accession: $42308
A;Molecule type: mRNA
A;Residues: 1-996 cAAAS
A;Cross-references: EMBL:D16482; NID:9473742; PIDN:BAA03943.1; PID:9538248
A;Accession: $71496
A;Molecule type: protein
A;Residues: 170-188;721-736;813-819;879-885 cAAX>
C;Superfamily: NAD-ADP-ribosyltransferase
C;Keywords: DNA binding; 91ycosyltransferase
C;Keywords: DNA binding #status predicted cANO>
F;370-507/Domain: auto-modification #status predicted cANO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nagasaki, K.; de Prati, A.C.; Kura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polymerase cDNA from Sare
                                                                                                                                                                                                                                                                          17;
                                                                                                                                                                                                                                                                                                                    64 YDCTLNQTNIGNNNNKFYIIQLLE--EGSRFFCWNRWGRVGEV-GQSKMNHFTCLEDAKK 120
                                                                                                                                                                                                                                                                                                                                                                                                             DFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVK-ALSPQVDSGPVRTVV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 KNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207 SQGSSESQIL-DLSNRFYTLIPHDFGMKKPPLLNNTDSVQAKVEMLDNLLDIEVAYSLLR 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 APGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQ----TGNSYRCPNL 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                472 RGQTEPDPAQDIELELDGQPVVVPQGPPVQCPS-FKSSSFSQSEYLIYKESQCRLRYLLE
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                                                                                                                                                                                                                                                                             41;
                                                                                                                                                                                                                              Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                           Query Match 24.3%; Score 682.5; DB 2; Best Local Similarity 36.0%; Pred. No. 1.3e-41; Matches 173; Conservative 86; Mismatches 181;
ibmitted to the EMBL Data Library, March 1992
Reference number: S78453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                531 I 531
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21;

Gaps

73;

Length Indels

pentosyltransferase

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C; Species: Drosophila melanogaster
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C; Accession: A47474
R; Uchida, K; Hanai, S.; Ishikawa, K.; Ozawa, Y.; Uchida, M.; Sugimura, T.; Miwa, M.
Proc. Natl. Acad. Sci. U.S.A. 90, 3481-3485, 1993
A; Title: Cloning of CDNA encoding Drosophila poly(ADP-ribose) polymerase: leucine zip
A; Reference number: A47474; MUID: 93234521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: A47474
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-994 <CUCH
A;Residues: 1-994 <CUCH
A;Cross-references: GB:D13806; GB:D13807; GB:D13808; NID:g303545; PIDN:BAA02964.1;
A;Note: sequence extracted from NCBI backbone (NCBIN:129703, NCBIP:129704)
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C;Superfamily: NAD+ ADP-ribosyltransferase
C;Keywords: DNA binding; glycosyltransferase; NAD; nucleus; pentosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAD+ ADP-ribosyltransferase (EC 2.4.2.30) – fruit fly (Drosophila melanogaster)
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                                                                                                                                                                                                                                                                                                                                                                                                                            296 TLQAAPGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQTGNSYRCP-- 353
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                                                                                                                                                                                                                                                                                                         EEAMKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQ
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                                                                                                                                                                               180 KPCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEAL----EAL
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996 KLQFLLKV 1003
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C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C; Accession: C84719
R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, R.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUID: 20083487
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KKKFWEKTKN----KWEERDRFVAQPNKYTLIEVQGEAESQEAVVKALSPQVDSGPVRTVV
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                                                                                                                      HSGGRVGKGIYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPP
                                                                                                                                                                                                                                                                                                                                  180 KPCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEAL----EAL
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Superfamily: NAD+ ADP-ribosyltransferase
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A;Molecule type: DNA
A;Residues: 1-1009 <STO>
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970 KLQFLLKV 977
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R; McMurray, A.
submitted to the EMBL Data Library, November 1996
A; Reference number: 218996
A; Recession: T18600
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DDA
A; Residues: 1-727 < WILL
A; Residues: 1-727 < WILL
A; Residues: EMBL: 283097; PIDN: CAB05448.1; GSPDB: GN00023; CESP: AC8.1
A; Experimental source: clone AC8
                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein AC8.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         375 V----KEVVMSIFDVENMKSALKSFEIDVNKMPLGRLSHNQINLAFEVLNDISDLLVKLP 430
                                           EGDRFQAH-SKLCNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKGIYFASENS 420
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--LDDKYMKLHCDITPLAHDSEDYKLIEQYLLNT----HAPTHKDWSLELEEVFSLDRDG 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     315 FHEKTKNDWIYRKHFRKMPGMFSYVETDYSEFVGTNNGHKKKITPGSKITPGSKTLLPKS 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQT-GNSYRCP-NLRHVWKV 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               362 NREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKGIYFAS 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------OGVGRQCPREIGSYKNPDGYTVPLGLTYMQLQGKQNVDYHL 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        860 KSAQY-----CYVDRNNPVGLMLLSEVALGDMYELK-KATSMDKPPRGKHSTKGLGKTVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 LDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEAMKNPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 GDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAAPGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KSAGYVTTMHC----GGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQTEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Introns: 31/3; 271/3; 312/3; 348/1; 466/3; 545/3; 617/3; 702/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDPAQDIELELDGQPVVVPQGPPVQCP----SFKSS-----SFSQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.9%; Score 475.5; DB 2; 30.2%; Pred. No. 2.2e-26; Live 68; Mismatches 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --SEYLIYKESQCRLRYLLEIHL 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LYNEFIVYDVDQIQLKYLVRVKM 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 30.29
Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Genetics:
A;Gene: CESP:AC8.1
A;Map position: 5
                                             366
    746
                                                                                      800
                                                                                                                                 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Zea mays (maize)
C;Decies: Zea mays (maize)
C;Dete: 24-Mar-1999 #text_change 20-Jun-2000
C;Accession: T0369;
C;Dete: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 20-Jun-2000
C;Dete: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 20-Jun-2000
C;Dete: 24-Mar-1999 #sequence_revision 70367
A;Description: Higher plants possess two poly(ADP-ribose) polymerases.
A;Recession: T03657
A;Recession: T03657
A;Recession: T03657
A;Recession: T03657
A;Recession: T03657
A;Readues: I-969 - RABA
A;Readues: I-969 - RABA
A;Readues: I-969 - RABA
Cross-references: EMBL:AJ222589; PIDN:CAA10889.1
C;Genetics:
A;Genetics:
C;Superfamily: NAD+ ADP-ribosyltransferase; NAD; pentosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEAMKNPTG 244
                                                               707
                                                                                                          304
                                                                                                                                                   761
                                                                                                                                                                                                 EEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQT-GNSYRCPNLR--HVWKV 361
                                                                                                                                                                                                                                            821
                                                                                                                                                                                                                                                                                     417
                                                                                                                                                                                                                                                                                                          477
                                                                                                                                                                                                                                                                                                                                                                                                882 MVSKSANYCCTSQ--QNSTGLMLLSEVALGDMMECT-SAKYINKLSNNKHSCFGRGRTMP 938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               468 ALESSKGSTVTVKVKGRSAVHESSGLQDTAHILEDGKSIYNATLNMSDLALGVNSYYVLQ 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85 LLE--EGSRFFCWNRWGRVG--EVGQSKMNHFTCLEDAKKDFKKKFWEKTKNKWEE---R 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DRFVAQPNKYTLIEVQGEAESQEAVVKALSPQVDSGPVRTVVKPCSLDPATQNLITNIFS 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNRFFTLIP----SIHPHIIRDEDDLMIKAKMLEALQDIEIASKIVGFDSDSDES---- 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQTGNSYRCP-----NLRHVWKVNREG 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 ALRAAPADNRVIRVDPSCPFSRNPGIQ----VHED----YDCTLNQTNIGNNNNKFYIIQ 84
                                                                                                        DGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAAPGEE
                                                                                                                                 648 EISVQNLIKLIFDIDSMNKTLMEFHIDMDKMPLGKLSAHQIQSAYRVVKEIYNVLECGSN
                                                                                                                                                                                                                            NREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRI-----MPHSGGRVGKGIYFAS
                                                                                                                                                                                                                                                                                                                                                                         ENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQTEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAAPGEEEEKVEEVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         478 DPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEI 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 20.8%; Score 584.5; DB 2; Best Local Similarity 30.7%; Pred. No. 4.1e-34; Matches 164; Conservative 98; Mismatches 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAD+ ADP-ribosyltransferase (EC 2.4.2.30) 2 - maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
                      185
                                                                                                          245
                                                                                                                                                                                                 305
                                                                                                                                                                                                                                                                                     362
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August 29, 2002, 07:59:37 ; Search time 69.02 Seconds (without alignments) 735.079 Million cell updates/sec Run on:

US-09-701-586B-10 2789 1 MAPKRKASVQTEGSKKQRQG......EYLIYKESQCRLRYLLEIHL 528 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	NAD+ ADP-ribosyltr	probable NAD+ ADP-	NAD+ ADP-ribosyltr	probable poly (ADP	NAD+ ADP-ribosyltr	NAD+ ADP-ribosyltr	hypothetical prote	hypothetical prote	NAD+ ADP-ribosyltr	protein ZK1005.1 [hypothetical prote	carbamoy1-phosphat	NAD+ ADP-ribosyltr	hypothetical prote		hypothetical prote	protein F19P19.26	Subunit A of ATP-d	hypothetical prote	exotoxin A precurs	probable GTP-bindi								
SUMMARIES	ID	T08713	T03656	A29725	JS0428	T01311	JH0581	S04200	S26057	S31735	S42208	T51353	C84719	A47474	T03657	T18600	T20414	PN0494	D88948	T17345	T33717	T03058	T20992	T43290	E96806	E86174	D86625	T12540	C83503	T38022
	DB	7	7	-	-	~	-	Н	7	7	٦	7	7	-	~	7	~	~	~	~	~	7	ď	~	~	~	7	~	7	~
	Query Match Length DB	459	653	1014	1016	635	1011	1013	200	866	966	983	1009	994	696	727	538	135	2004	1223	1092	181	5175	5198	935	954	1203	359	638	646
œ	Query	71.3	25.8	25.4	25.3	24.8	24.7	24.7	24.6	24.4	23.4	22.4	22.4	22.3	20.9	17.2	13.9	6.9	6.3	4.4	4.3	4.3	4.3	4.3	4.2	4.2	4.0	4.0	3.9	3.8
	Score	1987.5	719.5	707.5	704.5	691	689	688	989	681	652	624	624	621.5	584	481	389	193	172.5	121.5	121	120.5	120	120	118	117	112	111.5	107.5	106.5
	Result No.	1	7	Э	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

105.5 3.8 3075 2 \$14458 103.5 3.7 2285 2 \$14458 103.5 3.7 638 2 A30347 103 3.7 1031 1 A38713 103 3.7 1031 1 A38713 102.5 3.7 1435 2 \$69632 102.5 3.7 2484 2 \$726316 102.5 3.7 2607 2 \$726316 101.5 3.6 298 2 \$71424 101.5 3.6 434 2 H85175 101.5 3.6 434 2 H85175 101.5 3.6 436 2 \$69043 101.5 3.6 436 2 \$69043 101.5 3.6 108 2 \$71104
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A;Title: Nucleotide sequence of a full-length cDNA for human fibroblast poly(ADP-ribo A;Title: Nucleotide sequence of a full-length cDNA for human fibroblast poly(ADP-ribo A;Reference number: A29725; MUID:88076933
A;Reference number: A29725; MUID:88076933
A;Rocession: A29725
A;Molecule type: mRNA
A;Residues: 1-69, '0',71-1014 <UCH>
A;Cross-references: GB:MBHILZ: NID:9190166; PIDN:AAA60137.1; PID:9190167
A;Title: Primary structure of human poly (ADP-ribose) synthetase as deduced from cDNA
A;Reference number: A28498; MUID:88058958
A;Rocession: A28498
A;Residues: 1-16, 'E',18-211, 'K',213-236, 'R',238-366, 'H',369-1014 <KUR>
A;Residues: 1-16, 'E',18-211, 'K',213-236, 'R',238-366, 'H',369-1014 <KUR>
A;Residues: 1-16, 'E',18-211, 'K', 213-236, 'R', 238-366, 'H',369-1014 <KUR>
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A;Residues: 1-16, 'E',18-211, 'K', 213-236, 'R', 238-366, 'H',369-1014 <KUR>
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A;Residues: 1-490- MRNA
A;Residues: 1-49, 'D',51-612,'0',614-907, 'Y', 909-939, 'R', 941-979, 'I', 981-1014 <CHE>
A;Cross-references: GB:J0330
A;Title: Molecular cloning of CDNA for human poly(ADP-ribose) polymerase and expressi
A;Title: Molecular cloning of CDNA for human poly(ADP-ribose) polymerase and expressi
A;Molecular proper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 38-43:93-98:132-137;204-209;237-242;276-281;335-340;384-389;431-436;512-5
A; Cross-references: GB:M2954; GB:M22953
A; Cross-references: GB:M234ed the codon GTG for residue 54 as Glu
A; Note: the authors translated the codon GTG for residue 54 as Glu
A; Note: these fragments represent intron-exon boundaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Note: these fragments represent a zinc finger-containing DNA-binding region R; Gradwohl, G.; Menissier de Murcia, J.; Molinete, M.; Simonin, F.; Koken, M.; Hoeijm Proc. Natl. Acad. Sci. U.S.A. 87, 2990-2994, 1990
A; Title: The second zinc finger domain of poly(ADP-ribose) polymerase determines spec A; Reference number: A35635; MUID:90222155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 441-610, 'N', 612-880; 921-1014 <SUZ>
A; Residues: 441-610, 'N', 612-880; 921-1014 <SUZ>
A; Residues: 441-610, 'N', 612-880; 921-1014 <SUZ>
A; Rote: the sequence figure has an omission of forty residues
B; Ogura, T.; Nyunoya, H.; Takahashir Masurani, M.; Miwa, M.; Sugimura, T.; Esumi, H.
Biochem. Biophys. Res. Commun. 167, 701-710, 1990
A; Title: Characterization of a putative promoter region of the human poly(ADP-ribose)
A; Recession: I38096; MUID:90211250
A; Status: translation not shown
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A; Residues: 12-26, T7, 28-66;116-166 <GRA>
R; Schneider, R.; Auer, B.; Kuehne, C.; Herzog, H.; Klocker, H.; Burtscher, H.J.; Hirs Bur. J. Cell Biol. 44, 302-307, 1987

A; Title: Isolation of a cDNA clone for human NAD (+): protein ADP-ribosyltransferase. A; Reference number: A61559; MuID:88082900

A; Accession: A61559
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A;Status: nucleic acid sequence not shown; not compared with conceptual translation
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A; Residues: 1-40 - RES>

A; Cross-references: EMBL:X16674; NID:9510112; PIDN:CAA34663.1; PID:91017423

A; Cross-references: EMBL:X16674; NID:9510112; PIDN:CAA34663.1; PID:91017423

R; Auer, B.; Nagl, U.; Herzog, H.; Schneider, R.; Schweiger, M.

B; Auer, B.; Nagl, U.; Herzog, H.; Schneider, R.; Schweiger, M.

A; Title: Human nuclear NAD(+) ADP-ribosyltransferase(polymerizing): organization

A; Reference number: A33321; MUID:90091744
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R;Yokoyama, Y.; Kawamoto, T.; Mitsuuchi, Y.; Kurosaki, T.; Toda, K.; Ushiro, H.;
Eur. J. Biochem. 194, 521-526, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Accession: A35635
A, Status: not compared with conceptual translation
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A; Residues: 16-66;96;121-159,'D',161-167 <AU2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          S.; Fuangthong, M.; O'Farrell, M.; Van Monta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:AJ222588; NID:e1264090; PIDN:CAA10888.1; PID:e1264091
C;Genetics:
                                                                                                                                                                                                                                                                          probable NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - maize
C;Species: Zea mays (maize)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 PATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEAMKNPTGD 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : [|:|: |||||||:|| : | |::| |:|| :| |:|| | :|| | 364 RRHLEQLTGEFYTVIPHDFGFRKMREFIIDTPQKLKAKLEMVEALGEIEIATKLL---- 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQT---GNSYRCPNLRHVWK 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - EDDSSDQDDPLYARYKQLHCDFTPLEADSDEYSMIKSYLRNTHGKTHSGYTVDIVQIFK 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    412 SENSKSAGYVTTMHCGGHQV---GYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARG 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138 GAKEVIKGGDEEVEVKKEKMVTATKKGAAVLDQHIPDHIKVNYHV------LQVGDEIY 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DCTLNQTNIGNNNNKFYIIQLLEE--GSRFFCWNRWGRVGEVGQSKMNHFTCLED-AKKD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQ-GEAESQEAVVKVDSGPVRTVVKPCSLD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                251 FEGKFHNKTNNHWSDRKNFKCYAKKYTWLEMDYGETEKE----IEKGSITDQIKETKLE 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 GOSLEELSSCFYTVIPHNFG--RSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAAPGE 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKGIYFA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEIH 527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: PARP
C;Keywords: DNA binding; glycosyltransferase; NAD; pentosyltransferase
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R; Babyichuk, E.; Cottrill, P.; Storozhenko, S.; Fuangthong, M.; O'Farr submitted to the EMBL Data Library, November 1997
A; Description: Higher plants possess two poly(ADP-ribose) polymerases. A; Reference number: 214991
A; Accession: T03556
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-653 <BAB>
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420 VPQGQPVPCPEFSSSTFSQSFYLIYQESQCRLRYLLEVHL 459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.8%; Score 719.5; DB 2 35.3%; Pred. No. 5.5e-44;
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Best Local Similarity
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A; Reference number: S00328; MUID:88151954
A; Accession: S00328
A; Molecule type: mRNA
A; Residues: 648-714;838-904 <TAN>
A; Cross-references: EMBL:X06986
A; Accession: A30458
A; Molecule type: mRNA
A; Residues: 658-685;689-696;893-901 <TA2>
C; Superfamily: NAD+ ADP-ribosyltransferase
C; Keywords: DNA binding; glycosyltransferase; NAD; nucleotide binding; nucleus; P-loo F; 21-51/Region: zinc finger
F; 128-165/Region: zinc finger
F; 220-220/Region: helix-turn-helix motif
F; 250-270/Region: helix-turn-helix motif
F; 890-903/Region: nucleotide-binding motif A (P-loop)
F; 890-903/Region: nucleotide binding #status predicted
  Depression in gene expression for poly(ADP-ribose) synthetase during
nce number: S00328; MUID:88151954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAD+ App-ribosyltransferase (EC 2.4.2.30) - Arabidopsis thaliana N; Alternate names: poly(ADP-ribose) polymerase; protein T14P8.19 C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 21-Jul-2000 C; Accession: T01311; S65662 R; Kalicki, J.; Elliott, G.; Cloud, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        949 SVKGLGKTTPDPSASI--TVDG--VEVPLGTGIS-SGVNDTCLLYNEYIVYDIAOVHLKY 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   I - - QVHEDYDCTLNQTNIGNNNNKFYIIQLLEEG - - SRFFCWNRWGRVGEV - GQSKMNHF 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                291 TLQAAPGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQ----TGNSYR 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    403 RVGKGIYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFD 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              892 MFGKGIYFADMVSKSANYCHTSQ--GDPIGLILLGEAALGNMYELK-HARHISKLPKGKH 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           547 VLEKGGKVFSATLGLVDIVKCTNSYYKLQLLEDDKESRYWIFRSWGRVGTVIGSNKLEQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 TCLEDAKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVK--VDSGPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 RIVVKPCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231 EEAMKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :| :: | |:| :| |:| SLLRGGSDDSSK-----DPIDVNYEKLKTDIKVVDKDSEEAEIIRKYVKNTHATTHNAYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            347 CPNLRHVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAPKRKASVQTEGSKKQRQGTEEEDSFRSTAE---ALRAAPADNRVIRVDPSCPFSRNPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      833 L-EVVDIFKIEREGESQRYKPFKQLHNRRLLWHGSRTTNFAGILSQGLRIAPPEAPVTGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVIARGQTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.3%; Score 704.5; DB 1; 34.4%; Pred. No. 1.3e-42; ive 95; Mismatches 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 34.4% Matches 187; Conservative
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LLKL 1007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - bovine N:Alternate names: ADP-ribosyltransferase (polymerizing); poly(adenosine diphosphate rik C;Species: Bos primigenius taurus (cattle) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001 C;Accession: JS0428; S00328; A30458 R;Saito, I.
                                                                                                                                                                                                                                                                                                   pentosyltransfed
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A;Title: Human poly(ADP-ribose) polymerase gene. Cloning of the promoter region. A;Reference number: $14010; MUID:91099327 A;Accession: $14010
                                                                                                                                                                                                                                                                                                                                                                                                                17;
                                                           A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-95 < YOK>
A/Residues: 1-95 < YOK>
A/Residues: 1-95 < YOK>
A/Cross-references: EMBL:X56140; NID:935286; PIDN:CAA39606.1; PID:9825702
C/Comment: This protein can ADP-ribosylate itself as well as other proteins.
A/Gene: GDB.ADPRT; PPOL
A/Cross-references: GDB.119508; OMIM:173870
A/Map position: 1441-4442
C/Superfamily: NAD+ ADP-ribosyltransferase
C/Reywords: DNA binding; DNA repair; 91ycosyltransferase; NAD; nucleus; pent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 HEDYDCTLNQTNIGNNNNKFYIIQLLEEG -- SRFFCWNRWGRVGEV - GQSKMNHFTCLED 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVK--VDSGPVRTVVK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 PCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEAMK 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 NPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  352 HVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKG 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          296 PGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQ----TGNSYRCPNLR 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIAR 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MAPKRKASVQTEGSKKQRQGTEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GQTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEI
                                                                                                                                                                                                                                                                                                                                                                                                                39;
                                                                                                                                                                                                                                                                                                                                                                     Length 1014;
                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                Score 707.5; DB 1;
Pred. No. 7.6e-43;
1; Mismatches 216;
                                                                                                                                                                                                                                                                                                                                                                h 25.4%; Scc
Similarity 34.0%; Pre
83; Conservative 101;
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A; Residues: 1-1016 <SAI>
A; Experimental source: thymus
R; Taniguchi, T.; Yamauchi, K.; Yaman
Eur. J. Blochem. 171, 571-575, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to JIPID, February 1990
A; Reference number: JS0428
A; Accession: JS0428
                                                                                                                                                                                                                                                                                                                                                                                                             Matches 183;
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
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A; Accession: JH0581
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Cross-references: EMBL:X52690; NID:g63742; PIDN:CAA36917.1; PID:g63743
C; Comment: This protein is a chromatin-bound enzyme.
C; Comment: This protei
NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - chicken
N;Alternate names: poly(ADP-ribose) synthase
C;Species: dailus gallus (chicken)
C;Becies: 10. Sep-1999 #sequence_revision 10. Sep-1999 #text_change 10. Sep-1999
C;Accession: JH0581
R;Ittel, M.E.; darnier, J.M.; Jeltsch, J.M.; Niedergang, C.P.
R;Ittel, M.E.; darnier, J.M.; Jeltsch, J.M.; Niedergang, C.P.
A;Title: Chicken poly(ADP-ribose) synthetase: complete deduced amino acid sequence
A;Reference number: JH0581; MJID:91340148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    355 KVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKGIYF 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        299 EEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQ----TGNSYRCPNLRHVW 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 RKASVQTEGSKKQRQG-TEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQVHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 YDCTLNQTNIGNNNNKFYIIQLLEEG--SRFFCWNRWGRVGEV-GQSKMNHFTCLEDAKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 LDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEAMKNPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 GDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAAPGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                411 ASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEH-----HITIDDPSLKSPPPGFDSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               895 RDMVSKSANYCHTSQ--ADPIGLILLGEVALGNMYELKNASHIT-----KLPKGKHSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              465 IARGQTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 DFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVK--VDSGPVRTVVKPCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 24.7%; Score 689; DB 1; Length 1011; Best Local Similarity 33.9%; Pred. No. 1.7e-41; Matches 184; Conservative 97; Mismatches 205; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ::
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                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-635 < KALD.
A; Residues: 1-635 < KALD.
A; Cross-references: EMBL:AF069298; NID:g3193282; PID:g3193299
A; Experimental source: cultivar Columbia
R; Lepiniec, L.; Babiychuk, E.; Kushnir, S.; Van Montagu, M.; Inze, D.
A; Title: Characterization of an Arabidopsis thaliana cDNA homologue to animal poly(ADP-1A; Reference number: $65662; MUID:95269779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 4
A;Introns: 28/3; 116/1; 162/3; 190/1; 268/3; 312/1; 330/3; 355/2; 371/1; 387/3; 408/3;
A;Note: T14P8.19
C;Keywords: DNA binding; glycosyltransferase; NAD; pentosyltransferase; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-115,'GT',116-635 <LEP>
A;Cross-references: EMBL:248243; NID:9853721; PIDN:CAA88288.1; PID:9853722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPP--INSPDVLQAKKDMLLVLADIELA-Q 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VGKGIYFASENSKSAGYVTTMHC---GGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPG 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VHED-YDCTLNQTNIGNNNNKFYIIQLLEEGSR--FFCWNRWGRVGEVGQSKMN-HFTCL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDAKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKVDSGPVRTVVK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | | DRAIEIFTUKFUDKTKUYWSDRKEFIPHPKSYTWLEMDYGKEENDSPVNNDIPSSSSEVK 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176 P--CSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEA 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                461 FDSVIARGOTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRL 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 APVKSSNDEAE---DDNNGFEEEKKEEKIVTATKKGAAVLDQWI----PDEIKSQYHVLQ 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291 TLQAAPGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQT---GNSYRC 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153 VEIAQLFRASRAVEADRFQQFSSSKNRMLLWHGSRLTNWAGILSQGLRIAPPEAPVTGYM 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APKRKASVQTEGSKKQRQGTEEEDSFRS--TAEALRAAPADNRVIRVDPSCPFSRNPGIQ 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 24.8%; Score 691; DB 2; Length 635; Best Local Similarity 34.6%; Pred. No. 6.1e-42; Matches 189; Conservative 91; Mismatches 220; Indels
      submitted to the EMBL Data Library, May 1998
A;Description: The sequence of A. thaliana T14P8.
A;Reference number: 214290
                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S65662
A; Status: nucleic acid sequence not shown
                                                                                                                                           A;Status: translated from GB/EMBL/DDBJ
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RYVIQV 629
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                                                                                                           A; Accession: T01311
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Which apprints transferase (EC 2.4.2.30) - mouse C; Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C; Accession: S04200 E; Appropriate (R.): Siwarski, D.; Klinman, D.; Cherney, B.; Smulson, M. Nucleic Acids Res. 17, 3387-3401, 1989 A; Title: Sequence and organization of the mouse poly (ADP-ribose) polymerase gene.
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RESULT JH0581

17;

Length 500;

297

353

Length 998;

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NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - African clawed frog (fragment)

N.Alecrnate names: poly ADP-ribose polymerase
C.Species: Xenopus lacetis (African clawed frog)
C.Satuler: De Tradan, B.M.
S.Saulier: De Tradan, B.M.
S.Saulier: De Tradan, B.M.
S.Saulier: De Tradan, B.M.
A.Reference number: S31735
A.Reference number: S31735
A.Reference number: S31735
A.References: EMBL: Z12139; NID: 964967; PIDN: CAA78126.1; PID: 91334661
A.Residues: 1-998 <ANO-
A.Residues: Commun. 193, 119-125, 1993
A.Title: Isolation of cDNAs encoding the catalytic domain of poly(ADP-ribose)polymera
A.Reference number: PN049; MUID: 93277538
A.Residues: 742-745, 'E', 747-876 <OZA>
A.Residues: 742-745, 'E', 747-876 <OZA>
C.Comment: This zinc-finger protein plays a role in DNA repair, cell growth, and diff C.Superfamily: NAD+ ADP-ribosyltransferase; hexosyltransferase; NAD; nucleus; pento
                                                                A; Molecule type: mRNA
A; Residues: 1-124, /H', 126-127, /A', 129-238, 'D', 240-500 <POT>
A; Cross-references: EMBL: X65497
A; Cross-references: EMBL: X65497
C; Superfamily: NAD+ ADP-ribosyltransferase
C; Keywords: DNA binding; DNA repair; glycosyltransferase; NAD; nucleus; pentosyltrans
                                                                                                                                                                                                                                                                                                                            64 YDCTLNQTNIGNNNNKFYIIQLLE--EGSRFFCWNRWGRVGEV-GQSKMNHFTCLEDAKK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210 SSESQIL-DLSNRFYTLIPHDFGMKKPPLLNNTDSVQAKVEMLDNLLDIEVAYSLLRGGS 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             354 WKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKGIY 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        410 FASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQ 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 DFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKVDSGPVRTVVKP---C 177
                                                                                                                                                                                                                                                                                                                                                         470 TEPDPAQDIELELDGQPVVVPQGPPVQCPS-FKSSSFSQSEYLIYKESQCRLRYLLEI 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 HFMKLYEEKTGNAWHSKN-FTKYPKKFYPLEID-YGQDEEAVKKL-----AVKPGTKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 SLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEAMKNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQ----TGNSYRCPNLRHV
                                                                                                                                                                                                                                 24.6%; Score 686; DB 2; L4 36.2%; Pred. No. 9.9e-42; ive 86; Mismatches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 681; DB 2;
Pred. No. 6.1e-41;
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                                                                                                                                                                                                                                                         Best_Local Similarity 36.2
Matches 173; Conservative
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Best Local Similarity
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C; Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 18-Jun-1999
C; Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 18-Jun-1999
C; Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 18-Jun-1999
C; Accession: S2607; S78453; D2331
R; Thibodeau, J.; Gradwohl, G.; Dumas, C.; Clairoux-Moreau, S.; Brunet, G.; Penning, C.; Biochem. Cell Biol. 67, 653-660, 1989
A; Title: Cloning of rodent cDNA encoding the poly(ADP-ribose) polymerase catalytic domain A; Reference number: 152331; MUID:90027702
A; Molecule type: mRNA
                                                                                                                                                                               :Map position: 1
:Superfamily: NAD+ ADP-ribosyltransferase
:Keywords: DNA binding; glycosyltransferase; NAD; nucleus; pentosyltransferase; zinc
                                                                                                                                                                                                                                                                                                                                                    17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 HEDYDCTLNQTNIGNNNNKFYIIQLLEEG--SRFFCWNRWGRVGEV-GOSKMNHFTCLED 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 AKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKVDSGPVRTVVKP- 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQ----TGNSYRCPNL 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                351 RHVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGK 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GIYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIA 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RGQTEPDPAQDIELELDGQPVVVPQGPPVQCPS-FKSSSFSQSEYLIYKESQCRLRYLLE 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --CSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEAM 234
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                             1 MAPKRKASVQTEGSKKOROGTEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQV 60
A;Cross-references: EMBL:X65497; NID:956849; PIDN:CAA46478.1; PID:956850 R;Potvin, F. Submitted to the EMBL Data Library, March 1992 A;Reference number: S78453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQA
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                                                                                                                                                                                                                                                                                                Query Match 24.7%; Score 688; DB 1; Length 1013; Best Local Similarity 32.7%; Pred. No. 2e-41; Matches 177; Conservative 106; Mismatches 214; Indels 44
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NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - rat (fragment)
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A; Residues: 1-500 <THI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 KKQRQGTEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQVH----ED----YDC
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                                                                                                                                                                                                                                                         306 VPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQT-GNSYRCPNLR--HVWKVNREGEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                891 NYCCTSH--HNSTGLMLLSEVALGDMMECTAAKYVTKLPNDK-HSCFGRGRTMPNPSESI
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C;Superfamily: NAD+ ADP-ribosyltransferase
C;Keywords: DNA binding; glycosyltransferase; NAD; pentosyltransferase
                                                                                                                                                   604 YLEKSGNHFENRENFVKVAGRMYPIDIDYAEDS-----KIDLSAEHDIKSKLPL--SVQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKGIYFASENSKSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEIH 527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-983 <DOU>
A;Cross-references: EMBL:AJ131705; PIDN:CAA10482.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Experimental source: cultivar landsberg erecta C, Genetics:
A, Gene: parp-1
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A; Accession: T51353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
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N;Alternate names: poly(ADP-ribose) polymerase
C;Species: Sarcophaga peregrina
C;Species: Sarcophaga peregrina
C;Accession: S42208; S71496
R;Masutani, M.; Nozaki, T.; Hitomi, Y.; Ikejima, M.; Nagasaki, K.; de Prati, A.C.; Kurat
B:Masutani, M.; Nozaki, T.; Hitomi, Y.; Ikejima, M.; Nagasaki, K.; de Prati, A.C.; Kurat
A;Title: Cloning and functional expression of poly(ADP-ribose) polymerase cDNA from Sard
A;Reference number: S42208; WUID:94170813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Keywords: DNA binding; glycosyltransferase; NAD; pentosyltransferase; zinc finger 1.369/Domain: DNA binding #status predicted <DNA>
370-507/Domain: auto-modification #status predicted <AMO>
508-996/Domain: NAD binding #status predicted <NAD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
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A; Residues: 1-996 <MAS>
A; Cross -references: EMBL:D16482; NID:g473742; PIDN:BAA03943.1; PID:g538248
A; Accession: S71496
A; Molecule type: protein
A; Residues: 170-188;721-736;813-819;879-885 <MAX>
C; Superfamily: NAD+ ADP-ribosyltransferase
C; Superfamily: NAD+ binding; #status predicted <DNA>
F;1-359/Domain: DNA binding #status predicted <DNA>
A; Molecule type: DNA binding #status predicted <DNA>
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                                                                                                                                                                                                                                  185 NLITNIFSKEMFKNAMTLANLDVKKMPLGKLTKQQIARGFEALEALEEAMKNPTGDGQSL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245 EELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAAPGEEEEKVE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQTEPDPAQ 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 NQTNIGNNNNKFYIIQLLEEG--SRFFCWNRWGRVG-EVGQSKMNHFTCLEDAKKDFKKK 125
      Gaps
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                                                                                                         601 YODKTGNAWHS-PNFTKYPKKFYPLEIDYGQEEDVVKKLSVGAGTKSKLAKP-----VQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVPHPLDRDYQLLRCQLQLLDSGESEYKA1QTYLK - - - - QTGNSYRCPNLRHVWKVNREG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKGIYFASENSK
                                                                 QTEGSKKQRQGT-EEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQVHEDYDCTL
                                                                                                                                                                                                                                                                                                                           FWEKTKNKWEERDRFVAQPNKYTLIEVQ-GEAESQEAVVKVDSGPVRTVVKPCSLDPATQ
   42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        477 DIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEI 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.4%; Score 652; DB 1; Length 996; 33.3%; Pred. No. 7.6e-39;
   Indels
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   Mismatches 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ilarity 33.3%; Pred. No. 7.6e-39;
Conservative 100; Mismatches 205;
   95;
   Conservative
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Matches 176; Conserv
   Matches 178;
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C; Species: Drosophila melanogaster
C; Species: Drosophila melanogaster
C; Species: Drosophila melanogaster
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C; Accession: A4.4744
R; Uchida, K.; Hanai, S.; Ishikawa, K.; Ozawa, Y.; Uchida, M.; Sugimura, T.; Miwa, M.
Proc., Natl. Acad. Sci. U.S.A. 90, 3481-3485, 1993
A; Title: Cloning of CDNA encoding Drosophila poly(ADP-ribose) polymerase: leucine zip
A; Reference number: A4.474
A; Accession: A4.474
A; Accession: A4.474
A; Residues: 1-994 <UCH>
A; Rosidues: 1-994 <UCH>
A; Cross-references: GB:D13806; GB:D13807; GB:D13808; NID:g303545; PIDN:BAA02964.1; PI
A; Rosic : sequence extracted from NCBI backbone (NCBIN:129703, NCBIP:129704)
C; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: NAD+ ADP-ribosyltransferase
C; Keywords: DNA binding; glycosyltransferase
C; Keywords: DNA binding; glycosyltransferase
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                                                                                                                                 349 NLRHVWKVNREGEGDRFQAH-SKLGNRRLLWHGTNVAVVAAILTSGLRI----MPHSGGR
                                                                                                                                                          888 FGKGIYFADLVSKSAQYCYT--CKKNPVGLMLLSEVALGEIHELT-KAKYMDKPPRGKHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 KFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKVDSGPVRTVVKPCSLDPATQ
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                                                                      404 VGKGIYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDS
                                                                                                                                                                                                                                                                                                         464 VIARGQTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYL
                                             PGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAJQTYLKQTGNSYRCP----
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C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: O2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C.Accession: C84719
R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Macrman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A.Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A.Reference number: A84420; MUID:20083487
A.Accession: C84719
A.Accession: C84719
A.Accession: C84719
A.Accession: C84719
A.Accession: G8710
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                                                                                                                                                                                                                                                                                                                            404 VGKGIYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDS 463
                                                                                                                                                                                                                                                                                                                                                                                                                464 VIARGQTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYL 523
                                                                                                                                                                                                                                                                                                                                                                                                                                           TLNQTNIGNNNKFYIIQLLEE--GSRFFCWNRWGRVG--EVGQSKMNHFTCLEDAKKDF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 KKKFWEKTKN---KWEERDRFVAQPNKYTLIEVQGEAESQEAVVKVDSGPVRTVVKPCSL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 DPATONLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEAL----EALEEAMK 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 NPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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349 NLRHVWKVNREGEGDRFQAH-SKLGNRRLLWHGTNVAVVAAILTSGLRI----MPHSGGR
                                                                                                                                                                                                                                                                                                                                                       NPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAA
                                                                                                                                                      PGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKA IQTYLKQTGNSYRCP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                610 KRLFLEKTGNTWESWEQKTNFQKQPGKFLPLDIDYGVNKQVA----KKEPFQT---SSNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68;
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Pred. No. 8.1e-37;
7; Mismatches 209; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Map position: 2
Superfamily: NAD+ ADP-ribosyltransferase
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Best Local Similarity 33.09
Matches 179; Conservative
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917 EFVKWRDD----VVVPCGKPVP-SSIRSSELMYNEYIVYNTSQVKMQFLLKV 963
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                                                                                                                                                                                                                                                                                                                                        A; Gene: CESP: AC8.1
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                                                                                                                                                                                                                                                                                                                                               R. Bablychuk, E.; Cottrill, P.; Storozhenko, S.; Fuangthong, M.; O'Farrell, M.; Van Monta submitted to the EMBL Data Library, November 1997
A. Description: Higher plants possess two poly(ADP-ribose) polymerases.
A. Reference number: 214992
A. Accession: T03657
A. Molecule type: mRNA
A. Residues: preliminary; translated from GB/EMBL/DDBJ
A. Molecule type: mRNA
A. Residues: 1-969 < ABB>
A. Cross-references: EMBL.AJ22589; PIDN:CAA10889.1
C. Genetics:
A. Genetics:
A. Genetics:
A. Genetics:
A. Genetics:
A. Genetics:
C. Superfamily: NAD+ ADP-ribosyltransferase
C. Superfamily: NAD+ ADP-ribosyltransferase
C. Keywords: DNA binding: glycosyltransferase; NAD; pentosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
                                                                                                                                                                                                                                                                                                   Species: 2ea mays (maize)
Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 20-Jun-2000
                                                                                                              ANYCCTSQ--QNSTGLMLLSEVALGDMMECT-SAKYINKLSNNKHSCFGRGRTMPDPTKS 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 363
                417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAAPGEEEEKVEEVPHPL 310
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                                                                                    AGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQTEPDPAQD 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLE--EGSRFFCWNRWGRVG--EVGQSKMNHFTCLEDAKKDFKKKFWEKTKNKWEE---R 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 DRFVAQPNKYTLIEVQGEAESQEAVVKVDSGPVRTVVK--PCSLDPATQNLITNIFSKEM 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDKYMKLHCDITPLAHDSEDYKLIEQYLLNT----HAPTHKDWSLELEEVFSLDRDGELN 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RFQAH-SKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKGIYFASENSKSA 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      419 GYVTTMHC---GGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQTEPDPA 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 ALRAAPADNRVIRVDPSCPFSRNPGIQ----VHED----YDCTLNQTNIGNNNKFYIIQ 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -- MPHSGGRVGKGIYFASENSKS
                                 DRDYQLLRCQLQLLDSGESEYKAIQTYLKQTGNSYRCP-----NLRHVWKVNREGEGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.9%; Score 584; DB 2; Length 969; ilarity 30.9%; Pred. No. 5.9e-34; Conservative 94; Mismatches 201; Indels
                                                                                                                                                                              478 IELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEI 526
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                GDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRI-
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Best Local Similarity
Matches 164; Conserv
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hypothetical protein ACB.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Accession: T18600
R:McMurray, A.
submitted to the EMBL Data Library, November 1996
A:Reference number: 218996
A:Reference number: 218996
                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-727 VMLD-
A;Cross-references: EMBL:883097; PIDN:CAB05448.1; GSPDB:GN00023; CESP:AC8.1
A;Experimental source: clone AC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            315 FHEKTKNDWIYRKHFRKMPGMFSYVET----DYSEFVGTNNGHKKKITPGSKITPGSKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | ::|| |:::| | 370 ILPKSVKEVVMSIFDVENMKSALKSFEIDVNKMPLGRISHNQINLAFEVLNDISDLLVKL 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 EEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQT-GNSYRCP-NLRHVWK 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         356 VNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKGIYFA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               412 SENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITID-DPSLKSPPPGFDSVIARGQT 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            430 PIDASKILDFSNKFYTIIPHNFGMRVPEPIDSFHKIKEKNNMLNALLDIKFAYD-QISGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186 L------İTNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEAMKNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 TGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : |:|:|:|:| : | :| 489 DVPASTSLSIDPVDINYRKLKCIMEPLQQGCDDWNMIHQYLKNTHGATHDLKVELIDILK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            471 EPDPAQDIELELDGQPVVVPQGPPVQCP----SFKSS-----SFSQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: 5
A;Introns: 31/3; 271/3; 312/3; 348/1; 466/3; 545/3; 617/3; 702/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68; Mismatches 165; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 481; DB 2;
Pred. No. 1.1e-26;
                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
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30.0%;
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Best Local Similarity 30.0%
Matches 133; Conservative
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13;

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GenCore version 4.5
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OM protein - protein search, using sw model

August 29, 2002, 08:02:24; Search time 36.19 Seconds Run on:

(without alignments) 564.905 Million cell updates/sec

US-09-701-586B-10 2789 Title:

1 MAPKRKASVQTEGSKKQRQG......EYLIYKESQCRLRYLLEIHL 528 Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 Total number of hits satisfying chosen parameters:

105224 seqs, 38719550 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	O9v6f1 homo sapien	-	088554 mus musculu	P09874 homo sapien	P18493 bos taurus	Q9ugn5 homo sapien	P27008 rattus norv	Q11207 arabidopsis	-		P31669 xenopus lae				Q9ukk3 homo sapien	•	Q9d952 mus musculu		O13869 schizosacch	P25391 homo sapien	_	P35978 strongyloce			P42731 arabidopsis	Q10332 schizosacch	095235 homo sapien	P38904 saccharomyc	P49454 homo sapien	P53804 homo sapten		Q60974 mus musculu	Q9y913 aeropyrum p
SUMMARIES	ID	PPO3_HUMAN	PPOL_CRIGR	PPO2_MOUSE	PPOL_HUMAN	PPOL_BOVIN	PPO2_HUMAN	PPOL_RAT	PPOL_ARATH	PPOL_CHICK	PPOL_MOUSE	PPOL_XENLA	PPOL_SARPE	PPOL_DROME	YON4_CAEEL	PPOV_HUMAN	PPOL_ONCMA	EVPL_MOUSE	TOXA_PSEAE	YE14_SCHPO	LMA1_HUMAN	YO11_MOUSE	KINH_STRPU	EXO2_BPT5	RPOC_AQUAE	PAB2_ARATH	YBMA_SCHPO	RB6K_HUMAN	SP41_YEAST	CENF_HUMAN	TTC3_HUMAN	T2F1_FLAOK	NCR1_MOUSE	SYFB_AERPE
	Query Match Length DB	533 1	1012 1	559 1	1013 1	1015 1	583 1	1013 1	637 1	1011 1	1012 1	998 1	966	994 1	538 1	1724 1	135 1	2035 1	638 1	646 1	3075 1	379 1	1031 1	612 1	1574 1	629 1	830 1	890 1	1395 1	3210 1	2025 1	583 1	2453 1	548 1
σP	Query Match L	80.4	25.7	25.5	25.4	25.3	25.1	25.0	25.0	24.9	24.7	24.4	23.4	22.3	13.9	6.6	6.9		٠		•	•	٠	3.7	3.6	٠						3.5	•	3.5
	Score	2241.5	718	712.5	707.5	704.5	669	698	697.5	694	688	681	652	621.5	389	276.5	193	113.5	107.5	106.5	105.5	103	103	102.5	101	100.5	100.5	100.5	100.5	100.5	100	66	98	97.5
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Q91w85 arabidopsis P03003 escherichia	P98170 homo sapten P09010 xenopus lae	P31776 h penicilli O9pk79 chlamydia m	004747 bacillus su P09799 gossypium h	P33176 homo sapien Q02455 saccharomyc	Q9qyb8 mus musculu
MFP1_ARATH NUSA_ECOLI	BIR4_HUMAN LAM1_XENLA PMI, MOUSE	PBPA_HAEIN RPOC_CHLMU	SRF2_BACSU VCLA_GOSHI	KINH_HUMAN MLP1_YEAST	ADDB_MOUSE
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727 495	497 583 808	853 1396	3587 605	963 1875	725
3.5 5.5	ພ ພ ພ ໜ້ານັກ	, w w	3.5	ω ω 4. 4.	3.4
97 96.5	96.5 96.5 8.5	96.5	96.5 96	96 96	95.5
34 35	36 37	966	41	43 44	45

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEAR LOCALIZATION SIGNAL (POTENTIAL). 
K -> N (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Kidney;
Ansorge W., Wirkner U., Mewes H.-W., Gassenhuber J., Wiemann S.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: NAD(+) + {ADP-D-ribosyl}(N)-acceptor =
nicotinamide + {AADP-D-ribosyl}(N+1)-acceptor =
-!- SUBCELLUIAR LOCATION: Nuclear (Potential)
-!- TISSUE SPECIFICITY: Widely expressed; the highest levels are in
the kidney, skeletal muscle, liver, heart and spleen; also
detected in pancreas, lung, placenta, brain, leukocytes, colon,
small intestine, ovary, testis, prostate and thymus.
-!- SIMILARITY: BELONGS TO THE PARP FAMILY.
                                   PPO3_HUMAN STANDARD; PRT; 533 AA.
09Y6F1; 09UG81;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Poly [ADP-ribose] polymerase-3 (EC 2.4.2.30) (PARP-3) (NAD(+) ADP-ribosyltransferase-3) (Poly[ADP-ribose] synthetase-3) (PADPRT-3)
                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                 "A human poly(ADP-ribose) polymerase gene family (ADPRIL): cDNA cloning of two novel poly(ADP-ribose) polymerase homologues."; Genomics 57:442-445(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001290; PARP.
InterPro; IPR004102; PARP_reg.
InterPro; IPR004102; PARP_reg.
Pfam; PF000644; PARP; 1.
Pfam; PF0287; PARP_reg; 1.
Transferase; Glycosyltransferase; NAD; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                            MEDLINE-99263509; PubMed-10329013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF083068; AAD29855.1; -. EMBL; AL050034; CAB43246.1; -.
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                                                                                                                                                                               (hparp-3).
ADPRTL3 OR PARP3 OR ADPRT3.
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                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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RESULT 1
PPO3_HUMAN
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2 APKRKASVQTEGSKKQRQGTEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQVH 61
 EVENTS INVOLVED IN THE RECOVERY OF CELL FROM DNA DAMAGE (BY
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"Suppression of the radiation-sensitive phenotype of hamster irsl and irsl stains selected for resistance to 3-aminobenzamide.";

Int. J. Radiat. Biol. 77:609-616(2001).

-!- FUNCTION: POLY[ADP-RIBOSE] POLYMERASE MODIFIES VARIOUS NUCLEAR PROTEINS BY POLY(ADP-RIBOSE) POLYMERASE MODIFIES UNFORTION ON DAR AND IS INVOLVED IN THE REGULATION OF VARIOUS IMPORTANT CLELULAR PROCESSES SUCH AS DIFFERENTIATION, PROLIFERATION, AND
                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2002 (Rel. 41, Last annotation update)
16-DAP-ribose] polymerase-1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+)
ADP-ribosyltransferase-1) (Poly{ADP-ribose] synthetase-1).
                                                                                                                                      240
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                                                                                                                           QVHEDYDCTLNQTNIGNNNNKFYIIQLLEEGSRFF-CWNRWGRVGEVGQSKMNHFTCLED 117
                                                                                                                                                                  AKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKVDSGPVRTV---V 174
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                                                                                                                                                                                                                                             294
                                                                                                                                                                                                                                                                                                                                                                SKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQTEPDP 474
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                                                                   Gaps
                                                                                     MAPKRKASVQTEG--SKKQRQGTEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGI 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TUMOR TRANSFORMATION AND ALSO IN THE REGULATION OF THE MOLECULAR
                                                                                               KNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQA
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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                                                533;
                                                Length
                                                                  Indels
A -> G (IN REF. 2).
K -> E (IN REF. 2).
7C0AB89E64D1B9FD CRC64;
                                                DB 1;
                                                                  60;
                                               Query Match 80.4%; Score 2241.5; DB Best Local Similarity 80.5%; Pred. No. 4.4e-157 Matches 430; Conservative 37; Mismatches 60
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                   Ψ¥,
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171
411
533 AA;
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CONFLICT
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CATALYTIC ACTIVITY: NAD(+) + {ADP-D-ribosyl}(N)-acceptor = nicotinamide + {ADP-D-ribosyl}(N+1)-acceptor. COFACTOR: ZINC, CONTAINS TWO MOLES OF ZINC PER MOLE OF PROTEIN (BY
                                                                                                                      SUBGULT: HOMODIMER (Potential).
SUBCELULLAR LOCATION: Nuclear.
MISCELLANGOUS: THE ADP-D-RIBOSYL GROUP OF NAD(+) IS TRANSFERRED TO
AN ACCEPTOR CARBOXYL GROUP ON A HISTONE OR THE ENZYME ITSELE, AND
FURTHER ADP-RIBOSYL GROUPS ARE TRANSFERRED TO THE 2'-POSITION OF
THE TREMINAL ADBENOSINE MOLETY, BUILDING UP A POLYMER WITH AN
AVERAGE CHAIN LENGTH OF 20-30 UNITS.
SIMILARITY: BELONGS TO THE PARP FAMILY.
SIMILARITY: CONTAINS 1 BRCT DOMAIN.
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NUCLEAR LOCALIZATION SIGNAL 1ST PART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Interpro; IPR001357; BRCT. | Interpro; IPR001357; BRCT. | Interpro; IPR004102; PARP_reg. | Interpro; IPR004102; PARP_reg. | Refam; PP00533; BRCT; 1. | Pfam; PP006633; BRCT; 1. | Pfam; PP00663; Zf-PARP; 2. | Prodom; PD004675; Zf-PARP; 2. | Prodom; PD004675; Zf-PARP; 2. | SMART; SM00292; BRCT; 1. | RROSITE; PS00172; BRCT; 1. | RP0SITE; PS00347; PARP_ZN_FINGER_1; 2. | PROSITE; PS00647; PARP_ZN_FINGER_2; 2. | PROSITE; PS00647; PARP_ZN_FINGER_2; 2. | Iransferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protections of the product of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44;
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NUCLEAR LOCALIZATION SIGNAL 2ND
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INIT_MET 0 0 BY SIMILARITY.
DNA_BIND 1 371 BY SIMILARITY.
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TISSUE-Embryo;
MEDLINE-99292755; PubMed-10364231;
Ame J.-C., Rolli V., Schreiber V., Niedergang C., Apiou F., Decker P.,
Ame J.-C., Rolli V., Schreiber V., Murcia J., de Murcia G.M.;
Muller S., Hoger T., Menissier-de Murcia J., de Murcia G.M.;
"PARP-2, A novel mammalian DNA damage-dependent poly(ADP-ribose)
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                                                                                       KKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKVDSGPVRTVVKP--
                                                                                                                                                                NPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAA
                                                                                                                                                                                                                            PPO2_MOUSE STANDARD, PRT, 559 AA. 08854; 099N29; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Poly [ADP-ribose] polymerase-2 (EC 2.4.2.30) (PARP-2) (NAD(+) ADP-ribosyltransferase-2) (Poly[ADP-ribose] synthetase-2) (PADPRT-2)
193 APKGKSAAPSKKSK----GLYKEEGVNKSEKRMKLTLKGGAAVDPDSGLEHSAHVLEKGG
                             EDYDCTLNQTNIGNNNNKFYIIQLLEEG -- SRFFCWNRWGRVGEV - GQSKMNHFTCLEDA
                                                                                                          -CSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEAMK
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                                              PGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQ----TGNSYRCPNLR
                                                                                                                                                                                                                                                                                                                                HVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKG
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ame J.-C., Schreiber V., Fraulob V., Dolle P., de Murcia G.M., Niedergang C.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berghammer H., Ebner M., Marksteiner R., Auer B.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Chem. 274:17860-17868(1999).
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MEDLINE-99268466; PubMed-10338144;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADPRTL2 OR PARP2 OR ADPRT2.
Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata;
Mammalia; Butheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 9-559 FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25;
"pADPRT-2: a novel mammalian polymerizing(ADP-ribosyl)transferase gene related to truncated pADPRT homologues in plants and Caenorhabditis
                                                     -i- FUNCTION: HAS DNA DEPENDENT POLY (ADP-RIBOSE) POLYMERASE ACTIVITY.

SEEMS TO PLAY A ROLE IN THE RESPONSE TO DNA DAMAGE.

-i- CATALYTIC ACTIVITY: NAI+ + (ADP-D-ribosyl)(N)-acceptor—
nicotinamide + (ADP-ribosyl)(N+1)-acceptor.

-i- SUBCELLULAR LOCATION: Nuclear.

-i- TISSUE SPECIFICITY: Widely expressed; the highest levels were in testis followed by ovary.

-i- INDUCTION: By high levels of DNA-damaging agents.

-i- SIMILARITY: BELONGS TO THE PARP FAMILY.
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InterPro; IPR001290; PARP.
InterPro; IPR004102; PARP_reg.
Pfam; PF00644; PARP; 1
Pfam; PF02877; PARP_reg; 1.
Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41
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NUCLEAR LOCALIZATION SIGNAL 1ST (POTENTIAL).
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V -> I (IN REF. 2)
R -> Q (IN REF. 2)
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35.2%; Pred. No. 7.8e-45;
ive 87; Mismatches 207
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                                          FEBS Lett. 449:259-263(1999).
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559 AA;
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Best Local Similarity
Matches 204; Conserv
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DNA_BIND 1
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Erratum.
 456
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01-DEC-1992 (Rel. 24, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Poly [ADP-ribose] polymerase-1 (E. 2.4.2.30) (PARP-1) (ADPKT) (NAD(+)
ADP-ribosyltransferase-1) (Poly[ADP-ribose] synthetase-1).
 LQLLDSGESEYKAIQTYLKQTGNSYRCP-----NLRHVWKVNREGEGDRFQAHSKLGN 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular cloning of cDNA for human poly(ADP-ribose) polymerase and expression of its gene during HL-60 cell differentiation."; Biochem. Biophys. Res. Commun. 146:403-409(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primary structure of human poly(ADP-ribose) synthetase as deduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the
            RRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKGIYFASENSKSAGYVTTMHCGGH
                                                                                     QVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQTEPDPAQDIELELDGQPVVV
                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 440-1013 FROM N.A.
MEDLINE-87298455; PubMed=3113420;
Suzuki H., Uchida K., Shima H., Sato T., Okamoto T., Kimura T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cherney B.W., McBride O.W., Chen D., Alkhatib H., Bhatia K., Hensley P., Smulson M.E.; acDNa sequence, protein structure, and chronosomal location of human gene for poly(ADP-ribose) polymerase."; Proc. Natl. Acad. Sci. U.S.A. 84:8370-8374(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matsuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-88058958; PubMed=2824474;
Kroosaki T., Ushiro H., Mitsuuchi Y., Suzuki S., Matsuda M
Matsuda Y., Katunuma N., Kangawa K., Matsuo H., Hirose T.,
Inayama S., Shizuta Y.;
                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-90091744; PubMed=2513174;
Madr B., Majl U., Herzog H., Schneider R., Schweiger M.;
"Human nuclear NAD+ App-ribosyltransferase(polymerizing):
organization of the gene.";
                                                                                                                                PQGPPVQCPSFKSSSF--SQSEYLIYKESQCRLRYLLEI 526
                                                                                                                                           PRT; 1013 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from cDNA sequence.";
J. Biol. Chem. 262:15990-15997(1987)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Fibroblast;
MEDLINE=88076933; PubMed=3120710;
                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                      ADPRT OR PPOL OR PARP1.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                             8:575-580(1989)
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Rolli V., O'Farrell M., Menissier-de Murcia J., de Murcia G.M.;
"Random mutagenesis of the poly(ADP-ribose) polymerase catalytic
domain reveals anino acids involved in polymer branching.";
Biochemistry 36:12147-12154 (1997).
--- FONCTION: POLY[ADP-RIBOSE] POLYMERASE MODIFIES VARIOUS NUCLEAR
PROTEINS BY POLY(ADP-RIBOSYL)ATION. THE MODIFICATION IS DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The human poly(ADP-ribose) polymerase nuclear localization signal is a bipartite element functionally separate from DNA binding and
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MEDLINE=91035460; PubMed=2121735;
Simonin F., Menissier de Murcia J., Poch O., Muller S., Gradwohl G.,
Molinete M., Penning C., Keith G., de Murcia G.M.,
Expression and site-directed mutagenesis of the catalytic domain of
human poly(ADP-ribose)polymerase in Escherichia coli. Lysine 893 is
critical for activity.";
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[11] D.M., Miwa M.;
"The zinc fingers of human poly(ADP-ribose) polymerase are
differentially required for the recognition of DNA breaks and nicks
and the consequent enzyme activation. Other structures recognize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of
                                                                                                                                                                                                                              Yokoyama Y., Kawamoto T., Mitsuuchi Y., Kurosaki T., Toda K.,
Ushiro H., Terashima M., Sumimoto H., Kuribayashi I., Yamamoto Y.,
Maeda T., Ikeda H., Sagara Y., Shizuta Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-39 FROM N.A.
MEDLINE-90211250; PubMed-2108670;
Ogura T., Nyunoya H., Takahashi-Masutani M., Miwa M., Sugimura T.,
                                                                                                                                                                                                                                                                                                                                        "Human poly(ADP-ribose) polymerase gene. Cloning of the promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Characterization of a putative promoter region of the human poly(ADP-ribose) polymerase gene: structural similarity to that the DNA polymerase beta gene.";
H., Uchida K., Shima H., Sato T., Okamoto T., Kimura T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ikelima M., Noguchi S., Yamashita R., Ogura T., Sugimura T.,
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Herzog H., Schneider R., Hirsch-Kauffmann M., Schnitzer
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Submitted (JUL-1991) to the EMBL/GenBank/DDBJ databases
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Schreiber V., Molinete M., Boeuf H., de Murcia G.M.,
Menissier de Murcia J.;
                                                                        Biochem. Biophys. Res. Commun. 148:1549-1550(1987)
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Eur. J. Biochem. 194:521-526(1990).
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MEDLINE-91099327; PubMed-2125269;
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MEDLINE=91072398; Pubmed=2123876;
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MEDLINE=97461532; Pubmed=9315851;
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EMBO J. 11:3263-3269(1992).
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    Suzuki H.
Miwa M.;
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M17081; AAA51599.1; ALT_SEQ
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Pfam; PF00644; PARP;
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S14010; S14010
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SEQUENCE OF 647-714 AND 838-903 FROM N.A.
MEDLINE-88151954; PubMed-2450019;
Taniguchi T., Yamauchi K., Yamamoto T., Toyoshima K., Harada N.,
Tanaka H., Takahashi S., Yamamoto H., Fujimoto S.;
Tanaka H., Takahashi S., Yamamoto H., Fujimoto S.;
"Depression in gene expression for poly(ADP-ribose) synthetase during the interferon-gamma-induced activation process of murine macrophage
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                        MAPKRKASVQTEGSKKQRQGTEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQV
                                                                                                 61 HEDYDCTLNQTNIGNNNNKFYIIQLLEEG--SRFFCWNRWGRVGEV-GQSKMNHFTCLED
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                                      39;
Length 1013;
                                      Indels
 DB 1;
                                    Matches 183; Conservative 101; Mismatches 216;
                   Pred. No. 4.1e-44
25.4%; Score 707.5; 34.0%; Pred. No. 4.1
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EUT. J. Biochem. 171:571-575(1988).

- I- FUNCTION: POLY[ADP-RIBOSE] POLYMERASE MODIFIES VARIOUS NUCLEAR PROTEINS BY POLY[ADP-RIBOSE] POLYMERASE MODIFIES VARIOUS NUCLEAR PROTEINS BY POLY[ADP-RIBOSE] POLYMERASE MODIFIES ARROUND IS INVOLVED IN THE REGULATION OF VARIOUS IMPORTANT CELLULAR PROCESSES SUCH AS DIFFERENTIATION, PROLIFERATION, AND TENNOLVED IN THE RECOVERY OF CELL FROM DNA DAMAGE.

- CATALYTIC ACTIVITY: NAD(+) + {ADP-D-IIDOSY1](N)-acceptor = nicotinamide + {ADP-D-TIDOSY1](N)-acceptor = nicotinamide + {A
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NUCLEAR LOCALIZATION SIGNAL 2ND
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PROSITE; PS00347; PARP_ZN_FINGER_1; 2.
PROSITE; PS50064; PARP_ZN_FINGER_2; 2.
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EMBL; X06986; CAA30046.1; -.
EMBL; X06987; CAA30047.1; -.
PIR; JS0428; JS0428.
PIR; S00328; S00328.
HSSP; P26446; 1A26.
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Pfam; PF00644; PARP; 1.
Pfam; PF02877; PARP_reg; 1.
Pfam; PF00645; zf-PARP; 2.
ProDom; PD004675; Znf-PARP; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             403 RVGKGIYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPGFD 462
                                                                                                                                                                                                                                      1 MAPKRKASVQTEGSKKQRQGTEEDSFRSTAE---ALRAAPADNRVIRVDPSCPFSRNPG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Fetal brain;
MEDILNE-99292755; PubMed=10364231;
Ame J.-C., Rolli V., Schreiber V., Niedergang C., Apiou F., Decker
Ame J.-C., Rolli V., Menissier-de Murcia J., de Murcia G.M.;
Muller S., Hoeger T., Menissier-de Murcia J., de Murcia G.M.;
"PARP-2, a novel mammalian DNA damage-dependent poly(ADP-ribose)
                                                                                                                                                                                                                                                                                                               : || |: || || |- || || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291 TLQAAPGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQ----TGNSYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 L-EVVDIFKIEREGESQRYKPFKQLHNRRLLWHGSRTTNFAGILSQGLRIAPPEAPVTGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 I -- QVHEDYDCTLNQTNIGNNNNKFYIIQLLEEG -- SRFFCWNRWGRVGEV-GQSKMNHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                546 VLEKGGKVFSATLGLVDIVKGTNSYYKLQLLEDDKESRYWIFRSWGRVGTVIGSNKLEQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 TCLEDAKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVK--VDSGPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              171 RTVVKPCSLDPATONLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKOQIARGFEALEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 EEAMKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         090GN5; 09Y6C8; 09NUV2; 09UMR4;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Poly (ADP-ribose) polymerase-2 (EC 2.4.2.30) (PARP-2) (NAD(+) ADP-ribose)
ribosyltransferase-2) (Poly[ADP-ribose] synthetase-2) (PADPRT-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVIARGQTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
      Length 1015;
                                                                                                                         Indels
25.3%; Score 704.5; DB 1;
34.4%; Pred. No. 6.9e-44;
ive 95; Mismatches 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               583 AA.
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J. Biol. Chem. 274:17860-17868(1999).
[2]
SEQUENCE OF 2-583 FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 2).
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                                                                                                                         Conservative
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                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1003 LLKL 1006
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                                                                                                                   187;
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Query Match
Best Local S
Matches 187
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97; Mismatches 207;
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Biochem. Mol. Biol. Int. 43:755-761(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [3]
SEQUENCE OF 1-11 FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-Prostate;
MEDLINE-92290013; PubMed-1601134;
Matches 185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           520 LRYLLEI 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2]
REVISION TO 811.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Fibroblast;
MEDLINE-99268466; Pubmed-10338144;
MEDLINE-99268466; Pubmed-10338144;
Berghammer H., Ebner M., Marksteiner R., Auer B.;
"pADPRT-2: a novel mammalian polymerizing(ADP-ribosyl)transferase gene related to truncated pADPRT homologues in plants and Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Masuho Y., Kanehori K.;
"NECO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/Genbank/DDBJ databases.
-!- FUNCTION: HAS DNA-DEPENDENT POLY(ADP-RIBOSE) POLYMERASE ACTIVITY.
SEEMS TO PLAY A ROLE IN THE RESPONSE TO DNA DAMAGE (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ptam; PF02877; PARP_reg; 1.
Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein; ADP-ribosylation; Alternative splicing.
DNA_BIND 1 AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SIMILARITY: BELONGS TO THE PARP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEAR LOCALIZATION SIGNAL 2ND PART
                                                                             "A human poly(ADP-ribose) polymerase gene family (ADPRTL): cDNk cloning of two novel poly(ADP-ribose) polymerase homologues."; Genomics 57:442-445(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEAR LOCALIZATION SIGNAL 1ST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAD-BINDING (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -> H (ÎN REF. 2).
-> H (ÎN REF. 4).
5B7AE8AE531836AF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 699; DB 1;
Pred. No. 8.1e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
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                                                                                                                                                                             [3] SEQUENCE OF 22-583 FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AJ236912; CAB65088.1; -. EMBL; AF085734; AAD29657.1; ALT_INIT. EMBL; AJ236876; CAB41505.2; ALT_INIT. EMBL; AJ201019, BAA92017.1; ALT_TERM. HSSP; P26446; 1A26. InterPro; IPR001290; PARP.
                           MEDLINE-99263509; PubMed-10329013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR004102; PARP_reg.
                                                                                                                                                                                                                                                                                                                                                                                      elegans.";
FEBS Lett. 449:259-263(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66205 MW;
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33.8%;
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Pfam; PF00644; PARP; 1.
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   FISSUE=Fetal brain;
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Best Local Similarity
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                                                          Johansson M.;
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01-AUG-1992 (Rel. 23, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Poly [ADP-ribose] polymerase-1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+)
ADP-ribosyltransferase-1) (Poly[ADP-ribose] synthetase-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGRANKDRTEDKODGMPGRSWASKRVSESVKALLLKGKAP-----VDPECTAKVGKAH 106
                                                                                                                                                                                                                    --IQVHEDYDCTLNQTNIGNNNNKFYIIQLLEEGSR--FFCWNRWGRVGEVGQSKMNHFT 113
                                                                                                                                                                                                                                                         C---LEDAKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKVDSGPV 170
                                                                                                                                                                                                                                                                                                                                                                                               RTVVKPCS-LDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           225 KSPLKPESQLDLRVQELIKLICNVQAMEEMMMEMKYNTKKAPLGKLTVAQIKAGYQSLKK 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEEAMKNPTGD-GQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIEL 288
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
   Gaps
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MEDLINE-98046546; Pubbed-9285436;
Beneke S., Meyer R., Buerkle A.;
"Isolation of cDNA encoding full-length rat (Rattus norvegicus) poly
                                                                      GSKKQRQGTEEED-----SFRSTAEALRA-----APADNRVIRVDPSCPFSRNPG- 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         346 RCPNLRHVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SG
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   Indels
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Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE OF 514-1013 FROM N.A.

SEQUENCE OF 514-1013 FROM N.A.

SEQUENCE OD 27702; PubMed=2508731;

RATHID-INE-90027702; PubMed=2508731;

RATHID-Odeau J., Gradwohl G., Dumas C., Clairoux-Moreau S., Brunet G.;

"Cloning of rodent cDNA coding the poly(ADP-ribose) polymerase
RATHID-Odeau J. G7:653-660(1989).

"Cloning of rodent cDNA FRENCEST OF REAL MODIFIES VARIOUS NUCLEAR
RATHING PROFESSES SUCH AS DIFFERENTIATION OF VARIOUS IMPORTANT
CELLULAR PROCESSES SUCH AS DIFFERENTIATION OF THE MODIFICATION AND ALSO IN THE REGULATION OF THE MODIFICATION AND ALSO IN THE RECULANT DATE OF THE MODIFICATION AND ALSO IN THE RECULANT DATE OF THE MODIFICATION AND ALSO IN THE RECULANT LOCATION: NAD(+) + {ADP-D-ribosyl}{(NH-1)-acceptor.}

"INCOMPATED AND ADP-D-RIBOSYL GROUP OF NAD(+) IS TRANSFERRED TO AN ACCEPTOR CARBOXYL GROUP ON A HISTONE OR THE ENZYME HISTORIC OF THE TEXMINAL ADENOSINE MOIETY, BUILDING UP A POLYMER WITH AN FURTHER ADP-PREDORTE MATHER MODIFICATION OF THE TEXMINAL ADENOSINE MOIETY, BUILDING UP A POLYMER WITH AN AVERAGE CHAIN LENGTH OF 20-30 UNITS.

"INCOMPATION OF THE PARP FAMILY."

"INCOMPATION OF THE PARP FAMILY."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KW ADP-ribosylation; Zinc-finger; Zinc.
FT INIT_MET 0 BY SIMILARITY.
FT DOMAIN 373 523 AUTODDIFICATION DOMAIN.
FT DOMAIN 373 523 AUTODDIFICATION DOMAIN.
FT DOMAIN 374 524 1013 NAD-BINDING.
FT DOMAIN 375 524 TO SIMILARITY.
FT DOMAIN 377 574 TO SIMILARITY.
FT DOMAIN
Potvin F., Thibodeau J., Kirkland J.B., Dandenault B.,
Duchaine C., Poirier G.G.,
"Structural analysis of the putative regulatory region of the rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEAR LOCALIZATION SIGNAL 1ST PA
NUCLEAR LOCALIZATION SIGNAL 2ND PA
BLOCKED (BY SIMILARITY).
ADP-RIBOSYL[N] (POTENTIAL).
ADP-RIBOSYL[N] (POTENTIAL).
ADP-RIBOSYL[N] (POTENTIAL).
ADP-RIBOSYL[N] (POTENTIAL).
ADP-RIBOSYL[N] (POTENTIAL).
                                                                        gene encoding poly(ADP-ribose) polymerase.";
FEBS Lett. 302:269-273(1992).
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EEMBL; X65496; CAA46477.1; -.
EEMBL; X65497; CAA46478.1; ALT_INIT.
HSSP; P26446; IA26.
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Pfam; PF00644; PARP; 1.
Pfam; PF02877; PARP_reg; 1.
Pfam; PF00645; zf-PARP; 2.
ProDom; PD004675; Znf-PARP; 2.
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InterPro; IPR001290; PARP.
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Poly [ADP-ribose] polymerase (EC 2.4.2.30) (PARP) (ADPRT) (NAD(+) ADP-ribosyltransferase) (Poly[ADP-ribose] synthetase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                            61 HEDYDCTLNQTNIGNNNNKFYIIQLLE -- EGSRFFCWNRWGRVGEV - GQSKMNHFTCLED 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 --CSLDPATQNLITNIFSKEMFKNAMTIMNLDVKKMPLGKLTKQQIARGFEALEALEEAM 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     779 GGSDDSSK-----DPIDVNYEKLKTDIKVVDRDSEEAEVIRKYVKNTHATTHNAYDL-EV 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             351 RHVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILFSGLRIMPH----SGGRVGK 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  833 IDIFKIEREGESQRYKPFRQLHNRRLLWHGSRTTNFAGILSQGLRIAPPEAPVTGYMFGK 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            407 GIYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIA 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 KNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                    Length 1013;
                                                                                                                                                                                                                                                                                  Ouery Match 25.0%; Score 698; DB 1; Length 101
Best Local Similarity 33.6%; Pred. No. 2.1e-43;
Matches 182; Conservative 101; Mismatches 214; Indels
                                                                               (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                         (POTENTIAL).
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    (POTENTIAL)
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E -> A (IN REF. 4)
N -> D (IN REF. 4)
                  ADP-RIBOSYL[N]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 17;
                         405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 -YDCTLNQTNIGNNNNKFYIIQLLEEGSR--FFCWNRWGRVGEVGQSKMN-HFTCLEDAK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 VYDAILNQTNVRDNNNKFFVLQVLESDSKKTYMVYTRWGRVGVKGQSKLDGPYDSWDRAI 227
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                                                                                                                                                                                                                                                                                                                                                                              NAD-BINDING (BY SIMILARITY).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
527A8F464605D127 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 KASVQTEGSKKQRQGTEEEDSFRS--TAEALRAAPADNRVIRVDPSCPFSRNPGIQVHED 63
                                                                                                                                                                                                                                                                                                                                        SMART; SM00513; SAP; 2.
Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              406 DPGLQDD-----PLYYHYQQLNCGLTPVGNDSEEFSMVANYMENTHAKTHSGYTVEIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 SLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEAMKNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 TGDGQSLEELSSCFYTVIPHNFGRSRPPP--INSPDVLQAKKDMLLVLADIELA-QTLQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              295 APGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQT---GNSYRCPNLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                43;
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                                                                                                                                                                                                                                                                                Interpro; IPR001290; PARP.
Interpro; IPR004102; PARP_reg.
Interpro; IPR003034; SAP.
Pfam; PF00644; PARP; 1.
Pfam; PF02877; PARP_reg; 1.
Pfam; PF020377; SAP; 2.
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                                                                                                                                                                                                                                                             EMBL; 248243; CAA88288.1; -. HSSP; P26446; 1A26.
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                  SEQUENCE FROM N.A.
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01-AUG-1992 (Rel. 23, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
19-OY | ADP-ribose| polymerase-1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+)
ADP-ribosyltransferase-1) (Poly{ADP-ribose} synthetase-1).
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-!- FUNCTION: POLY[ADP-RIBOSE] POLYMERASE MODIFIES VARIOUS NUCLEAR PROTEINS BY POLY[ADP-RIBOSE].

-!- FUNCTION: POLY[ADP-RIBOSE] POLYMERASE MODIFICATION IS DEPENDENT ON DNA AND IS INVOLVED IN THE REGULATION OF VARIOUS IMPORTANT CELLULAR PROCESSES SUCH AS DIFFERENTIATION, PROLIFERATION, AND TUMORY TRANSFORMATION AND ALSO IN THE REGULATION OF THE MOLECULAR EVENTS INVOLVED IN THE RECOVERY OF CELL FROM DNA DAMAGE.

-!- CATALYTIC ACTIVITY: NADA(+) + (ADP-D-TIBOSY]!(N)-acceptor = nicotinamide + {ADP-D-TiBOSY]!(N)-acceptor = nicotinamide + {ADP-D-TiBOSY]!(N)-acceptor = nicotinamide + ADP-D-TiBOSY]!(N)-acceptor = nicotinamide + ADP-D-TiBOSY]!(N)-acceptor = nicotinamide + ADP-D-TiBOSY]!(N)-acceptor = nicotinamide + ADP-D-TiBOSY]!(N)-acceptor = nicotinamide + ADP-D-TiBOSY]!(N+1)-acceptor = nicotinamide + ADP-D-TIBOSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                574 KGVGKTAPNPSEAQTLE-DG--VVVPLGKPVE-RSCSKGMLLYNEYIVYNVEQIKMRYVI 629
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"Inhibitor and NAD+ binding to poly(ADP-ribose) polymerase as derived
from crystal structures and homology modeling.";
                                                       459 QLFRASRAVEADRFQQFSSSKNRMLLWHGSRLTNWAGILSQGLRIAPPEAPVTGYMFGKG 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 659-1011.
MEDLINE-296513881; PubMed-875549;
Ruf A., Mennissier de Aurcia G.M., Schulz G.E.;
"Structure of the catalytic fragment of poly(AD-ribose) polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 659-1011, AND REVISION TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                             465 IARGQTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLL
                                                                                                                                                                                                                                                                                                                        519 VYFADMFSKSANY----CYANTGANDGVLLLCEVALGDMNELLYSDYNADNLPPGKLST
                                                                                                                                                                                           408 IYFASENSKSAGYVTTMHC---GGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSV
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MEDLINE-98239716; Pubmed-9571033;
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MEDLINE=91340148; PubMed=1840535;
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                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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F
-1- MISCELLANEOUS: THE ADP-D-RIBOSYL GROUP OF NAD(+) IS TRANSFERRED TO AN ACCEPTOR CARROXYL GROUP ON A HISTONE OR THE ENZYME ITSELF, AND FURTHER ADP-RIBOSYL GROUPS ARE TRANSFERRED TO THE 2'-POSITION OF THE TERMINAL ADENOSINE MOIETY, BUILDING UP A POLYMER WITH AN AVERAGE CHAIN LENGTH OF 20-30 UNITS.
-! SIMILARITY: BELONGS TO THE PARP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                            DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PART.
PART.
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NUCLEAR LOCALIZATION SIGNAL 2ND
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PROSITE; PS00347; PARP_ZN_FINGER_1; 2.
PROSITE; PS50064; PARP_ZN_FINGER_2; 2.
Transferase; Glycosyltransferase; NAD; DNA-binding APP-ribosylation; Zinc-finger; Zinc; 3D-structure. DNA_BIND
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PDB; 3PAX; 27-MAY-98.
PDB; 4PAX; 27-MAY-98.
PDB; 1A26; 27-MAY-98.
InterPro; IPR001357; BRCT.
InterPro; IPR001290; PARP.
InterPro; IPR001290; PARP.
InterPro; IPR001510; 2nf-PARP.
Pfam; PF00644; PARR; 1.
Pfam; PF00644; PARR; 1.
Pfam; PP00645; 2F-PARP; 2.
ProDom; PP00645; 2F-PARP; 2.
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2PAW; 27-MAY-98.
1PAX; 15-MAY-97.
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1011 AA;
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PPOL_MOUSE STANDARD; PRT; 1012 AA.
PPOL_MOUSE (STANDARD; PRT; 1012 AA.
P1103; 0951x4; 0960x3;
01-JUL-1989 (Rel. 11, casted)
01-GCT-1989 (Rel. 12, Last sequence update)
16-GCT-2001 (Rel. 40, Last annotation update)
Poly (AnD-riboss) polymerase-1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+)
ADP-ribosyltransferase-1) (Poly[ADP-ribose] synthetase-1) (msPARP).
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polymerase
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YDCTLNQTNIGNNNNKFYIIQLLEEG -- SRFFCWNRWGRVGEV - GQSKMNHFTCLEDAKK
                                                                                                   FSATLGLVDIVKGTNSYYKLQLLEDDRESRYWVFRSWGRVGTVIGSNKLEQMPSKEDAVE
                                                                                                                                               DFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVK - - VDSGPVRTVVKPCS
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DGDK-----DPIDINYEKLRTDIKVVDKDSEEAKIIKQYVKNTHAATHNAYDL-KVVEIF
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RIEREGESORYKPFKQLHNRQLLWHGSRTTNFAGILSQGLRIAPPEAPVTGYMFGKGIYF
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION STRAIN-129/Sv X C57BL/6; TISSUE-Fibroblast; MEDLINE-20270268; PubMed=10809783;
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J. Biol. Chem. 275:15504-15511(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=BXSB;
MEDLINE=89263780; PubMed=2498841;
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KNOCK-OUT

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Gaps

56;

24.9%; Score 694; DB 1; Length 1011; 34.1%; Pred. No. 4e-43; ive 97; Mismatches 204; Indels 5

Best Local Similarity 34.1 Matches 185; Conservative

Similarity

Query Match

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PPOL_XENLA
P31669;
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                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
       Auer B., Flick K., Wang Z.Q., Haidacher D., Jaeger S., Berghammer H., Kofler B., Schweiger M., Wagner E.F.;
"On the biological role of the nuclear polymerizing NAD+: protein(ADP-ribosyl) transferase (ADPRT): ADPRT from Dictyostellum discoideum and linactivation of the ADPRT gene in the mouse.";
Blochimie 77:444-449(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00292; BRCT; 1.
PROSITE; PS50172; BRCT; 1.
PROSITE; PS50172; BRCT; 1.
PROSITE; PS50044; PARP_ZN_FINGER_1; 2.
Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein; ADP-ribosylation; Zinc-finger; Zinc; Alternative initiation.
INIT_MET 0 0 BY SIMILARITY
CHAIN 1012 POLY [ADP-RIBOSE] POLYMERASE-1, LONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PART.
PART.
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ADP-RIBOSYL[N] (POTENTIAL).
ADP-RIBOSYL[N] (POTENTIAL).
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POLY [ADP-RIBOSE] POLYMERASE-1,
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PIR; S04200; S04200.
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MEDLINE-96007847; PubMed-7578427
                                                                                                                                                                                                                                                                                                                                                            Interpro; IPR001357; BRCT.
Interpro; IPR001290; PARP.
Interpro; IPR004102; PARP_reg.
Interpro; IPR001510; Znf-PARP.
Pfam; PF00533; BRCT; 1.
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Pfam; PF00645; zf-PARP; 2.
ProDom; PD004675; znf-PARP; 2.
                                                                                                                                                                                                                                                                                                                    EMBL; X14206; CAA32421.1; -.
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MGD; MGI:1340806; Adprtl
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                       (POTENTIAL).
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ADP-RIBOSYL[N]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2010 (Rel. 40, Last annotation update)
Poly [ADP-ribose] polymerase (EC 2.4.2.30).(PARP) (ADPRT) (NAD(+) ADP-ribosyltransferase) (Poly[ADP-ribose] synthetase) (Fragment).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordets; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                    "Isolation of cDNAs encoding the catalytic domain of poly(ADP-ribose) polymerase from Xenopus laevis and cherry salmon using heterologous oligonucleotide consensus sequences."

Biochem. Biophys. Res. Commun. 193:119-125(1993).

-!- FUNCTION: POLY[ADP-RIBOSE] POLYMERASE MODIFIES VARIOUS NUCLEAR PROTEINS BY POLY(ADP-RIBOSYL)ATION. THE MODIFICATION IS DEPENDENT ON DAA AND IS INVOLVED IN THE REGULATION OF VARIOUS IMPORTANT CELLULAR PROCESSES SUCH AS DIFFERENTIATION, PROLIFERATION, AND TUMOR TRANSFORMATION AND ALSO IN THE REGULATION OF THE MOLECULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00292; BRCT; 1.
PROSITE; PS50172; BRCT; 1.
PROSITE; PS50047; PARP_ZN_FINGER_1; 2.
PROSITE; PS50064; PARP_ZN_FINGER_2; 2.
Transferase; 01ycosyltransferase; NAD; DNA-binding; Nuclear protein; ADP-ribosylation; Zinc-finger; Zinc.
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 742-876 FROM N.A.
MEDLINE-93277538; Pubmed-8503897;
Ozawa Y., Uchida K., Uchida M., Ami Y., Kushida S., Okada N.,
                                                                                                                                                                                                                                                                                      Saulier-Le Drean B.M.;
Thesis (1992), University of Rennes, France.
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Pfam; PF00644; PARP; 1.
Pfam; PF02847; PARP; 1.
Pfam; PF00645; zf-PARP; 2.
ProDom; PD004675; Znf-PARP; 2.
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IPR004102; PARP_reg.
IPR001510; Znf-PARP.
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InterPro; IPR001357; BRCT.
                                                                                                                                                                               Xenopodinae; Xenopus.
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                                                                                                                                                      SIGNAL
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95; Mismatches 215; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
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F5A25E4A3366BAE7 CRC64;
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(Rel. 34, Last sequence update)
(Rel. 40, Last annotation update)
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Q11208;
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01-OCT-1996 (
16-OCT-2001 (
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EEEDSFRSTAEALRAAPADNRV----IRVDPSCPF-----SRNPGIQVHEDYDCTL
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RA Masutani M., Nozaki T., Hitomi Y., Ikejima M., Nagasaki K.,
RA de Prati A.C., Kurata S., Natori S., Sugimura T., Esumi H.;
Cloning and functional expression of poly(ADP-ribose) polymerase
RT "Cloning and functional expression of poly(ADP-ribose) polymerase
RE cDNA from sarcophaga peregrina ":
RL U. J. Blochem. 220:607-614(1994).
CC PROTEINS BY POLY(ADP-RIBOSE) POLYMERASE MODIFICATION IS DEPENDENT
CC ON DNA AND IS INVOLVED IN THE REGULATION OF VARIOUS IMPORTANT
CC ON DNA AND IS INVOLVED IN THE REGULATION OF THE MOLECULAR
CC OTAURA PROCESSES SUCH AS DIFFERENTIATION, PROLIFERATION, AND
CC TUMOR TRANSFORMATION AND ALSO IN THE REGULATION OF THE MOLECULAR
CC C TOTALY PROCESSES SUCH AS DIFFERENTIATION, PROLIFERATION, AND
CC TOTALY PROLIFERATION OF THE PROPERMINA THE MOLECULAR
CC TOTALY PROLIFERATION OF THE PROPERMINA THE MOLECULAR
CC TOTALY CATIVITY: NDO(+) + {ADP-D-Tibosy1}(N-)-acceptor =
CC TOTALIAR LOCATION: Nuclear.
CC TOTALIAR CONTAINS THO MOLES OF ZINC PER MOLE OF PROTEIN.
CC TOTALIAR CONTAINS THO MOLES.
C THE TERMINAL ADDENOSINE MOLES.
C THE TERMINAL ADENOSINE MOLEY, BUILDING UP A POLYMER WITH AN
CC THE SIMILARITY: BELONGS TO THE PARP FAMILY.
C TOTALIARITY: BELONGS TO THE PARP FAMILY.
C TOTALIARITY: CONTAINS I BRCT DOMAIN.
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Poly [ADP-ribose] polymerase (EC 2.4.2.30) (PARP) (ADPRT) (NAD(+) ADP
                 ribosyltransferase) (Poly(ADP-ribose] synthetase).
Sarcophaga peregrina (Riesh fly) (Boettcherisca peregrina).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50172; BRCT; 1.
PROSITE; PS00347; PRRP_ZN_FINGER_1; FALSE_NEG.
PROSITE; PS50064; PARP_ZN_FINGER_2; 2.
Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein;
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NUCLEAR LOCALIZATION SIGNAL 2ND PART.
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                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-94170813; PubMed-8125121;
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                                                                                             Oestroidea; Sarcophagidae; Sarcophaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADP-ribosylation; Zinc-finger; Zinc.
DNA_BIND 1 369 BY SIM1
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InterPro; IPR004102; PARP_reg.
InterPro; IPR001510; Znf-PARP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF02877; PARP_reg; 1.
Pfam; PF00045; zf-PARP; 2.
ProDom; PD004675; znf-PARP; 2.
SMART; SM00292; BRCT; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00533; BRCT;
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Gaps

48;

Indels

23.4%; Score 652; DB 1; Length 996; 33.3%; Pred. No. 4.8e-40;

Query Match 23.4%; Score 652; DB 1; I Best Local Similarity 33.3%; Pred. No. 4.8e-40; Matches 176; Conservative 100; Mismatches 205;

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PPOL_DROME STANDARD, PRT; 994 AA.
P35875; Q9W5S1;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Poly [ADP-ribose] polymerase (EC 2.4.2.30) (PARP) (ADPRT) (NAD(+) ADP-ribosyltransferase) (Poly[ADP-ribose] synthetase).
PARP OR CG17696/CG17718.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                  418
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                                                                     126 FWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKVDSGPVRTVVKPCSLDPATQN 185
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                                                                                                                                                                               604 YLEKSGNHFENRENFVKVAGRMYPIDIDYAEDS-----KIDLSAEHDIKSKLPL--SVQD
EESKSSKSKSIYTKSVPKSMTLKIKDGLAVDPDSGLEDVAHVYVSRN-----KEKYNVVL
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DAINRFYTLIPHNFGTQSPPLLDTTEQVEQLRQMLDSLIEIECAYSLLQT---EDSKAD-
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Ordída K., Hanal S., Ishikawa K.-I., Ozawa Y.-I., Uchida M.,
Sugimura T., Miwa M.;
"Cloning of cDNA encoding Drosophila poly(ADP-ribose) polymerase:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., ALTERNATIVE SPLICING, DEVELOPMENTAL STAGE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                479 ELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEIH 527
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STRAIN=CANTON-S;
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Ananatides P.G., Solerer S.E., Lip FW., Blookins R.A., Galler.

Ananatides P.G., Solerer S.E., Lip FW., Blookins R.A., Galler.

B. Standon R.C., Mortran J.R., Tandall N.D., Change M., Feiffer B.D.,
B. Standon R.C., Mortran J.R., Tandall N.D., Change M., Feiffer B.D.,
Anna R. S.E., Mayer E. G., Batter E.G., Feiffer B.D.,
Anna R. S.E., Mayer B. C., Batter E.G., Feiffer B.D.,
Anna R. S.E., Mayer B. C., Batter E.G., Feiffer B.D.,
Anna R. S.E., Batter E.G., Batter E.G., Feiffer B.D.,
Anna R. S.E., Batter E.G., Feiffer B.D.,
B. Beilde J. R., Banca P., Washer B. S., Batter B.D., Batter B.,
B. Beilde J. R., Banca P., Washer B., B. Beilder G., Delander J.,
B. Beilde J. R., Banca P., Washer B., B. Beilder A., Beng S., M.,
B. Beilde B. Dellaher A., Beng Z., Maya R.D., Daw I.D. Diaka W.,
B. Beilde J. R., Banca P., Batter A., Beng Z., Maya R., Gala P., Bartis M.,
B. Beilde B., Dellaher A., Beng Z., Maya R., Gala P., Bartis M.,
B. Beilde J., Batter B., Batter A., Beng Z., Maya R., Gala P., Harris M.,
B. Beilde B., Beilder A., Beng Z., Maya R., Gala P., Harris M.,
B. Bottow B., Beilder A., Beng Z., Maya R., Gala P., Harris M.,
B. Batter B., Kodire C., Gorgel J. J. H., Gu Z., Guan P., Harris M.,
B. Batter B., Kodire C.D., Kraft C., Krayle M.-H., Libeyam C.,
B. Allahi M., Kalish P., Karpen G.H., Se Z., Kenniscon J.A., Mestchum K.A.,
B. Mayar R., Mayar R., Batter B., Mayar R., Beng M., Mayar R., Mayar R., Batter B., Mayar R., ```

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EMBL; D13806; BAA02964.1; -. EMBL; AF051548; AAC24518.1; -

DNA-binding; Nuclear protein; PART. R PROSITE; PS00129; BRCT; 1.

R PROSITE; PS00172; BRCT; 1.

R PROSITE; PS00172; BRCT; 1.

R PROSITE; PS0064; PARP\_ZN\_FINGER\_1; 1.

R PROSITE; PS0064; PARP\_ZN\_FINGER\_2; 2.

W Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear pr ADP-ribosylation; Zinc-finger; Zinc; Alternative splicing.

M ADP-ribosylation; Zinc-finger; Zinc; Alternative splicing.

M ADP-ribosylation; Zinc-finger; Zinc; Alternative splicing.

M ADP-ribosylation; Zinc-finger; Zinc; Alternative splicing.

DOMAIN 380 454 BRCT.

T DOMAIN 508 994 NAD-BINDING.

T ZN\_FING 19 54 PARP-TYPE.

T ZN\_FING 123 161 PARP-TYPE.

PARP-TYPE. 54 PARP-TYPE.

161 PARP-TYPE.

210 NUCLEAR LOCALIZATION SIGNAL 1ST

228 MUCLEAR LOCALIZATION SIGNAL 2ND

564 MISSING (IN SHORT ISOPORM).

113791 MW; ACA85A270DD29E08 CRC64; EMBL; AF051544; AAC24518.1; JOINED. EMBL; AF051545; AAC24518.1; JOINED. EMBL; AF051547; AAC24518.1; JOINED. EMBL; AE005147; AAC24518.1; JOINED. EMBL; AE002666; -; NOT\_ANNOTATED\_CDS. EMBL; AE002892; AAF45400.1; -DIR; A47474; A47474.

HSSP; P26446; 1A26.

HSSP; P26446; 1A26.

F1YBASS; FBGMO10247; PARP.

InterPro; IPR001357; BRCT.

InterPro; IPR001290; PARP.

InterPro; IPR001290; PARP.

InterPro; IPR001510; Znf-PARP.

Pfam; PF00633; BRCT; 1.

Pfam; PF00644; PARP; 1.

Pfam; PF00645; Zf-PARP; 2.

ProDom; PD004675; Znf-PARP; 2. 368 5 380 4 380 4 10 1 12 1 208 2 223 2 376 5 VARSPLIC SEQUENCE DOMAIN 

Gaps 39; Query Match 22.3%; Score 621.5; DB 1; Length 994; Best Local Similarity 31.6%; Pred. No. 8.3e-38; Matches 167; Conservative 102; Mismatches 221; Indels 39;

17;

68 LNQTNIGNNNNKFYIIQLL--EEGSRFFCWNRWGRVG-EVGQSKMNHFTCLEDAKKDFKK 124 125 KFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKVDSGPVRTVVKPCSLDPATQ 184 16 KQRQGTEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQ----VHED----YDCT 67 qq g Ω qq δ

NLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEAMKNPTGDGQSL 244 185 δý Dp

EELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAAPGEEEKVE 304 245 g οy

767 305

Db

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AGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQTEPDPAQD 477 887 ρp g

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------RRLLWHGTNVAVVAAILTS
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, E
Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
 -----SSFSQSEYLIYKESQCRLRYLLEI 526
 496 LETIEEETRLLYDEYVMFNKEHFKIKYVVEV 526
 Cell Biol. 146:917-928(1999).
 SEQUENCE OF 94-1724 FROM N.A.
 ADPRIL1 OR PARPL OR KIAA0177
 DNA Res. 3:17-24(1996).
 [5]
DISCUSSION OF SEQUENCE.
 Homo sapiens (Human)
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 polymerase,
 Mammalia;
 RESULT 15
PPOV_HUMAN
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 24;
 57 GIQVHEDYDCTLNQTNIGNNNNKFYIIQLLEEGSRFFCWNRWGRVGEVGQSKMNHFTCLE 116
 117 DAKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVV-----KVDS 167
 250 CFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVL----ADIELAQTLQAAPGEEEEKVE 304
 ---IYQRLYERLPCHLEPVSE------EIAGKIGDCLAMRGPTHCYKLSLIDA 339
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
 Gaps
 168 GPV----RTVVKPCSLDPATQNLITNIFSKEMFKNAMTL-----MNLDVKKM-----
 EVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQTGNSYRCPNLR---HVWKVN----
 --PLGKLTKQQIARGFEALEALEEAMKNPT---------GDGQSLEELSS
 86; Mismatches 181; Indels 156;
 Length 538;
 Smith A.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: SOME, TO THE MIDDLE PART OF NAD(+) ADP-
RIBOSYLTRANSFERASE (EC 2.4.2.30).
 01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Hypothetical 61.3 kDa protein E02H1.4 in chromosome II.
478 IELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEI
 3144E25465FC7341 CRC64;
 Score 389; DB 1;
Pred. No. 4.1e-21;
 WormPep; E02H1.4; CE01539.
InterPro; IPR001290; PARP.
InterPro; IPR004102; PARP_reg.
Pfam; PF00644; PARP; I.
Pfam; PF02877; PARP_reg; 1.
 61268 MW;
 EMBL; 247075; CAA87379.1; -. HSSP; P26446; 1A26.
 13.9%;
 148; Conservative
 STANDARD;
 Caenorhabditis elegans.
 l protein.
538 AA; (
 Best Local Similarity
 SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
 Hypothetical
SEQUENCE 53
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PPOV_HUMAN STANDARD; PRT; 1724 AA.
09UKK3; 075903; Q9H1M6; Q14682;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
Vault poly(ADP-ribose) polymerase (EC 2.4.2.30) (VPARP) (193-kDa vault protein) (PARP-related/lalphaI-related H5/proline-rich) (PH5P).
 "The nuclear protein PHSP of the inter-alpha-inhibitor superfamily: a missing link between poly(ADP-ribose)polymerase and the inter-alpha-inhibitor family and a novel actor of DNA repair?"; FEBS Lett. 446:6-8(1999).

-!- CATALYTIC ACTIVITY: NAD(+) + {ADP-D-ribosyl}(N)-acceptor = nicotinamide + {ADP-D-ribosyl}(N-acceptor = nicotinaminge + n
 ----IPAFKSN 495
340 FELKDPNEIPTEAPVEVQEVPKKRGRKSTKTAAPTVPPPTTKRLLWHGTRVTNVFSILMN 399
 .
by.
 400 GLOFPVGDRCGLMFGNGVYFANVPTKSANYC----CPEASKRV-FMLLCEVETANPLVLY
 EHHITIDDPSLKSPPPGFDSVIARGQTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKS-
 TISSUE-Bone marrow;
MEDLINE-96281124; PubMed-8724849;
Nagase T., Seki N., Ishikawa K.-I., Tanaka A., Nomura N.;
Prediction of the coding sequences of unidentified human genes.
The coding sequences of 40 new genes (KIAA0161-KIAA0200) deduced analysis of cDNA clones from human cell line KG-I.";
 Euteleostomi;
 MEDLINE-20112770; PubMed-10644454;
Still I.H., Vince P., Cowell J.K.;
"Identification of a novel gene (ADPRTL1) encoding a potential poly(ADP-ribosyl) transferase protein.";
Genomics 62:533-536(1999).
 GLR--IMPHSGGRVGKGIYFASENSKSAGYVTTMHC--GGHQVGYMFLGEVALGK--
 Streuli M., Rome L.H.;
"The 193 kBa vault protein, VPARP, is a novel poly(ADP-ribose)
polymerase.";
 SEQUENCE FROM N.A., AND SEQUENCE OF 306-319.
MEDLINE-99408776; PubMed-10477748;
Kickhoefer V.A., Siva A.C., Kedersha N.L., Inman E.M., Ruland
 MEDLINE-99198702; PubMed-10100603;
Jean L., Risler J.-L., Nagase T., Coulouarn C., Nomura N.,
Salier J.-P.;
 Tromans A.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
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 VWFA.
INTERACTION WITH THE MAJOR VAULT PROTEIN.
NUCLEAR LOCALIZATION SIGNAL IST PART
PROTEINS OF 193 AND 240-kDA.

-!- SUBCELLULAR LOCATION: CYTOPLASMIC, BUT IS ALSO FOUND IN THE NUCLEUS, ASSOCIATED WITH MITOTIC SPINDLES.
-!- TISSUE SPECIFICITY: WIDELY EXPRESSED; THE HIGHEST LEVELS ARE IN THE KIDNEY; ALSO DETECTED IN HEART, PLACENTA, LUNG, LIVER, SKELETAL MUSCLE, SPLEEN, LEGUKOCYTES AND PANCREAS.
-!- SIMILARITY: CONTAINS 1 BRCT DOMAIN.
-!- SIMILARITY: CONTAINS 1 WAFA DOMAIN.
 NUCLEAR LOCALIZATION SIGNAL 2ND PART
 Query Match 9.9%; Score 276.5; DB 1; Length 1724; Best Local Similarity 22.1%; Pred. No. 3.7e-12; Matches 122; Conservative 104; Mismatches 211; Indels 115;
 InterPro; 1PR001357; BRCT.
InterPro; 1PR001357; BRCT.
InterPro; 1PR001290; PARP:
InterPro; 1PR002035; vWFA.
InterPro; 1PR002035; vWFA.
InterPro; 1PR003035; vWFA.
InterPro; 1PR003035; vWFA.
InterPro; 1PR003035; vWFA; 1.
InterPro; 1PR003035; vWA; 1.
InterPro; 1PR003035; vWA; 1.
InterPro; 1PR003035; vWA; 1.
InterPro; 1PR03036; vWA; 1.
InterPro; 1PR03036; vWFA; 1.
InterPro; 1PR003036; vWFA; 1.
InterPro;
 NAD-BINDING (BY SIMILARITY).
 A009F34934460EDC CRC64;
 AND 4).
AND 4).
 2 AND 4).
2 AND 4).
 AND 4).
 REF. 1).
REF. 2 A REF. 1. A REF. 1. A REF. 1).
REF. 1).
REF. 3).
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 AA; 192587 MW;
 EMBL, AF158255; AAD47250.1; --
EMBL, AF057160; AAC62491.1; --
EMBL, AAL359763; CAC21562.1; --
EMBL, D79999; BAA11494.1; --
HSSP; P26446; 1A26.
 1046
1724
25
 1249
 1065
1080
11080
11265
1328
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11550
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345
55 NPGIQVHEDYDCTLNQTNIGNNNNKFYIIQ--LLEEG---SRFFCWNRWGRVGEVGQSKM 109
 249
 229
 304 VKAALKN----GETAEQLQKMMTEFYRLIPHK--GTMPKEVNL-GLLAKKADLCQLIRDM 356
 357 VNVCETNLSKPNP-----PSLAKYRALRCKIEHVEONTEEFLRVRKEVLQNHHSK 406
 401
 464
 ----GRVGKGIYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKS 456
 516
 : : | | :::|| : | ...| | :::|| : | ...| | : | | | :::|| : | | | :::|| : | | :::|| : | | :::|| : | | :::|| : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
 110 NHFTCLEDAKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKVDSGP
 -----BDASEYFENYIEELKKQGFLLREHFTPE-----ATQLASEQLQALL-----
 170 VRTVVKPCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEA
 250 LEEVMNSSTLSQEVSDLVEMIWAEALGHLEHMLLK-----PVNRISLNDVSKAEGILLL
 286 IELAQTLQAAPGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQTGNSY
 RCPNLRHVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGL----RIMPHSG-
 457 PPPGFDSVIARGQTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKES
 230 LEEAMKNPTGDGQSLEELSSC---FYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLAD-
 159 KVGMEGGQEAVVVELQCSRDSRDCPFLISSHFLLDDGMETRRQFAIKKTS----
 517 QCRLRYLLEIHL 528
 | :::|::: : 555 QVKMKYIIKFSM 566
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Search completed: August 29, 2002, 08:02:28 Job time: 305 sec

21;

Gaps

104 PDOKASSSEVKTEGLCPD-SATEEEDTVELTEFGMONVEIPHLPQDFEVAKYNT---LE 158

3 PKRKAS---VQTEGSKKQRQGTEEEDSFRSTAEALRAA----PADNRVIRVDPSCPFSR 54

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Perfect score:

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Scoring table:

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Database

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Q9x27 drosophila
Q9x27 drosophila
Q9vbp3 drosophila
Q9b8r9 homo sapien
Q9694 homo sapien
Q91f15 homo sapien
G91f15 homo sapien
G91f2 cymomonas m
G95721 chilo iride
Q9h2k2 homo sapien
 09ca26 arabidopsis
P93826 arabidopsis
P93826 arabidopsis
09v635 drosophila
09cj19 lactococcus
09h8f2 homo sapien
04y4p7 homo sapien
061595 mus musculu
0954k1 homo sapien
09hcr1 homo sapien
 Ogjkx5 mus musculu
Ogahk7 borrelia bu
 Q9fkn5 arabidopsis
 Q9has4 homo sapien
076518 caenorhabdi
 Q9ahl2 borrelia bu
Q9ahk8 borrelia bu
 PATQNLITNIFSKEMFKNAMTLANLDVKKMPLGKLTKQQIARGFEALEALEEAMKNPTGD 240
 DFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKVDSGPVRTVVKPCSLD 180
 HEDYDCTLNQTNIGNNNNKFYIIQLLEEGSRFFCWNRWGRVGEVGQSKMNHFTCLEDAKK 120
 1 MAPKRKASVQTEGSKKQRQGTEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQV 60
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 59.4 KDA PROTEIN.
HUS musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Mammalia; Eutheria; Rodentla; Sciurognathi; Muridae; Mus.
 09fk91
 99.9%; Score 2785; DB 11; Length 528; 99.8%; Pred. No. 6e-223; 1; Indels 0
 Strausberg R.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BCO14870; AAH14870.1; -. Hypothetical protein. SEQUENCE 528 AA; 59413 MW; 82EFB0C498EB5F74 CRC64;
 Q9H8F2
Q9Y4P7
Q61595
Q9S4K2
 Q9HAS4
O76518
Q9CA26
P93826
Q9V635
Q9CJ19
 Q96RT1
Q9HCR1
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Q9JKX5
 095271
09H8R9
0969W4
09UFI5
050236
055721
 PRT;
 16
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 Query Match 99.9
Best Local Similarity 99.8
Matches 527; Conservative
 PRELIMINARY;
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SEQUENCE FROM N.A.
 131.5
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 024570 zea mays (m
09zsv1 zea mays (m
09n4h4 caenorhabdi
09xua5 caenorhabdi
09txq1 caenorhabdi
 ; Search time 117.38 Seconds
(without alignments)
778.168 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Description
 EYLIYKESQCRLRYLLEIHL
 14.5
Compugen Ltd.
 hits satisfying chosen parameters:
 562222 seqs, 172994929 residues
 GenCore version
Copyright (c) 1993 - 2000
 SUMMARIES
 summaries
 - protein search, using sw model
 August 29, 2002, 08:01:37
 US-09-701-586B-10
2789
1 MAPKRKASVQTEGSKKQRQG...
 0917R6
0956C2
0916C2
0911R2
081294
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sp_fungi:*
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sp_human:*
sp_novertebrate:*
sp_mhc:*
sp_organelle:*
sp_phage:*
sp_plant:*
sp_rodent:*
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seq length: 200000000
 Minimum Match 0%
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Match
 Post-processing:
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2253.5 2253.5 71823.7 7055 691 689 689 681 624 612.5 612.5 584 584 584 584 584

Score

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Result

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PRELIMINARY;
 612 AA;
 NCBI_TaxID=44689;
 SEQUENCE
 Query Match
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 09TX06
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Matches
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 QVHEDYDCTLNQTNIGNNNNKFYIIQLLEEGSRFF-CWNRWGRVGEVGQSKMNHFTCLED 117
 AKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKVDSGPVRTV---V 174
 KNPTGDGQSLEELSSCFYTVIPHNFGRSRPPINSPDVLQAKKDMLLVLADIELAQTLQA 294
 APGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQTGNSYRCPNLRHVW 354
 Gaps
 9
 MAPKRKASVQTEG--SKKQRQGTEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGI 58
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 GOSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAAPGEEE
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 EGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPHSGGRVGKGIYFASENSKSAGY
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 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 ,;
 Length
 ELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEIHL 528
 Indels
 Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC014260; AAH14260.1; -.
 481 ELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEIHL
 Hypothetical protein.
SEQUENCE 533 AA; 60089 MW; 6296A0E439CC7767 CRC64;
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 60.1 KDA PROTEIN.
HOMEO Sapiens (Human).
 4;
 58;
 80.9%; Score 2253.5; DB 4
80.9%; Pred. No. 9.4e-179;
 Mismatches
 TISSUE-PRIMARY B-CELLS FROM TONSILS;
 PRT;
 37;
 Conservative
 PRELIMINARY;
 Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 Best Local Sim
Matches 432;
 Query Match
Best Local 9
 Q96CG2
 7
181
 481
 29
 118
 301
 301
 361
 421
 61
 175
 235
 361
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SEQUENCE FROM N.A.

MEDLINE=96007847; PubWed=7578427;
Auer B., Filex K., Wang Z.Q., Haidacher D., Jager S., Berghammer H.,
Kofler B., Schweiger M., Magner E.F.;
"On the biological role of the nuclear polymerizing NAD+: protein(ADP-
ribosyl) transferase (ADPRT): ADPRT from Dictyostellum discoideum and
inactivation of the ADPRT gene in the mouse.";
Biochimie 77:444-449(1995).
HSSP; P26446; 1A26
 419
 474
 231
 291
 407
 --YDCTLNQTVIGNNNNKFYIIQLLE--EGSRFFCWNRWGRVGEVGQSKMNHF--TCLED 117
 118 AKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQE---AVVKVDSGPVRTVV 174
 147 DVYDATLNQTEISQNNNKXYIIQLLEADDGSSYSVWNRWGREGLKGQSSRKDFGKGGLNQ
 175 ---KPCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALE
 267 EHKKECSLDERVQELVKLIFDVKMMERTMTEAKYDLKKMPLGKLSKNQITKGYLVLKQIE
 6 KASVQTEGSKKQRQGTEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQVHED--
 EAMKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQT
 LQAAPGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQTGNSYRCPNLR
 SKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQTEPDP
 HVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKG
 475 AQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEIHL
 480 TQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYLIYQESQCRLRYLLEVHL
 Length 612;
 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NAD+:PROTEIN(ADP-RIBOSYL)-TRANSFERASE (EC 2.4.2.30).
 Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
 CB340F7A88FF2364
 ;; Score 823; DB 5;
;; Pred. No. 9.9e-60;
79; Mismatches 204
 612
 PRT;
 7; PARP_reg; 1.
12 AA; 69241 MW;
 InterPro; IPR001290; PARP.
InterPro; IPR004102; PARP_reg.
Pfam; PF00644; PARP; I.
Pfam; PF02877; PARP_reg; 1.
 29.5%;
38.4%;
 Local Similarity 38.4% les 209; Conservative
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1 MAPKRKASVQTEGSKKQRQGTEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQV 60
 QTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEIH 527
 VNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKGIYFA
 SENSKSAGYVTTMHCGGHQV---GYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARG
 Mus musculús (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
 61 HEDYDCTLNQTNIGNNNNKFYIIQLLEEG--SRFFCWNRWGRVGEV-GQSKMNHFTCLED
 AKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKVDSGPVRTVVKP-
 177 -- CSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEAM
 235 KNPTGDGOSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQA
 APGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQ----TGNSYRCPNL
 GIYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIA
 RGQTEPDPAQDIELELDGQPVVVPQGPPVQCPS-FKSSSFSQSEYLIYKESQCRLRYLLE
 780 GGSDDSSK-----DPIDVNYEKLKTDIKVVDRDSEEAEVIRKYVKNTHATTHNAYDL-EV
 RHVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGK
 Ouery Match 25.3%; Score 705; DB 11; Length 1014; Best Local Similarity 33.6%; Pred. No. 1.4e-49; Matches 182; Conservative 101; Mismatches 214; Indels 44
 SDCE68E4CB3F46EB CRC64;
 Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012041; AAH12041.1;
Transferase.
SEQUENCE 1014 AA; 112721 MW; 5DCE68E4CB3F46EB CRC64;
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 SEQUENCE FROM N.A.
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 FKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQ-GEAESQEAVVKVDSGPVRTVVKPCSLD 180
 DCTLNQTNIGNNNNKFYIIQLLEE--GSRFFCWNRWGRVGEVGQSKMNHFTCLED-AKKD 121
 Gaps
 13 GSKKOROGTEEEDSFRS----TAEALRAAPADNRV---IRVDPSCPFSRNPGIQVHED-Y 64
 PATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEAMKNPTGD
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 EEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQT---GNSYRCPNLRHVWK
IYFASENSKSAGYVTTMHCGGHQVGY-MFLGEVALGKEHHITID---DPSLKSPPPGFDS
 464 VIARGQTEPDPAQDIELELDGQPVVVPQGPPVQCPS-FKSSSFSQSEYLIYKESQCRLRY
 53;
 Length 653;
 91; Mismatches 205; Indels
 5FD01923C4ABCD1D CRC64;
 01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
POLY(ADP-RIBOSE) POLYMERASE.
 DB 10;
 Score 719.5; DB 1
Pred. No. 4.4e-51;
 653 AA
 PRT;
 InterPro; IPR001290; PARP.
InterPro; IPR001290; PARP_reg.
InterPro; IPR003034; SAP.
Ffam; PF00644; PARP_i.
Pfam; PF02877; PARP_reg; 1.
Pfam; PF020377; PARP_reg; 1.
SMART; SM00513; SAP; 2.
SEQUENCE 653 AA; 72995 MW; SF
 25.8%;
 Matches 190; Conservative
 PRELIMINARY;
 Similarity
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SEQUENCE FROM N.A.
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LEQL 610
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MEDLINE=96007847; PubMed=7578427;
Auer B., Filck K., Wang Z.Q., Haidacher D., Jager S., Berghammer H.,
Kofler B., Schweiger M., Wagner E.F.;
"On the biological role of the nuclear polymerizing NAD+: protein(ADP-
ribosyl, transferase (ADPRT): ADPRT from Dictyostellum discoideum and
inactivation of the ADPRT gene in the mouse.";
Biochimie 77:444-449(1995).
HSSP: P26446; IAZ6.
 282 PEQSKLDTRVAKFISLICUVS#MAQHWEIGYNANKLPLGKISKSTISKGYEVLKRISEV 341
 234 MKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPP--INSPDVLQAKKDMLLVLADIELA-Q 290
 : | ||||| ||||||||||||| 342 IDR--YDRTRLEELSGEFYTYIPHDFGFKKMSQFVIDTPQKLKQKIEMVEALGEIELATK 399
 453 VEIAQLFRASRAVEADRFQQFSSSKNRMLLWHGSRLTNWAGILSQGLRIAPPEAPVTGYM 512
 FDSVIARGOTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEXLIYKESQCRL 520
 EDAKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKVDSGPVRTVVK 175
 348 PNLRHVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGR 403
 404 VGKGIYFASENSKSAGYVTTMHC---GGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPG 460
 513 FGKGVYFADMFSKSANY-----CYANTGANDGVLLLCEVALGDMNELLYSDYNADNLPPG 567
 : |:::: | |: || :: | |: || 3 || || 3 || || 3 || || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 ||
 222 DRAIEIFTNKFNDKTKNYWSDRKEFIPHPKSYTWLEMDYGKEENDSPVNNDIPSSSEVK 281
 291 TLQAAPGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQT---GNSYRC 347
 Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 RKASVQTEGSKKQRQG-TEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQVHED 63
 176 P--CSLDPATONLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEA
 24.7%; Score 689; DB 13; Length 6
33.9%; Pred. No. 1.4e-48;
ive 97; Mismatches 205; Indels
 68033 MW; 75F6EE1D30D8F402 CRC64;
 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NAD+:PROTEIN(ADP-RIBOSYL)-TRANSFERASE, ADPRT.
 607 AA
 InterPro; IPR004102; PARP_reg
 Pfam; PF00533; BRCT; 1.
Pfam; PF00644; PARP; 1.
Pfam; PF02877; PARP_reg; 1.
PROSITE; PS50172; BRCT; 1.
 Query Match
Best Local Similarity 33.99
Matches 184; Conservative
 InterPro; IPR001357; BRCT
InterPro; IPR001290; PARP
 PRELIMINARY;
 607 AA;
 NCBI_TaxID=9031;
 521 RYLLEI 526
 624 RYVIQV 629
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951 LGKTTPDPSASITLE----GVEVPLGTGI--PSGVNDTCLLYNEYIVYDIAQVNLKYLLK 1004
 01-NOY-1998 (TrEMBLrel. 08, Created)
01-NOY-1998 (TrEMBLrel. 08, Last sequence update)
01-NOY-1998 (TrEMBLrel. 19, Last annotation update)
101-DCC-2001 (TrEMBLrel. 19, Last annotation update)
114P8.19 PROTEIN (NAD+ ADP-RIBOSYLTRANSFERASE).
114PB.19 OR AT4G02390.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae, Arabidopsis.
 60 VHED-YDCTLNQTNIGNNNNKFYIIQLLEEGSR--FFCWNRWGRVGEVGQSKMN-HFTCL 115
 Gaps
 2 APKRKASVQTEGSKKQRQTEEEDSFRS--TAEALRAAPADNRVIRVDPSCPFSRNPGIQ 59
 ; Score 691; DB 10; Length 635;
; Pred. No. 9.9e-49;
91; Mismatches 220; Indels 46;
 Lamar B., Stoneking T., Stumpf J., Mewes H.W., Lemcke K. Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 [2]
SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
Kalicki J., Eliott G., Cloud J.;
"The sequence of A. thaliana T14P8.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
 "The A. thaliana Genome Sequencing Project.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
 EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF069293 AAC12283.1;
EMBL; AL161494; CAB80732.1; -.
 to the EMBL/GenBank/DDBJ databases
 E3F1CBE4D367A377 CRC64;
 635 AA.
 PRT;
 635 AA; 72017 MW;
 InterPro; IPR001290; PARP.
InterPro; IPR004102; PARP_reg.
InterPro; IPR003034; SAP.
 24.8%;
34.6%;
 PF02877; PARP_reg; 1. PF02037; SAP; 2.
 Query Match
Best Local Similarity 34.6%
Matches 189; Conservative
 PRELIMINARY;
 Pfam; PF00644; PARP; 1.
 SMART; SM00513; SAP; 2.
 Submitted (MAY-1998)
 SEQUENCE FROM N.A. STRAIN=CV. COLUMBIA;
 SEQUENCE FROM N.A. STRAIN-CV. COLUMBIA;
 HSSP; P26446; 1A26
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=3702;
 Waterston R.;
 Transferase.
SEQUENCE 6:
 1005 L 1005
 526 I 526
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Gaps

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Length 607;

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18;

Gaps

42;

215; Indels

Mismatches

95;

Conservative

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178;
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 Q92P54
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 MEDLINE-96007847; PubMed-7578427;
Auer B., Flick K., Wang Z.Q., Haidacher D., Jager S., Berghammer H.,
Kofler B., Schweiger M., Wagner E.F.;
"On the biological role of the nuclear polymerizing NAD+: protein(ADP-
ribosyl) transferase (ADPRT): ADPRT from Dictyostelium discoideum and
inactivation of the ADPRT gene in the mouse.";
Blochimie 77:444-449(1995).
InterPro; IPR001357; BRCT.
 64 YDCTLNQTNIGNNNNKFYIIQLLEEG--SRFFCWNRWGRVGEV-GQSKMNHFTCLEDAKK 120
 355 KVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKGIYF 410
 464
 299 EEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQ----TGNSYRCPNLRHVW 354
 465 IARGQTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLL 524
 DFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVK--VDSGPVRTVVKPCS
 LDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEAMKNPT
 |:|| || || || :::|||||| || 262 ----IQDLIKWIFDVESMKKAMVEFEIDLQKMPLGKLSKRQIQSAYSILNEVQQAVSDGG
 411 ASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEH-----HITIDDPSLKSPPPGFDSV
 GDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAAPGE
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae.
 Pfam; PF02877; PARP_reg; 1.
PROSITE; PS50172; BRCT; 1.
SEQUENCE 607 AA; 67496 MW; 54CDEBBE22079886 CRC64;
 01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEZ-2001 (TrEMBLrel. 19, Last annotation update)
NAD+:PROTEIN(ADP-RIBOSYL)-TRANSFERASE, ADPRT.
 607 AA
 PRT;
 InterPro; IPR001290; PARP.
InterPro; IPR004102; PARP_reg.
 PRELIMINARY;
 Pfam; PF00533; BRCT; 1.
 Pfam; PF00644; PARP; 1.
 SEQUENCE FROM N.A.
 NCBI_TaxID-8353;
 525 EI 526
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 Xenopus.
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Length 607;

Score 681; DB 13; Pred. No. 6.3e-48;

24.4%;

Query Match Best Local Similarity

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21;
 ---DPIDVKYEKIKTDIKVVAKDSEESRIICDYVKNTHADTHNAYDLEVL-EIFKIDREG 435
 | |:: :| ||:||||| |:
EYQRYKPFKQLHNRQLLWHGSRTTNFAGILSQGLRIAPPEAPVTGYMFGKGIYFADMVSK 495
 263 ELIKLIFDVESMKKAMVEFEIDLQKMPLGKLSKRQIQSAYSILSQVQQAVSESLSEARLL 322
 305 EVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLK----QTGNSYRCPNLRHVWKVNREG 360
 EGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKGIYFASENSK 416
 SAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQTEPDPAQ 476
 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Erassicales; Brassicaceae; Arabidopsis.
 NQTNIGNNNNKFYIIQLLE--EGSRFFCWNRWGRVGEV-GOSKMNHFTCLEDAKKDFKKK 125
 FWEKTKNKWEERDRFVAQPNKYTLIEVQ-GEAESQEAVVKVDSGPVRTVVKPCSLDPATQ 184
 NLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEAMKNPTGDGQSL 244
 245 EELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAAPGEEEEKVE 304
 |||||: :: |:||:| |: |KRQRKILPFDKYKIEDTSESLVTVKVKGRSAVHEAS-----GLQEHCHILEDGNSIYNT 524
 Gaps
QTEGSKKQRQGT-EEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQVHEDYDCTL 68
 15 KKQRQGTEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQVH----FD----YDC 66
 210 YODKTGNAMHS-PNFTKYPKKFYPLEIDYGQEEDVVKKLSVGAGTKSKLAKP-----VQ
 68;
 22.4%; Score 624; DB 10; Length 983; 33.0%; Pred. No. 7.2e-43;
 DIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEI 526
 Transferase, Glycosyltransferase, NAD.
CHAIN 2 983
POLY(ADP-RIBOSE) POLYMERASE.
SEQUENCE 983 AA; 111232 MW; 468E12A8EF1B6F4F CRC64;
 209; Indels
 Doucet-chabeaud G., Kazmaier M.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AJ131705; CAA10482.1; -.
 01-MAY-1999 (TrEMBLrel. 10, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
10-DEC-2001 (TrEMBLrel. 19, Last annotation update)
POLY(ADP-RIBOSE) POLYMERASE (EC 2.4.2.30).
 87; Mismatches
 983
 PRT;
 SEQUENCE FROM N.A.
STRAIN=CV. LANDSBERG ERECTA;
 Best Local Similarity 33.03
Matches 179; Conservative
 PRELIMINARY;
 1A26.
 NCBI_TaxID=3702;
 P26446;
 Query Match
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InterPro;
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 STRAIN-CV. COLUMBIA;
MEDLINE-20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Luin X., Mason T.M., Bowman C.L., Barnstead M.E., Feldhlyum T.V.,
Buell C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldhlyum T.V.,
Buell C.Y., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronlin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
 348
 636
 235
 801
 403
 463
 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 180 DPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEAL----EALEEAMK
 236 NPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAA
 NLRHVWKVNREGEGDRFQAH-SKLGNRRLLWHGTNVAVVAAILTSGLRI-----MPHSGGR
 104 VGKGIYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDS
 TLNQTNIGNNNNKFYIIQLLEE--GSRFFCWNRWGRVG--EVGQSKMNHFTCLEDAKKDF
 123 KKKFWEKTKN---KWEERDRFVAQPNKYTLIEVQGEAESQEAVVKVDSGPVRTVVKPCSL
 296 PGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQTGNSYRCP-----
 VIARGOTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYL
 EMBL/GenBank/DDBJ databases.
 Last sequence update)
Last annotation update)
 PRT; 1009 AA
 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seque
01-DEC-2001 (TrEMBLrel. 19, Last annot
PUTATIVE POLY (ADP-RIBOSE) POLYMERASE.
 Submitted (MAR-2000) to the BEMBL; AC006593; AAD20677.1; HSSP; P26446; 1A26.
 InterPro; IPR001357; BRCT.
 PRELIMINARY;
 Nature 402:761-768(1999)
 SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
 SEQUENCE FROM N.A.
 NCBI_TaxID=3702;
 524 LEI 526
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21;
 723 QPTMKESLLVDASNRFFTMIP----SIHPHIIRDEDDFKSKVKMLEALQDIEIASRI--- 775
 01-MAY-2000 (TERMELTE). 13, Last sequence update)
01-DEC-2001 (TERMELTE). 19, Last annotation update)
NAD+:PROTEIN(ADP-RIBOSYL)-TRANSFERASE, ADPRT.
Drosophila sp. (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
 827
 463
 464 VIARGQTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYL 523
 498 KKORKLPFDKYKIEDTSESLVTVKVKGRSAVHEAS-----GLOEHCHILEDGNSIYNT 550
 TLNQTNIGNNNNKFYIIQLLEE--GSRFFCWNRWGRVG--EVGQSKMNHFTCLEDAKKDF 122
 KKKFWEKTKN -- - KWEERDRFVAQPNKYTLIEVQGEAESQEAVVKVDSGPVRTVVKPCSL 179
 DPATONLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEAL----EALEEAMK 235
 349 NLRHVWKVNREGEGDRFQAH-SKLGNRRLLWHGTNVAVVAAILTSGLRI----MPHSGGR 403
 Gaps
 15 KKQRQGTEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQVH----ED----YDC 66
 ELEEVFALEREGEFDKYAPHREKLGNKMLLWHGSRLTNFVGILNQGLRIAPPEAPATGYM
 TLSMSDLSTGINSYYILQIIQEDKGSDCYVFRKWGRVGNEKIGGNKVEEMS-KSDAVHEF
 776 VGFDVDSTES----LDDKYKKLHCDISPLPHDSEDYRLIEKYL----NTTHAPTHTEWSL
 236 NPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAA
 404 VGKGIYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDS
 PGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQTGNSYRCP-----
 68;
 Length 1009;
 22.4%; Score 624; DB 10; Length 1 33.0%; Pred. No. 7.5e-43; ive 87; Mismatches 209; Indels
 SMART; SM00292; BRCT; 1.
PROSITE; PS50172; BRCT; 1.
PROSITE; PS50064; PARP_IN_FINGER_2; 2.
SEQUENCE 1009 As: 114133 MW; CDE6E41CC2A3A2DB CRC64;
 Created)
 PRT;
 Pfam; PF00533; BRCT; 1.
Pfam; PF00644; PARP; 1.
Pfam; PF02877; PARP_reg; 1.
Pfam; PF00645; zf-PARP; 2.
ProDom; PD004675; znf-PARP; 2.
SMART; SM00292; BRCT; 1.
PARP_reg.
Znf-PARP.
 01-MAY-2000 (TrEMBLrel. 13,
 Query Match 22.49
Best Local Similarity 33.09
Matches 179; Conservative
 PRELIMINARY;
 IPR004102;
 IPR001510;
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1001 LKV 1003
 524 LEI 526
 interPro;
 09TX05;
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138 DRFVAQPNKYTLIEVQGEAESQEAVVKVDSGPVRTVVK--PCSLDPATQNLITNIFSKEM 195
 419 GYVTTMHC---GGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQTEPDPA 475
 468 ALESSKGSTVIVKVKGRSAVHESSGLØDTAHILEDGKSIXNATLNMSDLALGVNSYYVLØ 527
 85 LLE--EGSRFFCWNRWGRVG--EVGQSKMNHFTCLEDAKKDFKKKFWEKTKNKWEE---R 137
 33 ALRAAPADNRVIRVDPSCPFSRNPGIQ----VHED----YDCTLNQTNIGNNNKFYIIQ 84
 196 FKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEAMKNPTGDGQSLEE----LSSC
 698 FFTLIP----SIHPHIIRDEDDLMIKAKMLEALQDIEIASKIVGFDSDSDES-----L
 SO3 KYSRYKNNLHNKMLLWHGSRLTNFVGILSQGLRIAPPEAPVTGYMFGKGLYFADLVSKSA
 863 QY-----CYVDRNNPVGLMLLSEVALGDMYELK-KATSMDRPPRGKHSTKGLGKTVPLES
 587 TNFRKQPGRFYPLDVD-----YGVKKAPKRKDISEMKSSLAPQLLELMKMLFNVET
 FYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAAPGEEEEKVEEVPHPL
 DRDYQLLRCQLQLLDSGESEYKAIQTYLKQTGNSYRCP-----NLRHVWKVNREGEGD
 364 RFQAH-SKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKGIYFASENSKSA
 476 QDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEI 526
 EFVKWRDD----VVVPCGKPVP-SSIRSSELMYNEYIVYNTSQVKMQFLLKV 963
 Length 969;
 SEQUENCE FROM N.A.
Bablychuk E., Cottrill P., Storozhenko S., Fuangthong M.,
O'Farrell M., Van Montagu M., Inze D., Kushnir S.;
"Higher plants possess two poly(ADP-ribose) polymerases.";
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ222589; CAA10889.1; -.
 94; Mismatches 201; Indels
 PROSITE; PS50172; BRCT; 1.
PROSITE; PS50064; PARP_XN_FINGER_2; 2.
SEQUENCE 969 AA; 109128 MW; EB23AC62EEC14009 CRC64;
 Created)
Last sequence update)
Last annotation update)
 20.9%; Score 584; DB 10; 30.9%; Pred. No. 1.5e-39;
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InterPro; IPR003034; SAP_
InterPro; IPR001510; Znf-PARP.
Pfam; PF00533; BRCT; 1.
Pfam; PF00644; PARP; 1.
Pfam; PF00645; Zf-PARP; 2.
ProDom; PD004675; Znf-PARP; 2.
SWART; SM00292; BRCT; 1.
 (TrEMBLrel. 10, C (TrEMBLrel. 10, I (TrEMBLrel. 19, I
 InterPro; IPR001357; BRCT
InterPro; IPR001290; PARP
 Matches 164; Conservative
 PRELIMINARY;
 Best Local Similarity
 HSSP; P26446; 1A26.
 NCBI_TaxID-4577;
 Q9ZSV1;
Q9ZSV1;
01-MAY-1999 (
01-MAY-1999 (
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 Query Match
 RESULT 13
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SEQUENCE FROM N.A.

MEDLINE-96007847; PubMed-7578427;

Auer B., Flick K., Wang Z.Q., Haidacher D., Jager S., Berghammer H.,

Kofler B., Schweiger M., Wagner E.F.;

"On the biological role of the nuclear polymerizing NAD+: protein(ADP-
ribosyl) transferase (ADPRT): ADPRT from Dictyostellum discoideum and
lnactivation of the ADPRT gene in the mouse.";

HSSP; P26446; 1A26.

InterPro; IPR001290; PARP.

InterPro; IPR001290; PARP.
 Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
 KSRIPKETTKSLNSNSIYTKSMPV-SRTFKVKDGLAVDPDSGLEDIAHVYVDSNNKYSVV 138
 : :: |||:||||| | | : :: || ||:||:| : : | | |
311 IDAINRFYTLIPHNEGVQLPTLIETHQQIEDLRQMLDSLAEIEVAXSI----IKSEDVS 365
 : :||| | :: || || |: |: || || DACNPLDNHYAQIKTQLVALDKNSEEFSILSQYVKNTHASTHKSYDLKIVDVFKVSRQGE 425
 LNQTNIGNNNNKFYIIQLL -- EEGSRFFCWNRWGRVG-EVGQSKMNHFTCLEDAKKDFKK 124
 245 EELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAAPGEEEEKVE 304
 305 EVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQT-GNSYRCPNLR--HVWKVNREGE 361
 GDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRI----MPHSGGRVGKGIYFASENSKS 417
 AGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQTEPDPAQD 477
 486 ANYCCTSQ--QNSTGLMLLSEVALGDMMECT-SAKYINKLSNNKHSCFGRGRTMPDPTKS 542
 KFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKVDSGPVRTVVKPCSLDPATQ 184
 39; Gaps
 KQRQGTEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQ----VHED----YDCT 67
 NLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEAMKNPTGDGQSL
 Query Match 22.0%; Score 612.5; DB 5; Length 593; Best Local Similarity 31.4%; Pred. No. 3e-42; Matches 166; Conservative 102; Mismatches 222; Indels 39
 478 IELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEI 526
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 D9BA37E38B8E7CCD CRC64;
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Last annotation update)
 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last anno
 PRT;
 Pfam; PF00533; BRCT; 1.
Pfam; PF00644; PARP; 1.
Pfam; PF02877; PARP-reg; 1.
PROSITE; PS550172; BRCT; 1.
SEQUENCE 593 AA; 68018 MW;
 POLY (ADP-RIBOSE) POLYMERASE
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 MEDILINE=99026291; PubMed=9808734;
Mahajan P.B., Zuo Z.;
"Purification and cDNA cloning of maize Poly(ADP)-ribose polymerase.";
Plant Physiol. 118:895-905(1998).
EMBL: AF093627; AAC79704.1; -.
HSSP; P26446; 1A26.
 Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
 648
 757
 758 DDKYMKLHCDITPLAHDSEDYKLIEQYLLNT---HAPTHKDWSLELEEVFSLDRDGELN 813
 85 LLE--EGSRFFCWNRWGRVG--EVGQSKMNHFTCLEDAKKDFKKKFWEKTKNKWEE---R 137
 DRFVAQPNKYTLIEVQGEAESQEAVVKVDSGPVRTVVK--PCSLDPATQNLITNIFSKEM 195
 FYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAAPGEEEEKVEEVPHPL 310
 DRDYQLLRCQLQLLDSGESEYKAIQTYLKQTGNSYRCP-----NLRHVWKVNREGEGD 363
 364 RFQAH-SKLGNRRLLWHGINVAVVAAILTSGLRIMPH----SGGRVGKGIYFASENSKSA 418
 419 GYVTTMHC---GGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQTEPDPA 475
 874 QY-----CYVDRNNPVGLMLLSEVALGDMYELK-KATSMDKPPRGKHSTKGLGKTVPLES 927
 33 ALRAAPADNRVIRVDPSCPFSRNPGIQ----VHED----YDCTLNQTNIGNNNKFYIIQ 84
 FKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEEALEEAMKNPTGDGQSLEE----LSSC
 709 FFTLIP----SIHPHIIRDEDDLMIKAKMLEALQDIEIASKIVGFDSDSDES-----L
 598 TNFRKQPGRFYPLDVD-----YGVKKAPKRKDISEMKSSLAPQLLELMKMLFNVET
 72;
 476 QDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEI 526
 Length 980;
 : :: | |||| | || | ::::|| :: | :::|| :: | ::::||:: | EFVKWRDD---VVVPCGKPVP-SSIRSSELMYNEYIVYNTSQVKMQFLLKV
 Indels
 Transferase; Glycosyltransferase.
SEQUENCE 980 AA; 110475 MW; 9D8AED26BC37E5C1 CRC64;
 94; Mismatches 201;
 20.9%; Score 584; DB 10; 30.9%; Pred. No. 1.5e-39;
POLY(ADP)-RIBOSE POLYMERASE (EC 2.4.2.30)
 Pfam; PF02877; PARP_reg; 1.
Pfam; PF00645; zf-PARP; 2.
ProDom; PD00457; znf-PARP; 2.
SMART; SM0292; BRCT; 1.
PROSITE; PS50172; BRCT; 1.
PROSITE; PS50064; PARP_ZN_FINGER_2; 2.
 Panicoideae; Andropogoneae; Zea
 InterPro; IPR004102; PARP_reg.
InterPro; IPR003034; SAP.
InterPro; IPR001510; Znf-PARP.
 Best_Local Similarity 30.9%
Matches 164; Conservative
 InterPro; IPR001357; BRCT
 InterPro; IPR001290; PARP.
 PF00644; PARP;
 Pfam; PF00533; BRCT;
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64 YDCTLNQTNIGNNNNKFYIIQLLEEGSR--FFCWNRWGRVG-EVGQSKMNHFTCLEDAKK 120
 181 PATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEAMKNPTGD 240
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 121 DFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKVDSGPVRTVVKPCSLD 180
 EKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQT-GNSYRCP-NLRHVWKVNR 358
 EGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKGIYFASEN 414
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
 Gaps
 48;
 "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
 Length 945;
 202; Indels
 Bradshaw-Cordum H., Scott K., Graves T.;
"The sequence of C. elegans cosmid Y71F9AL.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 EMBL/GenBank/DDBJ databases
 Hypothetical protein.
SEQUENCE 945 AA; 108006 MW; 1D0A62C954BC6AD9 CRC64;
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Last annotation update)
 20.7%; Score 576; DB 5; 31.8%; Pred. No. 6.6e-39; iive 83; Mismatches 202;
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 SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
 01-0CT-2000 (TrEMBLrel. 15, Cre 01-0CT-2000 (TrEMBLrel. 15, Las 01-0CT-2001 (TrEMBLrel. 19, Las HYPOTHETICAL 108.0 KDA PROTEIN
 InterPro; IPR001290; PARP.
InterPro; IPR001510; Znf-PARP.
 "Direct Submission.";
Submitted (SEP-2001) to the
EMBL; AC024200; AAF36011.1;
HSSP; P26446; 1A26.
 Matches 155; Conservative
 PRELIMINARY;
 Caenorhabditis elegans
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
 STRAIN-BRISTOL N2;
 SEQUENCE FROM N.A.
 NCBI_TaxID=6239;
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13;
415 SKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITID-DPSLKSPPPGFDSVIARGQ---- 469
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 885 EIGSYNHPDGYTIPLGLTYMQLQGKQDV------DYHLLYNEFIVYDVDQIQL 931
 EEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQT-GNSYRCP-NLRHVWK 355
 FWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKVDSGPVRTVVKPCSLDPATQN 185
 186 L-----ITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEAMKNP 237
 238 TGDGQSLEELSSCFYTVIPHNFGRSRPPINSPDVLQAKKDMLLVLADIELAQTLQAAPG 297
 VNREGEGDREQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKGIYFA 411
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
 17.2%; Score 481; DB 5; Length 727; 11arity 30.0%; Pred. No. 3.5e;31; Conservative 68; Mismatches 165; Indels
 none;
"Genome sequence of the nematode C.elegans: A platform for
 [1]
SEQUENCE FROM N.A.
McMurray A.A.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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SEQUENCE FROM N.A.
MEDLINE-99069613; Pubmed-9851916;
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PARP; poly(ADP-ribose) polymerase; human; murine; detection; sepsis; diagnosis; therapy; necrosis; apoptosis; neurodegenerative illness; ischemic tissue damage; PARP1.
 Novel genes and proteins, antibodies and binding partners useful in diagnosis and therapy of energy deficiency associated disease
 Otterbach B, Lubisch W,
 ALIGNMENTS
 Murine PARP1 (short) homologue protein.
 AAY68840
AAU20129
AAU21810
 AAY49939
AAU29020
AAY68835
AAB93513
ABB66431
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AAY68833
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AAY51174
AAB11480
 AAB42909
AAU29023
AAB47029
 AAY54373
AAB51022
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 ABB60894
 AAB66297
 AAY51178 standard; Protein; 528 AA
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 99WO-EP03889
 98DE-1025213.
99DE-1008837.
 Kroeger
 (first entry)
WPI; 2000-087218/07.
N-PSDB; AAZ44291.
 Kock M, Hoeger T,
(BADI) BASF AG.
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 04-JUN-1999;
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1 MAPKRKASVQTEGSKKQRQG......EYLIYKESQCRLRYLLEIHL
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Copyright (c) 1993 - 2000 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 747574 segs, 111073796 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 AAY51178
AAY51177
 AAV51176
AAV29021
AAY68834
AAR99642
AAU29022
AAY58043
AAU29019
AAU29019

 protein search, using sw model

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 polymerase (PARP) homologues, which are characterised by an amino acid sequence with a functional NAD^+-binding site and no zinc finger sequence motif, of general formula CX_ZCX_ZMMX_ZC (I). The nucleic acid sequences motif, of general formula CX_ZCX_ZMMX_ZC (I). The nucleic acid detection of PARP homologues and antibodies are useful for analytic detection of PARP homologues and for identifying PARP effectors or binding partners, as well as for determining their effectiveness. PARP-binding partners are useful for the diagnosis or therapy of a disease condition, which is the result of a PARP protein, especially an energy deficiency, which may comprise tissue damage from cell death following necrosis or apoptosis. The disease condition may be chosen from a neurodegenerative illness, or sepsis or ischemic tissue damage, in particular neurotoxic disturbances, etc. This sequence represents the murine PARPI protein used in the method of the invention.
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 HEDYDCTLNQTNIGNNNNKFYIIQLLEEGSRFFCWNRWGRVGEVGQSKMNHFTCLEDAKK 120
 61 hedydctlnqtnignnnnkfyiiqlleegsrffcwnrwgrygeyggskmnhftcledakk 120
 240
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 GQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAAPGEEE 300
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 EKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQTGNSYRCPNLRHVWKVNREG
 MAPKRKASVQTEGSKKQRQGTEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQV
 DFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKVDSGPVRTVVKPCSLD
 PATONLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKOQIARGFEALEALEEAMKNPTGD
 EGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPHSGGRVGKGIYFASENSKSAGY
 VTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQTEPDPAQDIEL
 This invention describes novel human and murine poly(ADP-ribose)
 ;
0
 100.0%; Score 2789; DB 21; Length 528; 100.0%; Pred. No. 4.3e-239;
 481 ELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEIHL 528
 ; Pred. No. 4.
 Murine PARP1 (long) homologue protein.
 Claim 4; Page 71-73; 96pp; German
 AAY51177 standard; Protein; 533
 (first entry)
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nes 528; Conserv
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conditions
 AAY51177;
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This invention describes novel human and murine poly(ADP-ribose) polymerase (PARP) homologues, which are characterised by an amino acid sequence with a functional NAD⁺+-binding site and no zinc finger sequence motif, of general formula CX_2CX_2NHX_2C (I). The nucleic acid detection of PARP homologues and antibodies are useful for analytic detection of PARP homologues and for identifying pARP effectors or binding partners, as well as for determining their effectiveness. PARP-binding partners are useful for the diagnosis or therapy of a disease condition, which is the result of a PARP protein, especially an energy deficiency, which may comprise tissue damage from cell death following necrosis or apoptosis. The disease condition may be chosen from a neurodegenerative illness, or sepsis or ischemic tissue damage, in particular neurotoxic disturbances, etc. This sequence represents the murine PARPI protein used in the method of the invention.
 DFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVK-----VDSGPVRTVVK 175
 121 dfkkkfwektknkweerdrfvagpnkytlievggeaesgeavvkalspgvdsgpvrtvvk 180
 9
 9
PARP; poly(ADP-ribose) polymerase; human; murine; detection; sepsis; diagnosis; therapy; necrosis; apoptosis; neurodegenerative illness; ischemic tissue damage; PARP1.
 Gaps
 proteins, antibodies and binding partners useful in
 Lemaire
 1 MAPKRKASVQTEGSKKQRQGTEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQV
 PCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEAMK
 nptgdgqsleelsscfytviphnfgrsrpppinspdvlqakkdmllvladielaqtlqaa
 NPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAA
 PGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQTGNSYRCPNLRHVWK
 DB 21; Length 533;
 5
 Novel genes and proteins, antibodies and binding partners used diagnosis and therapy of energy deficiency associated disease
 Lubisch W,
 Score 2776.5; DB 21
Pred. No. 5.7e-238;
0; Mismatches 0;
 Otterbach B,
 Claim 4; Page 67-69; 96pp; German.
 Kroeger B,
 99.68;
 98DE-1025213.
99DE-1008837.
 Matches 528; Conservative
 Kock M, Hoeger T,
 WPI; 2000-087218/07
 Local Similarity
 533 AA;
 N-PSDB; AAZ44290
 (BADI) BASF AG.
 WO9964572-A2
 04-JUN-1999;
 01-MAR-1999;
 16-DEC-1999
 conditions
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240

294 300 354 414 419 474 479

117 120

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AKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKVDSGPVRTV---V 174
 MAPKRKASVQTEG--SKKQRQGTEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGI
 QVHEDYDCTLNQTNIGNNNNKFYIIQLLEEGSRFF-CWNRWGRVGEVGOSKMNHFTCLED
 175 KPCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEAM
 KNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQA
 295 APGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQTGNSYRCPNLRHVW
 KVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPHSGGRVGKGIYFASEN
 SKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQTEPDP
 475 AQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEIHL 528
 W09964572-A2
 Homo sapiens
 04-JUN-1999;
 (BADI) BASF
 01-MAR-1999;
 05-JUN-1998;
 31-MAR-2000
 16-DEC-1999
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 118
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 This invention describes novel human and murine poly(ADP-ribose)
polymerase (PARP) homologues, which are characterised by an amino acid
sequence with a functional NAD⁺-binding site and no zinc finger
sequence motif, of general formula CX_2CX_ZMHX_2C (I). The nucleic acid
sequences, PARP homologues and antibodies are useful for analytic
detection of PARP homologues and for identifying PARP effectors or
binding partners, as well as for determining their effectiveness.
PARP-binding partners are useful for the diagnosis or therapy of a
disease condition, which is the result of a PARP protein, especially an
energy deficiency, which may comprise tissue damage from cell death
following necrosis or apoptosis. The disease condition may be chosen
from a neurodegenerative lilhess, or sepsis or ischemic tissue damage,
in particular neurotoxic disturbances, etc. This sequence represents the
human PARP3 protein used in the method of the invention.
 415
 475
 480
 PARP; poly(ADP-ribose) polymerase; human; murine; detection; sepsis; diagnosis; therapy; necrosis; apoptosis; neurodegenerative illness; ischemic tissue damage; PARP3.
 Η;
 in
 VNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPHSGGRVGKGIYFASENS
 KSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQTEPDPA
 Lemaire
 Novel genes and proteins, antibodies and binding partners useful diagnosis and therapy of energy deficiency associated disease
 Otterbach B, Lubisch W,
 Š
 Claim 4; Page 57-59; 96pp; German.
 AAY51175 standard; Protein; 533
 Kroeger B,
 98DE-1025213
99DE-1008837
 99WO-EP03889
 (first entry)
 Human brain PARP3 protein
 WPI; 2000-087218/07.
 Hoeger T,
 533 AA;
 N-PSDB; AAZ44288
 (BADI) BASF AG
 31-MAR-2000
 W09964572-A2
 Homo sapiens
 04-JUN-1999;
 05-JUN-1998;
 01-MAR-1999;
 16-DEC-1999
 conditions
 AAY51175;
 Sequence
 Kock M,
326
 476
 481
 AAY51175
 RESULT
```

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PARP; poly(ADP-ribose) polymerase; human; murine; detection; sepsis; diagnosis; therapy; necrosis; apoptosis; neurodegenerative illness; ischemic tissue damage; PARP3.
 Lemaire H;
 Novel genes and proteins, antibodies and binding partners useful in diagnosis and therapy of energy deficiency associated disease conditions -
 Kroeger B, Otterbach B, Lubisch W,
 Š
 Human uterus type 2 PARP3 protein.
AAY51176 standard; Protein; 540
 99WO-EP03889
 98DE-1025213
99DE-1008837
 (first entry)
 WPI; 2000-087218/07.
N-PSDB; AAZ44289.
 Kock M, Hoeger T,
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Gaps

7;

DB 21; Length 533;

80.8%; Score 2253.5; DB 21; Lengt 80.9%; Pred. No. 1.8e-191; ive 37; Mismatches 58; Indels

Query Match
Best Local Similarity 80.95
Matches 432; Conservative

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cytostatic; nootropic; neuroprotective; antiinflammatory; antidiabetic;
 61
 118
 175
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 241
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 4;
 polymerase (PARP) homologues, which are characterised by an amino acid sequence with a functional NAD^+-binding site and no zinc finger sequence motif, of general formula CX_ZXZAMXZ_C(I). The nucleic acid sequences, parP homologues and antibodies are useful for analytic detection of PARP homologues and for identifying PARP effectors or binding partners, as well as for determining their effectiveness. PARP-binding partners are useful for the diagnosis or therapy of a disease condition, which is the result of a PARP protein, especially an energy deficiency, which may comprise tissue damage from cell death following necrosis or apoptosis. The disease condition may be chosen from a neurodegenerative illness, or sepsis or ischemic tissue damage, in particular neurotoxic disturbances, etc. This sequence represents the human PARP3 protein used in the method of the invention.
 426
 474
 QVHEDYDCTLNQTNIGNNNNKFYIIQLLEEGSRFF-CWNRWGRVGEVGQSKMNHFTCLED 117
 AKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKVDSGPVRTV---V 174
 295 APGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQTGNSYRCPNLRHVW 354
 355 KVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPHSGGRVGKGIYFASEN 414
 Human; PARP; Poly (ADP-ribose) polymerase; antisense oligonucleotide;
 Gaps
 1 MAPKRKASVQTEG--SKKQRQGTEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGI 58
 KPCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEAM
 KNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQA
 SKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGOTEPDP
 This invention describes novel human and murine poly(ADP-ribose)
 DB 21; Length 540;
 7;
 475 AQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEIHL
 58;
 Score 2253.5; DB 2. Pred. No. 1.9e-191;
 Mismatches
 Š
 4; Page 62-64; 96pp; German.
 AAU29021 standard; Protein; 533
 37;
 80.8%;
80.9%;
 (first entry)
 Conservative
 Human PARP-3 protein.
 Similarity
 540 AA;
 18-DEC-2001
 Best Local Sim
Matches 432;
 Sequence
 AAU29021;
 Query Match
 Claim
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 æ
 59
 89
 128
 235
 118
 175
 188
 308
 367
 415
 427
 487
 AAU29021
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The invention relates to antisense oligonucleotides targeted to human PARP nucleic acid and inhibiting expression of human PARP. PARP (PDI) (ADP-Tibose) polymerase plays an important role in chromatin decondensation, DNA replication, DNA repair, game expression, malignant transformation, cellular differentiation and apoptosis. The antisense oligonucleotide inhibitors are useful for inhibiting the expression of PARP in human cells or tissues. They are also useful for treating a human with a disease associated with PARP especially hyperproliferative disorders (e.g. cancer), cellular injury resulting from oxidative stress, neurological (e.g parkinsonism, meningitis-associated intraoranial arthritis) and dischaemia) inflammatory and autoimmune disorders (e.g. cancer). The present sequence is a PARP protein, the cody, ending which was used to design the antisense
immunosuppressant; hyperproliferative disorder; cancer; cellular injury; oxidative stress; neurological disorder; parkinsonism; apoptosis; meningitis-associated intracranial complication; ischaemia; inflammatory disorder; autoimmune disorder; arthritis; diabetes.
 240
 111
 234
 294
 300
 295 APGEEBEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYRAIQTYLKQTGNSYRCPNLRHVW 354
 28
 Gaps
 QVHEDYDCTLNQTNIGNNNNKFYIIQLLEEGSRFF-CWNRWGRVGEVGQSKMNHFTCLED
 1 MAPKRKASVQTEG--SKKQRQGTEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGI
 AKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKVDSGPVRTV---V
 KPCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEAM
 KNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQA
 ound useful for treating hyperproliferative, inflammatory and autoimmune disorders and diabetes
 7;
 22; Length 533;
 60; Indels
 ; Score 2241.5; DB ;
; Pred. No. 2.1e-190;
37; Mismatches 60;
 Example 13; Page 105-107; 168pp; English.
 compound useful for
 80.4%;
 01-MAR-2001; 2001WO-US06572
 32-MAR-2000; 2000US-0517467
 Query Match
Best Local Similarity 80.53
Matches 430; Conservative
 (ISIS-) ISIS PHARM INC.
 Cowsert LM;
 WPI; 2001-602570/68.
 neurological, inflam
inhibits human PARP
 533 AA;
 N-PSDB; AAS45590
 oligonucleotides
 WO200164955-A1
 Homo sapiens
 07-SEP-2001
 Popoff I,
 Antisense
 Sequence
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653 AA;

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Sequence
 Query Match
Best Local S
 Matches
 13
 138
 241
 65
 191
 306
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 419
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 478
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 RESULT
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 The present sequence represents the NAP protein of Zea mays. This protein is a poly(ADP-ribose) polymerase (PARP) protein (also known as poly(ADP-ribose) transferase). The PARP enzyme is involved in programmed cell death or apoptosis, and is a nuclear enzyme. The NAP polymucleotide sequences can be used for modulation of programmed cell death in plants, to induce, or protect against, programmed cell death, depending on the extent to which PARP activity is reduced. Reducing expression of endogenous NAP class PARP only is also used to modulate programmed cell death, to increase growth rate and to produce plant cells that are more tolerant of stress (cold, chemical treatments, pathogens, pests, drought, heat, etc., or during transformation). Particular applications are generation of plants that are resistant to fungl or nematodes; are malle or female sterile, or have better seed-shatter properties. The methods are also used to increase growth of transformed plant cells (and derived calli or
 Modulating cell death, growth and stress resistance in eukaryotes, specifically plants, used, e.g. to impart fungus or nematode resistance
 NAP; poly(ADP-ribose) polymerase; PARP; poly(ADP-ribose) transferase; programmed cell death; apoptosis; growth rate; stress; cold; pathogen; pest; drought; heat; fungl; nematode; seed-shatter.
 KVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPHSGGRVGKGIYFASEN 414
v-seqektveevphpldrdyqllkcqlqlldsgapeykviqtyleqtgsnhrcptlqhiw 359
 /note- "these residues are specifically claimed in claim 18"
 SKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQTEPDP
 A poly(ADP-ribose) polymerase NAP protein of Zea mays.
 Σ
 Claim 18; Page 92-95; 126pp; English.
 Location/Qualifiers
1..159
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 De Block
 AAY68834 standard; Protein; 653
 (PLBZ) PLANT GENETIC SYSTEMS
 99WO-EP04940.
 98US-0118276
 16-MAY-2000 (first entry)
 Kushnir S,
 WPI; 2000-182436/16.
 N-PSDB; AAZ60616
 complete plants)
 Key
Misc-difference
 WO200004173-A1
 Babiychuk E,
 17-JUL-1998;
 12-JUL-1999;
 27-JAN-2000
 AAY68834;
 Zea mays
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17;
 181 PATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEBAMKNPTGD 240
 363
 418
 355
 122 FKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQ-GEAESQEAVVKVDSGPVRTVVKPCSLD 180
 GOSLEELSSCFYTVIPHNFG--RSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAAPGE 298
 477
 DCTLNQTNIGNNNNKFYIIQLLEE--GSRFFCWNRWGRVGEVGQSKMNHFTCLED-AKKD 121
 VNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKGIYFA 411
 412 SENSKSAGYVTTMHCGGHQV---GYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARG 468
 Gaps
 GSKKQRQGTEEEDSFRS----TAEALRAAPADNRV---IRVDPSCPFSRNPGIQVHED-Y 64
 PARP; DNA-binding domain; poly(ADP-ribose) polymerase; gene therapy;
tumour treatment; DNA repair; over-expression.
 |: | | | : ::|||| | | triaqfislicnismmkqrmveigynaeklplgklrkatilkgyhvlkrisdvisk--ad
 EEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQT---GNSYRCPNLRHVWK
 469 QTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEIH
 53;
 Length 653;
Score 719.5; DB 21; Length
Pred. No. 6.7e-55;
91; Mismatches 205; Indels
 Poly(ADP-ribose) polymerase contg. DNA-binding domain.
 AAR99642 standard; Protein; 1013 AA
 (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
 Buerkle A, Kuepper J, Zur Hausen H;
25.8%;
 95WO-DE01817.
 94DE-4444949.
 (first entry)
 Conservative
 WPI; 1996-300654/30
 Similarity
 Homo sapiens
 WO9618737-A2
 15-DEC-1995;
 16-DEC-1994;
 31-OCT-1996
 20-JUN-1996
 190;
 AAR99642;
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Sequence
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 contg. a DNN-binding domain (DBD). It is encoded by AAT13732, from which a fragment comprising nucleotides 67-1220 (-29 to + 1127) encoding the DBD can be inserted into vectors which are used for gene therapy. Over expression of the DBD inhibits the DNN repair function of PARP, so the vectors are useful for gene therapy or tumours, esp. in combination with conventional chemo- and/or radiotherapy.
 Human; PARP; Poly (ADP-ribose) polymerase; antisense oligonucleotide;
cytostatic; nootropic; neuroprotective; antiinflammatory; antidiabetic;
immunosuppressant; hyperproliferative disorder; cancer; cellular injury;
 235
 61 HEDYDCTLNQTNIGNNNNKFYIIQLLEEG--SRFFCWNRWGRVGEV-GQSKMNHFTCLED 117
 608
 118 AKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVK--VDSGPVRTVVK 175
 236 NPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAA 295
 296 PGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQ----TGNSYRCPNLR 351
 HVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKG 407
 893
 IYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIAR 467
 Gaps
 1 MAPKRKASVQTEGSKKQRQGTEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQV 60
 present sequence is that of a poly(ADP-ribose) polymerase (PARP)
 PCSLDPATONLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEAMK
 468 GQTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEI
 of
 DB 17; Length 1013;
 39;
 insert encoding DNA-binding domain of e) polymerase - useful for gene therapy, esp.
 Indels
 Query Match 25.4%; Score 707.5; DB 17; Best Local Similarity 34.0%; Pred. No. 1.5e-53; Matches 183; Conservative 101; Mismatches 216;
 Ą
 522
 Disclosure; Fig 1; 22pp; German.
 Vectors contg. insert encodi
poly(ADP-ribose) polymerase
 Protein;
 Mouse PARP-2 protein.
 1013 AA;
 AAU29022 standard;
N-PSDB; AAT13732.
 18-DEC-2001
 Sequence
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 352
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The invention relates to antisense oligonucleotides targeted to human PARP nucleic acid and inhibiting expression of human PARP. PARP (POLY (ADP-ribose) polymerase plays an important role in chromatin decondensation, DNA replication, DNA repair, gene expression, malignant transformation, cellular differentiation and apoptosis. The antisense oligonuclectide inhibitors are useful for inhibiting the expression of PARP in human cells or tissues. They are also useful for treating a human with a disease associated with PARP especially hyperproliferative disorders (e.g. cancer), cellular injury resulting from oxidative stress, neurological (e.g parkinsonism, meningitis-associated intracranial complications and ischaemia), inflammatory and autoimmune disorders (e.g arthritis) and diabetes. The present sequence is a PARP protein,
 VEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQTGNSYRCP-----NLRHVWK 355
 | :|||| ||:|:| | || ||:::: | :| || ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
 QNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEAMKNPTGD-GQ 242
 SLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAAPGEEEEK 302
 Gaps
 71 TNIGNNNNKFYIIQLLEEGSR--FFCWNRWGRVGEVGQSKMNHFTC---LEDAKKDFKKK 125
 FWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQ-EAVVKVDSGPVRTVVKPCS-LDPAT 183
 20 GTEEEDSFRSTAEALRA-----APADNRVIRVDPSCPFSRNPG---IQVHEDYDCTLNQ 70
 64
 12 ggkdadrtkdnrdsvktlllkgkap-----vdpecaaklgkahvycegddvydvmlng
oxidative stress; neurological disorder; parkinsonism; apoptosis; meningitis-associated intracranial complication; ischaemia; inflammatory disorder; autoimmune disorder; arthritis; diabetes.
 oound useful for treating hyperproliferative, inflammatory and autoimmune disorders and diabetes
 64;
 Length 522;
 88; Mismatches 195; Indels
 Score 707; DB 22;
Pred. No. 6.2e-54;
 Example 13; Page 109-111; 168pp; English.
 Antisense compound useful for
 25.3%;
 02-MAR-2000; 2000US-0517467.
 01-MAR-2001; 2001WO-US06572
 Matches 190; Conservative
 (ISIS-) ISIS PHARM INC
 Cowsert LM;
 neurological, inflamma
inhibits human PARP -
 WPI; 2001-602570/68.
 Query Match
Best Local Similarity
 522 AA;
 N-PSDB; AAS45597
 WO200164955-A1
 Mus musculus.
 07-SEP-2001.
 Popoff I,
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MAPKRKASVQTEGSKKQRQCTEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPG1QV
 18-DEC-2001
 07-SEP-2001
 AAU29019;
 176
 353
 899
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 This is the human poly (ADP-ribose) polymerase protein (PARP) sequence.
PARP is a 116kD DNA-binding protein that binds tightly to single-strand and double-strand breaks. The PARP protein and Bscherichia coli UvrA and UVRB proteins (see AAY58041-Y58042) are used in a method for the detection and quantitation of DNA base damage. The method involves quantifying at least one modification of inferest in a nucleic acid sequence through the used of capillary electrophoresis, laser induced fluorescence and a fluorescently labeled polypeptide (e.g. fluorescently labeled parper of fluorescently labeled anti-PARP antibody) that is specific for the modification. The new method is useful for quantifying nucleic acid modifications, especially a mutation (including deletions, insertions and substitutions), mismatch, DNA adduct, or strand break (single or double). The method is useful for identifying and detecting exposure to caracthogens, and in early risk assessment for cancer, and is
 Poly (ADP-ribose) polymerase; DNA excision repair; DNA damage; PARP; carcinogen; cancer therapy; base modification; human; cancer; UvrA; UvrB.
 Quantifying nucleic acid modifications useful for identifying and detecting exposure to carcinogens, in early risk assessment for cancer, and in monitoring cancer therapy -
 356 VNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKGIYFA 411
 412 SENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQTE 471
 472 PDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSF--SQSEYLIYKESQCRLRYLLEI 526
 | || | |:| ||||| || pspahfi-tlngs--tvplgpasdtgilnpegytlnynefivyspnqvrmryllki 514
 Human poly (ADP-ribose) polymerase protein sequence.
 AAY58043 standard; peptide; 1014 AA
 Example 6; Fig 9; 65pp; English.
 Weinfeld M, Xing JZ;
 99WO-CA00444
 98US-0078347
 (first entry)
 WPI; 2000-062317/05
 (LEXX/) LE X.
(WEIN/) WEINFELD M.
 1014 AA;
 (XING/) XING J Z.
 14-MAR-2000
 Homo sapiens.
 W09958971-A2
 13-MAY-1999;
 13-MAY-1998;
 18-NOV-1999.
 AAY58043;
 Sequence
 Le x,
 462
 AAY58043
 g
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17;

Gaps

Query Match 25.2%; Score 702.5; DB 21; Length 1014; Best Local Similarity 33.8%; Pred. No. 4.3e-53; Matches 182; Conservative 102; Mismatches 217; Indels 37;

```
Human; PARP; Poly (ADP-ribose) polymerase; antisense oligonucleotide; cytostatic; nootropic; neuroprotective; antiinflammatory; antidiabetic; immunosuppressant; hyperproliferative disorder; cancer; cellular injury; oxidative stress; neurological disorder; parkinsonism; apoptosis; meningitis-associated intracranial complication; ischaemia; inflammatory disorder; autoimmune disorder; arthritis; diabetes.
 408
 609
 118 AKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVK--VDSGPVRTVVK 175
 667
 235
 236 NPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAA 295
 296 PGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQT-GNSYRCPNLR--H 352
 109 YFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARG 468
 896 yfadmvsksanyyhtsq--gdpiglillgevalgnmyelk-hashisrlpkgkhsvkglg 952
 469 QTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEI 526
 493 vaprgksga---alskkskgqvkeeginksekrmkltlkggaavdpdsglehsahvlekg
 61 HEDYDCTLNOTNIGNNNNKFYIIOLLEEG--SRFFCWNRWGRVGEV-GOSKMNHFTCLED
 | : | | : ||| | | :: | | | |: :|
610 aieqfmklyeektgnawhskn-ftkypkkfypleid-ygqdeeavkkltvnpgtksklpk
 PCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEAMK
 VWKVNREGEGDRFQAHSKLGNRRLLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKGI
 Antisense compound useful for treating hyperproliferative, neurological, inflammatory and autoimmune disorders and diabetes
 AAU29019 standard; Protein; 1014
 01-MAR-2001; 2001WO-US06572.
 02-MAR-2000; 2000US-0517467.
 (first entry)
 (ISIS-) ISIS PHARM INC.
 Popoff I, Cowsert LM;
 Human PARP-1 protein.
 WPI; 2001-602570/68.
N-PSDB; AAS45582.
 WO200164955-A1
 Homo sapiens,
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Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasm; aging
 inflammatory disorder
 Sequence
 Query Match
Best Local S
 Matches
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 17;
 The invention relates to antisense oligonucleotides targeted to human PARP nucleic acid and inhibiting expression of human PARP. PARP (Poly (ADP-ribose) polymerase plays an important role in chromatin decondensation, DNA replication, DNA repair, gene expression, malignant transformation, cellular differentiation and apoptosis. The antisense oligonucleotide inhibitors are useful for inhibiting the expression of PARP in human cells or tissues. They are also useful for treating a human with a disease associated with PARP especially hyperproliferative disorders (e.g. cancer), cellular injury resulting from oxidative stress, neurological (e.g parkinsonism, meningitis-associated intracranial complications and ischaemia), inflammatory and autoimmune disorders (e.g arthritis) and diabetes. The present sequence is a PARP protein, the cdNA encoding which was used to design the antisense
 549
 VWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKGI 408
 YFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARG 468
 236 NPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAA 295
 296 PGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQT-GNSYRCPNLR--H 352
 61 HEDYDCTLNQTNIGNNNNKFYIIQLLEEG--SRFFCWNRWGRVGEV-GQSKMNHFTCLED 117
 yfadmvsksanyyhtsq--gdpiglillgevalgnmyelk-hashisrlpkgkhsvkglg 952
 1 MAPKRKASVQTEGSKKQRQGTEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQV 60
 QTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEI 526
 AKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVK--VDSGPVRTVVK
 | : | | : ||| | | :: | | | | : |
alegfmklyeektgnawhskn-ftkypkkfypleid-yggdeeavkkltvnpgtksklpk
 PCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEAMK
 DB 22; Length 1014;
 Human tankyrase2 related protein sequence SEQ ID NO: 137
 Conservative 102; Mismatches 217;
 .3e-53;
 25.2%; Score 702.5; 33.8%; Pred. No. 4.3
 Page 97-101; 168pp; English.
 Ā
 Protein; 1014
 (first entry)
inhibits human PARP
 1014 AA;
 Similarity
 oligonucleotides.
 05-APR-2001
 Best Local Sim
Matches 182;
 AAB66296
 AAB66296;
 Sequence
 Query Match
 968
 118
 610
 176
 899
 181
 353
 469
 953
 AAB66296
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New tankyrase2 polypeptides, useful for treating conditions mediated by poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers, inflammatory and autoimmune disorders -
 The present invention provides the protein and coding sequence for the human tankyrase2 protein. This is found in two different versions, designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has polyADP-ribosylation activity and is involved in the modification of TRFI, which is a telomere-specific binding protein. The regulation of telomere length, in which TRFI has a role, is linked to ageing and cancer. The sequences are useful in the treatment of cancers and inflammatory disorders.
 780
 408
 952
 118 AKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVK--VDSGPVRTVVK 175
 296 PGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQT-GNSYRCPNLR--H 352
 409 YFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARG 468
 Gaps
 61 HEDYDCTLNQTNIGNNNNKFYIIQLLEEG--SRFFCWNRWGRVGEV-GQSKMNHFTCLED
 668 p-----vqdlikmifdvesmkkamveyeidlqkmplgklskrqiqaaysilsevqqavs
 1 MAPKRKASVQTEGSKKQRQGTEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQV
 493 vaprgksga---alskkskgqvkeeginksekrmklilkggaavdpdsglehsahvlekg
 | : | | : || | | : | | | : | 610 aiegfmklyeektgnawhskn-ftkypkkfypleid-yggdeeavkkltvnpgtksklpk
 236 NPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAA
 353 VWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKGI
 176 PCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEAMK
 37;
 b; Score 702.5; DB 22; Length
b; Pred. No. 4.3e-53;
102; Mismatches 217; Indels
 McElligott DL;
 Goldman PS,
 Example 2; Page 207-210; 242pp; English.
 25.2%;
 Demaggio AJ,
 2000WO-US17827.
 Conservative
 2001-102896/11.
 1014 AA;
 Local Similarity
 (ICOS-) ICOS CORP.
 N-PSDB; AAF63954
 Christenson E,
 WO200100849-A1
Homo sapiens
 28-JUN-2000;
 29-JUN-1999;
 04-JAN-2001
 182;
```

```
AKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVK--VDSGPVRTVVK 175
 WO200112645-A1.
 Homo sapiens.
 10-AUG-2000;
 12-AUG-1999;
 11-MAY-2001
 22-FEB-2001
 AAB60693;
 899
118
 RESULT 1
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 This invention describes a novel vector (A), suitable for gene therapy, which contains a DNA insert (I) that encodes a practically complete to ply(adenosine diphosphate-ribose) polymerase (PARP) which has antitumor activity. PARP is a nuclear DNA repair enzyme (activated by strand breakage), that allows recovery of proliferating cells from the toxic effects of DNA damage claused by alkylating or oxidizing agents or radiation), and protects cells against such damage or other causes of genomic instability. (A) are used for treatment of cancer and for cancer prevention in subjects at high risk (e.g. those with tumor-associated genetic defects). Tumor-cells treated with (A) show an increased tendency to die when treated with radiation or chemotherapeutic agent, and in cells that survive this treatment they inhibit genomic instability, so should reduce the likelihood of further development of both malignant cells and resistance to chemotherapy. This sequence
 17;
 HEDYDCTLNQTWIGNNNNKFYIIQLLEEG--SRFFCWNRWGRVGEV-GQSKMNHFTCLED 117
 Gaps
 Gene therapy; poly(adenosine diphosphate-ribose) polymerase; treatmen PARP; antitumor; nuclear DNA repair; proliferating cell; DNA damage; protection; genomic instability; cancer; prevention; human.
 MAPKRKASVQTEGSKKQRQGTEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQV 60
 poly(adenosine
treating or preventing tumors
QTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEI
 DB 20; Length 1014;
 Indels
 Score 701.5; DB 20;
Pred. No. 5.3e-53;
); Mismatches 218;
 Human poly(ADP-ribose)polymerase protein.
 (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 AAY33699 standard; Protein; 1014 AA
 New gene therapy vector expressing diphosphate-ribose)-polymerase for
 25.2%; Sco
34.0%; Pre
tive 99;
 Disclosure; Fig 2; 12pp; German.
 98DE-1008889.
 98DE-1008889
 (first entry)
 Conservative
 Meyer R;
 WPI; 1999-509563/43.
 1014 AA;
 Similarity
 N-PSDB; AAZ23799
 DE1980889-A1
 03-MAR-1998;
 18-JAN-2000
 Homo sapiens
 03-MAR-1998;
 09-SEP-1999
 Best Local Sim
Matches 183;
 Buerkle A,
 invention
 AAY33699;
 Sequence
 Query Match
 61
469
 AAY33699
 RESULT
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New human polypeptide of the polyADPribose synthetase family for use in diagnostic assays and for screening modulators used for preventing and treating inflammation, autoimmune disease and Alzheimers disease
 drug screening;
 295
 | : | | : ||| | | : : | | |: :|: | | |: || | | : || | |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || | |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: |
 p-----vqdlikmifdvesmkkamveyeidlqkmplgklskrqiqaaysilsevqqavs 721
 296 PGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQ----TGNSYRCPNLR 351
 834
 352 HVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAAVIAAILTSGLRIMPH----SGGRVGKG 407
 894
 408 IYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIAR 467
 468 GQTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEI 526
 Human; poly(ADP-ribose) synthetase; sbhPARS2; vaccine; drug screen. ischaemic disorder; cerebral ischaemia; cardiac ischaemia; myocardial infarction; strcke; inflammation; autoimune disease; diabetes; multiple sclerosis; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; chromosome localisation.
 236 NPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAA
 PCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEAMK
 This sequence represents a novel human poly(ADP-ribose) synthetase, sbhParKS2. The invention also relates to fragments, variants and sequences with at least 95% identity to the sbhPaRS2 profeain or nucleotide sequence; expression systems and host cells
 χ,
 Zhu
 Li X, McQueney MS,
 Human poly(ADP-ribose) synthetase sbhPARS2.
 AAB60693 standard; Protein; 521 AA.
 Kabnick KS,
 Claim 1; Page 21; 30pp; English.
 (SMIK) SMITHKLINE BEECHAM CORP
 99US-0373441.
 2000WO-US21775
 (first entry)
 Barone F, Field J,
 WPI; 2001-211196/21.
 N-PSDB; AAF59996
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of shipARS2; and an antibody specific for shipARS2. shipARS2; and an antibody specific for shipARS2. shipARS2 proteins an anceotides are useful as vaccines for inducing an immunological response in anamual. The shipARS2 protein is useful for identifying compounds which inhibit or stimulate its activity or expression level. Such agonists and antagonists of shipARS2 are useful for treating human diseases including ischaemia and ischaemic tissue injury (e.g., cerebral and cardiac ischaemia, myocardial infarction, stroke), inflammation, autoimmune disease (e.g. diabetes, multiple sclerosis) and neurodegenerative diseases (e.g., Parkinson's disease and Alzheimer's disease). shipARS2 uncleic acids are useful as diagnostic reagents for disease. ShipARS2 uncleic acids are useful as diagnostic reagents for detecting mutations in the associated gene; as hybridisation probes to isolate full-length shipARS2 couns and shipARS2 genomic clones; and for chromosome localisation studies. The shipARS2 protein is also useful as an immunogen to produce antibodies for therapeutic use, sbhpARS2 proteins, uncleotides and antibodies are also useful in screening methods for detecting the effect of added compounds on the production of mRNA and
 the recombinant expression
 comprising an sbhPARS2 nucleic acid sequence;
$$$$$$$$$$$$$$$$$$$$$$
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521 AA; Sequence

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17;
 NQTNIGNNNNKFYIIQLLEEGSR--FFCWNRWGRVGEVGQSKMNHFTC---LEDAKKDFK 123
 ||| :|||| ||:||:|| | || :::
116 kkfldktknnwedrekfekvpgkydmlqmdyatntqdeeetkkeeslksplkpesqldlr 175
 405
 ngtnlgfnnnkyyliglleddagrnfsvwmrwgrvgkmgghsl--vacsgnlnkakeifg 115
 124 KKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKVDSGPVRTVVKPCS-LDPA 182
 183 TONLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEAMKNPTGD-G 241
 242 QSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAAPGEEEE 301
 KVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQT---GNSYRCPNLRHVWKVNR 358
 EGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKGIYFASEN 414
 SKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQTEPDP 474
 sksanycfasrl--kntgllllsevalgqcnelleanpkaegllqgkhstkglgkmapss 463
 57
 13 GSKKQRQGTEEEDSFRSTAEALRA-APADNRVIRVDPSCPFSRNPG---IQVHEDYDCTL 68
 348 dgekeafr--edlhnrmllwhgsrmsnwvgilshglriappeapitgymfgkgiyfadms
 45;
 DB 22; Length 521;
 475 AQDIELELDGQPVVVPQGPPVQCPSFKSSSF--SQSEYLIYKESQCRLRYLLEI
 .,3e-53;
les 212;
25.1%; Score 700.5; 34.6%; Pred. No. 2.3e
 Conservative
 Query Match
Best Local Similarity
Matches 185; Conserv
 406
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 302
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464 ahfv--tlngs--tvplgpasdtgilnpdgytlnyneyivynpngvrmryllkv

AAY51174 standard; Protein; 570

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(first entry)

31-MAR-2000

XEXEXEX

AAY51174;

Human brain PARP2 protein.

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polymerase (PARP) homologues, which are characterised by an amino acid sequence with a functional NAD++binding site and no zinc finger sequence with a functional NAD++binding site and no zinc finger sequences with a functional NAD++binding site and no zinc finger sequences. PARP homologues and antibodies are useful for analytic detection of PARP homologues and for identifying PARP effectors or binding partners as well as for determining their effectiveness. PARP-binding partners are useful for the diagnosis or therapy of a disease condition, which is the result of a PARP protein, especially an energy deficiency, which may comprise tissue damage from cell death following necrosis or apoptosis. The disease condition may be chosen from a neurodegenerative illness, or sepsis or ischemic tissue damage, in particular neurotoxic disturbances, etc. This sequence represents the human PARP2 protein used in the method of the invention.
 NQTNIGNNNNKFYIIQLLEEGSR--FFCWNRWGRVGEVGQSKMNHFTC---LEDAKKDFK 123
 KKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKVDSGPVRTVVKPCS-LDPA 182
 KVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQT ---GNSYRCPNLRHVWKVNR 358
 54 ggkankdrtedkgdesvkalllkgkap----vdpectakvgkahvycegndvydvml 106
 Gaps
 13 GSKKQRQGTEEEDSFRSTAEALRA-APADNRVIRVDPSCPFSRNPG---IQVHEDYDCTL 68
poly(ADP-ribose) polymerase; human; murine; detection; sepsis;
osis; therapy; necrosis; apoptosis; neurodegenerative illness;
 Novel genes and proteins, antibodies and binding partners useful in diagnosis and therapy of energy deficiency associated disease
 Lemaire
 QSLEELSSCFYTVIPHNFGRSRPPINSPDVLQAKKDMLLVLADIELAQTLQAAPGEEEE
 TONLITNIFSKEMPKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEAMKNPTGD-G
 This invention describes novel human and murine poly(ADP-ribose)
 45;
 25.1%; Score 700.5; DB 21; Length 570; 34.6%; Pred. No. 2.7e-53; ive 92; Mismatches 212; Indels 45;
 Lubisch W,
 B,
 Otterbach
 Claim 4; Page 52-54; 96pp; German.
 Kroeger B,
 99WO-EP03889.
 98DE-1025213.
99DE-1008837.
 Best Local Similarity 34.6
Matches 185; Conservative
 ischemic tissue damage.
 WPI; 2000-087218/07
 Kock M, Hoeger T,
 570 AA;
 N-PSDB; AAZ44287
 (BADI) BASF AG.
 Homo sapiens
 W09964572-A2
 04-JUN-1999;
 05-JUN-1998;
 01-MAR-1999;
 16-DEC-1999
 conditions
 diagnosis;
 Sequence
 Query Match
 165
 242
 69
 107
 124
 183
 302
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transplantation), revascularization of critically constricted coronary arteries (e.g. after PCTA or by-pass operations) or peripheral arteries (e.g. leg arteries), treating acute myocardial ischemia and damage during or after its mechanical or dury-induced lysis and treating tumors and their metastasis, sepsis and septic shock, inflammatory and rheumatic disease (e.g. rheumatoid arthritis), and diabetes mellitus. Although (I) inhibit PARP (i.e. the known form designated PARPI), they especially selectively and strongly inhibit PARP homologs, specifically the homolog PARP2. In particular (I) have very strong PARP2 inhibitory activity (e.g. with K.i values of 1-20 nM) and high selectivity for PARP2 relative to PARPI (generally by a factor of more than 5).

 $\begin{array}{c} \mathbb{C} & \mathbb$ 

570 AA;

Sequence

heart valve replacement, aneurysm resectioning and heart

```
Human; poly ADP-ribose polymerase; PARP; neuroprotective; nootropic; cerebroprotective; antiparkinsonian; nephrotropic; cardiant; vasotropic; anticonvulsant; cytostatic; antibacterial; immunosuppressive; treatment; antinflammatory; antirheumatic; antiarthritic; antidiabetic; epilepsy; antinflammatory; neurodegenerative disease; tumor; neuronal damage; Alzheimer's disease; Huntington's disease; tumor; Parkinson's disease; ischemic damage; microinfarction; sepsis;
 454
 474
 Drugs for inhibiting PARP or especially homologous enzymes comprising
 EGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKGIYFASEN
 4-substituted phthalazinone derivatives, useful e.g. for treating neurodegenerative disease, ischemic damage, tumors or diabetes
 SKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQTEPDP
 AQDIELELDGQPVVVPQGPPVQCPSFKSSSF--SQSEYLIYKESQCRLRYLLEI 526
 Human brain poly-ADP-ribose-polymerase protein.
 Ë
 Hoeger
 Example A; Page 12-13; 14pp; German.
 ¥.
 Σ
 AAB11480 standard; Protein; 570
 Kock
 99DE-1021567
 99DE-1021567
 (first entry)
 Sadowski J,
 WPI; 2001-032983/05
 diabetes mellitus
 N-PSDB; AAC82090
 (BADI) BASF AG.
 DE19921567-A1
 02-MAR-2001
 Homo sapiens
 11-MAY-1999;
 11-MAY-1999;
 16-NOV-2000.
 Lubisch W,
 AAB11480;
 12
 475
359
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 nqtnlqfnnnkyyliqlleddaqrnfsvwmrwgrvgkmgqhsl--vacsgnlnkakeifq 164
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 KVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQT---GNSYRCPNLRHVWKVNR
 ::: ||||: |: || |: || |::| ::| :| elgspehpldghyrnlhcalrpldhesyefkvisgylgsthapthsdytmtlldlfevek
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 DB 22; Length 570;
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25.1%; Score 700.5; DB 22;
llarity 34.6%; Pred. No. 2.7e-53;
Conservative 92; Mismatches 212;
 Similarity
 Best Local Sim
Matches 185;
 Query Match
 13
 54
 107
 124
 165
 225
 242
 283
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Search completed: August 29, 2002, 07:57:21 Job time: 298 sec

This invention describes novel 4-substituted 2H-phthalazin-1-one derivatives (1) which are used for the treatment or prophylaxis of diseases associated with elevated poly. (ADP-ribose)-polymerase (PARP; EC 2.4.2.30) activity. The products of the invention have nootropic, neuroprotective, cerebroprotective, antiparkinsonian, nephrotropic, cardiant, vasotropic, anticonvulsant, cytostatic, antibacterial, immunosuppressive, antionnvulsant, cytostatic, antibacterial, antidiabetic. (1) are especially used for treating or preventing neurodegenerative disease or neuronal damage (specifically associated with ischemia, trauma or massive bleeding, especially apoplaxy or spinal-cranial trauma or massive bleeding, especially apoplaxy or spinal-cranial treating or preventing ischemic damage (specifically renal damage after renal ischemia or during and after (specifically renal damage after renal ischemia cischemia), treating epilepsy, specifically generalized epileptic attacks (e.g. petit mal and conplexy partial attacks), treating microinfarction (e.g. temporal lope and complex partial attacks), treating microinfarction (e.g. during and

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Appli

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Sequence 2, Al Sequence 11, Page 11, Pa
 Sequence 1
Sequence 2
Sequence 2
Sequence 2
 Sequence
 Sequence
 Sequence
 DB 4; Length 1013;
 GENERAL INFORMATION:
APPLICANT: Burkle, Alexander
APPLICANT: Burkle, Alexander
APPLICANT: Jan Heiner, Kupper
TITLE OF INVENTION: VECTORS AND VIRUSES FOR USE
TITLE OF INVENTION: IN GENE THERAPY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STREET: US Avenue of the Americas
CITY: New York
STREET: 10356-2811
 US-08-465-473B-14
US-09-046-992-4
US-08-391-259-1
US-08-839-425-2
US-08-839-425-1
US-08-839-425-1
US-08-235-838-16
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US-08-923-992A-6
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US-08-333-700-1
 COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FESTENG for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,886
 PCT-US95-16216-1
US-08-451-715A-2
US-08-923-992A-8
 -08-235-838-14
 25.4%; Score 707.5;
 30,742
SR: 8484-0028-999
 ALIGNMENTS
 Sequence 2, Application US/08860886
Patent No. 6335009
 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LEUTE A
REGISTRATION NUMBER: 30,742
REFERENCE/POCKET NUMBER: 8484
TELECHOMICATION INFORMATION:
TELEPAN: 650-493-4935
TELEFAX: 660-493-5556
TELEFAX: 660-493-5556
TELEEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1013 amino acids
 03-0CT-1997
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
 TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-860-886-2
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 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
 STRANDEDNESS: single
 TYPE: amino acid
 CLASSIFICATION:
 FILING DATE:
 US-08-860-886-2
Query Match
 (without alignments)
275.630 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-076-347A-3
US-09-046-992-2
US-09-308-375-2
US-08-461-234-1
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 Total number of hits satisfying chosen parameters:
 231628 segs, 24425594 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 August 29, 2002, 07:58:21
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Gapop 10.0 , Gapext 0.5
 Issued_Patents_AA:*
 US-09-701-586B-10
 seq length: 0 seq length: 2000000000
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 Length
 613
613
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614
614
614
638
462
3075
 Query
Match 1
 707.5
702.5
143
106.5
 104
103.5
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103.5
103.5
102.5
100.5
100.5
 Perfect score:
 Scoring table:
 Score
 Minimum DB
Maximum DB
 OM protein
 Sequence:
 Searched:
 Database
 Run on:
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Result

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TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1014 amino acids
 ; MOLECULE TYPE: protein US-09-078-347A-3
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber &
 CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
 TOPOLOGY: unknown
 07601
 US-09-196-387-2
 STREET:
 Query Match
 Best Loca
Matches
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 17;
 492 VAPRGKSGA---ALSKKSKGQVKEEGINKSEKRMKLTLKGGAAVDPDSGLEHSAHVLEKG 548
 61 HEDYDCTLNQTNIGNNNNKFYIIQLLEEG -- SRFFCWNRWGRVGEV - GQSKMNHFTCLED 117
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 HVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKG 407
 IYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIAR 467
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 39;
 GENERAL INFORMATION:
APPLICANT: Le, Xiao-Chun
APPLICANT: Weinfeld, Michael
APPLICANT: Xing, Janes Z.
TITLE OF INVENTION: Methods for Quantitating Low Level
TITLE OF INVENTION: Modifications of Nucleotide Sequences
 Indels
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
 Best Local Similarity 34.0%; Pred. No. 3.3e-60; Matches 183; Conservative 101; Mismatches 216;
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STRRET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: USA
 APPLICATION NUMBER: US/09/078,347A
PILING DATE: 13-MAY-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARTOIL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: UALB-03283
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
 OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 3, Application US/09078347A Patent No. 6132968
 IBM PC compatible
 COUNTRA
ZIP: 94104
COMPUTER READABLE FORM: "TOPE: Floppy disk
 NUMBER OF SEQUENCES:
 COMPUTER:
 -09-078-347A-3
 408
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17;
 493 VAPRGKSGA---ALSKKSKGQVKEEGINKSEKRMKLTLKGGAAVDPDSGLEHSAHVLEKG 549
 353 VWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKGI 408
 61 HEDYDCTLNQTNIGNNNNKFYIIQLLEEG -- SRFFCWNRWGRVGEV - GOSKMNHFTCLED 117
 118 AKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVK--VDSGPVRTVVK 175
 296 PGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQT-GNSYRCPNLR--H 352
 409 YFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARG 468
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 469 QTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEI 526
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 37;
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 Match 25.2%; Score 702.5; DB 4; Local Similarity 33.8%; Pred. No. 1e-59; les 182; Conservative 102; Mismatches 217;
 3: Klauber & Jackson
411 Hackensack Avenue, 4th Floor
 Sequence 2, Application US/09196387
Patent No. 6277613
GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: OF USE THEREOF
IUMBER OF SEQUENCES: 12
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
TYPE: amino acid
STRANDEDNESS: not relevant
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148 TLIEVQGEAESQEAVVKVDSGPVRTVVKP------CSLDPATQNLITNIFSKEM 195
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 3.8%; Score 106.5; DB 4; Length (19.0%; Pred. No. 0.11; tive 55; Mismatches 154; Indels
 US-09-308-375-2
Sequence 2, Application US/09308375
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Sequence 10: Percent No. 10: Perce
 SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/046,992 FILING DATE: 24-MAR-1998
 CLASSIPCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY, AGENT INFORMATION:
NAME: POISSANT, BITAN M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 9457-0013-999
TELECOMMUNICATION INFORMATION:
TELEFAX: 650-493-4935
TELEFAX: 650-493-556
TENGTH: 635-40100 acids
TYPE: amino acid
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 MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-046-992-2
 196 FKNAMTLMNLDVK----
 Query Match
Best Local Similarity
 linear
 TOPOLOGY:
 Matches
 357
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 13;
 1223 QYVYGIGGGTGCPTHKDRSCYICHRQMLFCRVTLGKS-FLQFSTMKMAHAPPGHHSVI-- 1279
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PatentIn Release #1.0, Version #1.30
 Sequence 2, Application US/09046992
Patent NO. 6140066
GENERAL INFORMATION:
APPLICANT: Lorberboum-Galski, Haya
APPLICANT: Yarkoni, Shai
APPLICANT: Ren-Yehudah, Ahmi
APPLICANT: Pen-Yehudah, Mami
APPLICANT: US Ben-Yehudah, METHODS OF CANCER DIAGNOSIS
TITLE OF INVENTION: USING A CHIMERIC TOXIN
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26/72
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
 ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
 APPLICATION NUMBER: US/09/196,387 FILING DATE:
 TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
 TELER: 133521
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1327 amino acids
 ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
 201-343-1684
 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
 HYPOTHETICAL: NO
 NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
 CLASSIFICATION:
 USA
 TELEFAX:
 US-09-196-387-2
 US-09-046-992-2
 COUNTRY:
 STATE:
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NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15;
 TELECOMMUNICATION INFORMATION:
 Ouery Match
Best Local Similarity 19.7%
Matches 78, Conservative
 COMPUTER READABLE FORM:
 California
 COUNTRY: USA
ZIP: 94105-1492
 209 -----
 US-08-461-234-1
 JS-08-405-615-1
 CITY:
STATE:
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 1000 KMQKALDSGD--EKAFDNAKKDLQSLLETYSKSDSSIDVFKMSFDKAQ-----KNIKDG 1051
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 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
 94;
 276 KKDMLLVLADI-ELAQTLQAAPGEEEEKVEEVPHPLD 311
 47; Mismatches
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 3.0
 NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15280-36
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/901,709
FILING DATE:
 APPLICATION NUMBER: US/08/405,615
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
 TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
 LENGTH: 613 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
 ; ORGANISM: Bacillius subtilis
US-09-308-375-2
 ATTORNEY/AGENT INFORMATION:
 Query Match 3.7
Best Local Similarity 21.2
Matches 46; Conservative
 CLASSIFICATION: 435
 OPERATING SYSTEM:
 94105
 FILING DATE
 SEQ ID NO 2
LENGTH: 2285
 US-08-405-615-1
 TYPE: PRT
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17;
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247 RLHFPEGGSLAALTAHQACHLPLETFTRHRQPRGWEQLEQCGYPVQRLVALYLAARLSWN 306
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 167 SGPVRTVVKP-----CSLDPATQNLITNIFSKEMFKNAMTLMNLDVK---- 208
 307 QVDQVIRNALASP-GSGGDLGEAI------REQPE-----QAR--LALTLA 343
 285 DIELAQTLQAAPGEEEEKVEEVPHPLDRDYQLLRCQLQL-----LDSG----ESEYKAI 334
 344 AAESERFVRQGTGNDEAGA-----ANADVVSLTCPVAAGECAGPADSGDALLERNYPTG 397
 335 QTYLKQTGNSYRCPNLRHVWKVNREGEGDRFQAHSKLGNRRLL---WHGTNVAVVAAILT 391
 392 SGLRIMPHSGGRVGKGIYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDD 451
 453 GGVRARSQDLDAIWRGFYIAGDPALAYGYAQDQEPDAR-----GRIRNGALLRVYVPR 505
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 ----KMPLGKLTKQQIARGFEALE------
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 47; Mismatches 144; Indels 127;
Length 613;
 Sequence 1, Application US/08461234
Patent No. 5821238
GENERAL INFORMATION:
APPLICANT: Pastan, Ira H.
APPLICANT: FitzGerald, David J.
TITLE OF INVENTION: Recombinant Pseudomonas Exotoxin with
TITLE OF INVENTION: Increased Activity
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
 ADDRESSEE: Townsend and Townsend and Crew STREET: One Market Plaza, Steuart Street Tower CITY: San Francisco
 Version #1.30
 DB 1;
 452 PSLKSPPPGFDSVIARGQTEPDPAQDIELELDGQPV 487
 Score 103.5; D
Pred. No. 0.21;
 FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PROOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,709
FILING DATE: 18-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405,615
FILING DATE: 15-MAR-1995
ATTORNEY/AGENT INFORMATION:
 15280-36-3
 SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/461,234
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: 15280-36-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 613 amino acids
 US 08/405,615
 FILING DATE: 18-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405
FILING DATE: 15-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
 Sequence 1, Application US/08225224 Patent No. 5635599
 Conservative
 TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
 TYPE: amino acid
 Query Match
Best Local Similarity
Matches 78; Conservi
 COUNTRY: US
ZIP: 94105-1493
 STRANDEDNESS:
 US-08-463-480-1
 RESULT 9
US-08-225-224-1
 209
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 17;
 192 SGKVLCLLDPLDGVYNYLAQQRCNLDDTWEGKIYRVLAGNPAKH-----DLDIKPTVISH 246
 247 RLHFPEGGSLAALTAHQACHLPLETFTRHRQPRGWEQLEQCGYPVQRLVALYLAARLSWN 306
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 ----ALEEAMKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLA 284
 307 QVDQVIRNALASP-GSGGDLGEAI------REQPE-----OAR--LALTLA 343
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 344 AAESERFVROGTGNDEAGA-----ANADVVSLTCPVAAGECAGPADSGDALLERNYPTG 397
 335 QTYLKQTGNSYRCPNLRHVWKVNREGEGDRFQAHSKLGNRRLL---WHGTNVAVVAAILT 391
 398 AEFLGDGGDVSFSTRGTQNWTVER-----LLQAHRQLEERGYVFVGYHGTFLEAAQSIVF 452
 392 SGLRIMPHSGGRVGKGIYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDD 451
 Gaps
 3.7%; Score 103.5; DB 2; Length 613;
19.7%; Pred. No. 0.21;
ive 47; Mismatches 144; Indels 127;
 Sequence 1, Application US/08463480
Patent No. 5844044
GENERAL INFORMATION:
APPLICANT: Pastan, Ira H.
APPLICANT: FitzGerald, David J.
TITLE OF INVENTION: Recombinant Pseudomonas Exotoxin with TITLE OF INVENTION: Increased Activity
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
 ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
 STREET: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco CTATE: Caraffernia COUNTRY: USA
 452 PSLKSPPPGFDSVIARGQTEPDPAQDIELELDGQPV 487
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,480
FILING DATE: 05-UUN-1995
(415) 543-9600
 TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 613 antho acids
 Best_Local Similarity 19.7%
Matches 78; Conservative
 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-461-234-1
 FILING DATE: 05-JUN-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
 amino acid
 TYPE: amino
STRANDEDNESS:
TELEPHONE:
 US-08-463-480-1
 Query Match
 209
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:|| | | : || || 306
247 RIHFPEGGSLAALTAHQACHLPLETFTRHRQPRGWEQLEQCGYPVQRLVALYLAARLSWN 306
 167 SGPVRTVVKP-----CSLDPATQNLITNIFSKEMFKNAMTLMNLDVK---- 208
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 392 SGLRIMPHSGGRVGKGIYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDD 451
 DB 2; Length 613;
 GENERAL INFORMATION:
APPLICANT: PASTAN, Ira
APPLICANT: PASTAN, Ira
APLICANT: KEITMAN, ROBERT J.
TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND
TITLE OF INVENTION: CIRCULARLY PERMUTED FUSION PROTEINS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco STATE: California
3.7%; Score 103.5; DB 2;
19.7%; Pred. No. 0.21;
iive 47; Mismatches 144;
 -----KMPLGKLTKQQIARGFEALE----
 452 PSLKSPPPGFDSVIARGQTEPDPAQDIELELDGQPV 487
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California
 COUNTRY: USA
ZIP: 94111-3834
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 167 SGPVRTVVKP------CSLDPATQNLITNIFSKEMFKNAMTLMNLDVK----- 208
 229 ----ALEEAMKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLA 284
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 454 GGVRARSODLDAIWRGFYIAGDPALAYGYAQDQEPDAR-----GRIRNGALLRVYVPR 506
 209 ------KMPLGKLTKQQIARGFEALE----------
 Length 614;
 APPLICANT: Pastan, Ira
APPLICANT: Kreitman, Robert J.
APPLICANT: Puri, Raj K.
TITLE OF INVENTION: Circularly Permuted Ligands and
TITLE OF INVENTION: Circularly Permuted Chimeric Molecules
 COMPUTER REALIZED FORGY.

MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/225,224
FILING DATE: 8 APPL-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Weber: Blanch
REGISTRATION NUMBER: 15280-193
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRATION NUMBER: 15280-193
TELEPRATION INFORMATION:
TELEPRATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TENDENCE CHARACTERISTICS:
 3.7%; Score 103.5; DB 1;
19.7%; Pred. No. 0.21;
tive 47; Mismatches 144;
 452 PSLKSPPPGFDSVIARGQTEPDPAQDIELELDGQPV 487
 ; LOCATION: 1..614
; OTHER INFORMATION: /label= native-PE
US-08-225-224-1
 Sequence 1, Application US/08722258
Patent No. 6011002
GENERAL INFORMATION:
 614 amino acids
 Query Match 3.7%
Best Local Similarity 19.7%
Matches 78; Conservative
 unknown
 MOLECULE TYPE: protein
COMPUTER READABLE FORM:
 NAME/KEY: Protein
 unknown
 amino acid
 TYPE: amino a STRANDEDNESS:
 US-08-722-258-1
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:| |: :|||: :|| 399 AEFLGDGGDVSFSTRGTQNWTVER-----LLQAHRQLEERGYVFVGYHGTFLEAAQSIVF 453
 Gaps
 167 SGPVRTVVKP------CSLDPATQNLITNIFSKEMFKNAMTLMNLDVK----- 208
 193 SGKVLCLLDPLDGVYNYLAQQRCNLDDTWEGKIYRVLAGNPAKH-----DLDIKPTVISH 247
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 308 QVDQVIRNALASP-GSGGDLGEAI-------REQPE-----QAR--LALTLA 344
 285 DIELAQTLQAAPGEEEEKVEEVPHPLDRDYQLLRCQLQL-----LDSG----ESEYKAI 334
 345 AAESERFVROGTGNDEAGA----ANADVVSLTCPVAAGECAGPADSGDALLERNYPTG 398
 335 QTYLKQTGNSYRCPNLRHVWKVNREGEGDRFQAHSKLGNRRLL---WHGTNVAVVAAILT 391
 392 SGLRIMPHSGGRVGKGIYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDD 451
 Query Match 3.7%; Score 103.5; DB 3; Length 614; Best Local Similarity 19.7%; Pred. No. 0.21; Matches 78; Conservative 47; Mismatches 144; Indels 127;
 209 ---------KMPLGKLTKQQIARGFEALE-------
 ; NAME/KEY: Protein
; LOCATION: 1..614
; OTHER INFORMATION: /note= "native Pseudomonas exotoxin
; OTHER INFORMATION:
US-08-722-258-1
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
 Townsend and Townsend and Crew LLP
 : Two Embarcadero Center, Eighth Floor
San Francisco
 APPLICATION NUMBER: US/08/722,258
FILING DATE: 08-JAN-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US95/04468
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/225,224
FILING DATE: 08-APR-1994
ATTORNEY/AGBNT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-193100US
TELEFAN: (415) 576-0200
TELEFAN: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTER/STICS:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 LENGTH: 614 amino acids
TYPE: amino acid
STRANDEDNESS:
 TOPOLOGY: linear
MOLECULE TYPE: protein
CORRESPONDENCE ADDRESS:
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Rockford
METHODS AND COMPOSITIONS FOR USING
MEMBRANE-PENETRATING PROTEINS TO CARRY MATERIALS ACROSS
 | : :: | :| | | | | 369 AAESERFVRQGTGNDEAGA-----ANADVVSLTCPVAAGECAGPADSGDALLERNYPTG 422
 335 QTYLKQTGNSYRCPNLRHVWKVNREGEGDRFQAHSKLGNRRLL---WHGTNVAVVAAILT 391
 332 QVDQVIRNALASP-GSGGDLGEAI-------REQPE------QAR--LALTLA 368
 167 SGPVRTVVKP-----CSLDPATQNLITNIFSKEMFKNAMTLMNLDVK---- 208
 272 RIHFPEGGSLAALTAHQACHLPLETFTRHRQPRGWEQLEQCGYPVQRLVALYLAARLSWN 331
 285 DIELAQTLQAAPGEEEEKVEEVPHPLDRDYQLLRCQLQL-----LDSG----ESEYKAI 334
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 Indels 127;
 DB 3; Length 638;
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATE: US/09/047,148 FILING DATE: Concurrently Herewith
 3.7%; Score 103.5; DB 3;
19.7%; Pred. No. 0.22;
tive 47; Mismatches 144;
 ---KMPLGKLTKQQIARGFEALE---
 452 PSLKSPPPGFDSVIARGQTEPDPAQDIELELDGQPV 487
 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Draper, Rockford
TITLE OF INVENTION: METHODS AND COMPC
TITLE OF INVENTION: MEMBRANE-PENETRAT
TITLE OF INVENTION: CELL MEMBRANES
NUMBER OF SEQUENCES: 13
CORRESPONDENCES 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: HOUSTON
STATE: Texas
COUWTRY: United States
ZIP: 77210
COMPUTER PROFILE
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/042,056
FILING DATE: 26-MAR-1997
ATTORNEY AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTSF:072
TELEPHONE: (512) 418-3000:
TELEPHONE: (512) 474-777
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 638 amino acids
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 78; Conservative
 Best Local Similarity
 FILING DATE: C
 STRANDEDNESS
 RESULT 12
US-09-047-148-2
 Query Match
 Matches
 209
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 17;
 167 SGPVRTVVKP------CSLDPATQNLITNIFSKEMFKNAMTLMNLDVK----- 208
 229 ----ALEEAMKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLA 284
 308 QVDQVIRNALASP-GSGGDLGEAI-------REQPE-----QAR--LALTLA 344
 399 AEFLGDGGDVSFSTRGTQNWTVER----LLQAHRQLEERGYVFVGYHGTFLEAAQSIVF 453
 248 RLHFPEGGSLAALTAHQACHLPLETFTRHRQPRGWEQLEQCGYPVQRLVALYLAARLSWN 307
 285 DIELAQTLQAAPGEEEEKVEEVPHPLDRDYQLLRCQLQL-----LDSG----ESEYKAI 334
 335 QTYLKQTGNSYRCPNLRHVWKVNREGEGDRFQAHSKLGNRRLL---WHGTNVAVVAAILT 391
 SGLRIMPHSGGRVGKGIYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDD 451
 454 GGVRARSQDLDAIWRGFYIAGDPALAYGYAQDQEPDAR-----GRIRNGALLRVYVPR 506
 Query Match 3.7%; Score 103.5; DB 5; Length 614; Best Local Similarity 19.7%; Pred. No. 0.21; Matches 78; Conservative 47; Mismatches 144; Indels 127;
 CIRCULARLY PERMUTATED LIGANDS AND CIRCULARLY PERMUTED FUSION PROTEINS 59
 209 ---------KMPLGKLTKQQIARGFEALE-------
 APPLICANT:
TITLE OF INVENTION: CIRCULARLY PERMUTATED LICANDS AN TITLE OF INVENTION: CIRCULARLY PERMUTED FUSION PROTENUMBER OF SEQUENCES: 59
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04468
FILING DATE: 07-APR-1995
 452 PSLKSPPPGFDSVIARGQTEPDPAQDIELELDGOPV 487
 NAME: Weber, Ellen L. REGISTRATION UNMBER: 32,762
REFERENCE/DOCKET NUMBER: 15280-193-1PC
TELECOMMUNICATION INFORMATION:
 ; LOCATION: 1..614
; OTHER INFORMATION: /label= native-PE
PCT-US95-04468-1
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/225,224
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
 Sequence 1, Application PC/TUS9504468 GENERAL INFORMATION:
 TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
 LENGIH: 614 amino acids
 S: unknown unknown
 MOLECULE TYPE: protein
 NAME/KEY: Protein
 amino acid
 STRANDEDNESS:
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266 PINSPDVLQAKKDMLLVLADIELAQTLQAAPGEEEEKVEEVPHPLDRDYQLLRCQLQL-- 323
 184 ------QAR--LALTLAAAESERFVRQGTGNDEAGA-----ANADVVSLTCPVAAGE 227
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 376 LL---WHGTNVAVVAAILTSGLRIMPHSGGRVGKGIYFASENSKSAGYVTTMHCGGHQVG 432
 283 YVFVGYHGTFLEAAQSIVFGGVRARSODLDAIWRGFYIAGDPALAYGYAQDQEPDAR--- 339
 433 YMFLGEVALGKEHHITIDDPSLKSPPPGFDSVI-----ARGQTEPDPAQDIELELD-- 483
 340 ----GRIRNGALLRVXVPRSSL----PGFYRTSLTLAGGEAAGEVERLIGHPLFLFLDAI 391
 181 -PATQNLITNIFSK--EMFK-----NAMTLMNLDVKKMPLGKLTKQQIARGFEALE-- 228
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 Nucleic Acids Encoding Merosin, Merosin
Fragments and Uses Thereof
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,309
 E: Campbell and Flores 4370 La Jolla Village Drive, Suite 700
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/125,077
FILING DATE: 22-5EP-1993
APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-5EP-1994
 484 -------GQP-----VVVPQGPP 494
 392 TGPEEEGGRLETILGWPLAERTVVIPSAIP 421
 NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9721
 APPLICATION NUMBER: US 07/472,319 FILING DATE: 30-JAN-1990 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/919,951
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 5, Application US/08460309
Patent No. 5837496
GENERAL INFORMATION:
 27-JUL-1992
 FILING DATE: 27-JUL-1992
ATTORNEY/AGENT INFORMATION:
 APPLICANT: Engvall, Eva
APPLICANT: Leivo, Ilmo
TITLE OF INVENTION: Nucl
TITLE OF INVENTION: Frag
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
 FILING DATE: 21-SEP-1
PRIOR APPLICATION DATA:
 CITY: San Diego
STATE: California
 COUNTRY: U
 FILING DATE
 ADDRESSEE:
 US-08-460-309-5
 STREET:
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 21;
 Query Match 3.7%; Score 103; DB 2; Length 462;
Best Local Similarity 21.1%; Pred. No. 0.15;
Matches 95; Conservative 46; Mismatches 181; Indels 128; Gaps
 123 KKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKVDSGPVRTVVKPCSLD-- 180
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 392 SGLRIMPHSGGRVGKGIYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDD 451
 478 GGVRARSQDLDAIWRGFYIAGDPALAYGYAQDQEPDAR------GRIRNGALLRVYVPR 530
 APPLICANT: Culouscou, Jean-Michel
APPLICANT: Shoyab, Mohammed
APPLICANT: Siegall, Clay B.
APPLICANT: Hellstr m, Ingegerd
APPLICANT: Hellstr m, Karl E.
TITLE OF INVENTION: HER4 HUMAN RECEPTOR TYROSINE KINASE
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/484,438
FILING DATE: U7-JUN-1995
CLASSIFICATION: 530
 452 PSLKSPPPGFDSVIARGQTEPDPAQDIELELDGQPV 487
 ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,442
FILING DATE: 14-0CT-1994
FILING DATE: 10-NOV-1993
CLASSIFICATION: 530
 APPLICATION NUMBER: US 07/981,165
FILING DATE: 24-NOV-1992
CLASSIFICATION: 530
 5624-230
 Sequence 42, Application US/08484438
Patent No. 5811098
Patent No. 5811098 5780031
 TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
 Plowman, Gregory D.
 ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 56
TELECOMMUNICATION INFORMATION:
 TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
 LENGTH: 462 amino acids
 ; MOLECULE TYPE: protein US-08-484-438-42
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie &
 COMPUTER READABLE FORM:
 PRIOR APPLICATION DATA:
 amino acid
 STATE: New York COUNTRY: U.S.A. ZIP: 10036-2711
 GENERAL INFORMATION:
 TOPOLOGY:
 TELEFAX:
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us-09-701-586b-10.rai

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
 SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
 1656 DLAVAIE-----
 TOPOLOGY:
 US-08-125-077-5
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 1500 QTPGGSCQKCDCNPHGSVHGDCDRTSGQCVCRLGASGLRCDECEPRHILMETDCVSCDDE 1559
 1611
 1656 DLAVAIE------RLQMSITEIMEK-----TTLNOTLDEDFLLPNSTLQ 1693
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 Sequence 5, Application US/08125077
Patent No. 5872231
APPLICANT: Leivo, Ilmo
APPLICANT: Leivo, Ilmo
TITLE OF INVENTION: Pragments and Uses Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
 1905 V-----HYNIQSLIEESEELARDAHRIVTETSLLS-----ESLVSNGK 1942
 421 VTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQ 469
 E: Campbell and Flores 4370 La Jolla Village Drive, Suite 700
: LEBERAX: (619) 535-9001
; TELEFAX: (619) 535-9001
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTER.STICS:
; LENGTH: 3075 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-460-309-5
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
 San Diego
: California
 COUNTRY:
 RESULT 15
US-08-125-077-5
 STREET:
 STATE:
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23;
 745 VLKEAASHVLSKHNNEL-KAAEALVREAEAKMQESNHLLLMVNANLREFSDKKLHVQEEQ 1803
 ----RLOMSITEIMEK-----TTLNOTLDEDFLLPNSTLQ 1693
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 366 QAHSKLGNR-----RLLWHGTNVAVVAAILTSGLRIMPHSGGRVGKGIYFASENSKSAGY 420
 217 KQQIARGFEALEALE----EAMKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPD 271
 10 QTEGSKKQR----QGTEEEDSFRST-----AEALRAAPADNRVIRVDPSCPFSRNP 56
 272 VLQAKKDMLLVLADIELAQTLQAAPGEEEEKVEEVPHPL-----DRDYQLLRCQLQ---
 57 --GIQVHE-----DYDCTLNQTNI------GNNNNKFYIIQLLEEGSRFFCWNRWG
 160 EAVVKVDSGPVRTVVKPCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKK---MPLGKLT
 Length 3075;
 1905 V-----HYNIQSLIEESEELARDAHRTVTETSLLS-----ESLVSNGK 1942
 421 VTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQ 469
 Indels
 Query Match 3.7%; Score 102.5; DB 2; Best Local Similarity 19.7%; Pred. No. 3.3; Matches 104; Conservative 79; Mismatches 191;
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-JUL-1992
 NAME: Campbell, Cathryn A.
REGISTRAITON NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9721
TELECOMMUNICATION INFORMATION:
TELEFONE: (619) 535-9001
TELEFONE: (619) 535-9049
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERESTICS:
LENGTH: 3075 amino acids
TYPE: amino acid
 APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-JUL-1992
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US/08/125,077 FILING DATE: 22-SEP-1993 CLASSIFICATION: 435
```

Search completed: August 29, 2002, 07:58:25

Job time: 302 sec

us-09-701-586b-10.rai

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

August 29, 2002, 08:02:19 ; Search time 36.19 Seconds Run on:

(without alignments) 570.255 Million cell updates/sec

US-09-701-586B-8

Perfect score: Title:

2813 1 MAPKRKASVQTEGSKKQRQG......EYLIYKESQCRLRYLLEIHL 533 Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

105224 Total number of hits satisfying chosen parameters:

105224 seqs, 38719550 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description           | homo sap   | crice      | 4 mus musculu | 4 homo sapien | bos t      | 5 homo sapien | rattus   |            | arabido    |            |            |            | -            | 5 caenorhabdi | 3 homo sapien | _          | 2 mus musculu | 9 pseudomonas | 8 strongyloce |            |            |            | _          |            | 0 bos taurus |            | aguifex    |            | esche  |        | m          | schiz | 5 homo sapien |
|-----------|-----------------------|------------|------------|---------------|---------------|------------|---------------|----------|------------|------------|------------|------------|------------|--------------|---------------|---------------|------------|---------------|---------------|---------------|------------|------------|------------|------------|------------|--------------|------------|------------|------------|--------|--------|------------|-------|---------------|
|           | Descri                | Q9y6£1     | 09r152     | 088224        | P09874        | P18493     | ubn60         | P27008   | P26446     | 011207     | P3166      | P11103     | 01120      | P3587        | 00952         | Q9ukk3        | Q08824     | 56P60         | P1143         | P35978        | P33176     | P38904     | P49454     | 008404     | P12222     | P4882(       | P25391     | 067763     | . P09010   | P03003 | P98170 | 36         | 386   | 095235        |
| SUMMARIES | ΩI                    | PPO3_HUMAN | PPOL_CRIGR | PPO2_MOUSE    | PPOL_HUMAN    | PPOL_BOVIN | PPO2_HUMAN    | PPOL_RAT | PPOL_CHICK | PPOL_ARATH | PPOL_XENLA | PPOL_MOUSE | PPOL_SARPE | PPOL_DROME   | YON4_CAEEL    | PPOV_HUMAN    | PPOL_ONCMA | EVPL_MOUSE    | TOXA_PSEAE    | KINH_STRPU    | KINH_HUMAN | SP41_YEAST | CENF_HUMAN | CAT1_MYCFO | YCF1_TOBAC | RBP2_BOVIN   | LMA1_HUMAN | RPOC_AQUAE | LAM1_XENLA | - 1    | - 1    | RPA1_EUPOC |       | RB6K_HUMAN    |
|           | DB                    | -          | 7          | 7             | ٦             | Н          | ٦             | ٦        | Н.         | -          | ٦          | -          | -          | <del>-</del> | -             | -1            | -          | -             | -             | -             | -          | -          | -          | -          | Н          |              | 7          |            |            |        | Н      | -          | -     | -             |
|           | Query<br>Match Length | 533        | 1012       | 559           | 1013          | 1015       | 583           | 1013     | 1011       | 637        | 966        | 1012       | 966        | 994          | 538           | 1724          | 135        | 2035          | 638           | 1031          | 963        | 1395       | 3210       | 752        | 1901       | 1085         | 3075       | 1574       | 583        | 495    | 497    | 638        | 646   | 890           |
| de        | Query                 | 79.2       | 25.4       | 25.2          | 25.1          | 25.0       | 24.8          | 24.7     | 24.6       |            |            |            | 22.9       |              |               | 9.8           | ٠          | ٠             | •             | 3.8           | ٠          | ٠          | ٠          | 3.6        | ٠          |              | ٠          | ٠          | ٠          | •      | ٠      |            | ٠     |               |
|           | Score                 | ~          | 713.5      | 708           | 705           | 702        | 696.5         | 694.5    | 691.5      | 069        | 686.5      | 683.5      | 645.5      | 619          | 396.5         | 275           | 193        | 117           | 106.5         | 106.5         | 104.5      | 104        | 104        | 102        | 101.5      | 101          | 101        | 100.5      | 100        | 66     | 66     | 66         | 66    | 66            |
|           | Result<br>No.         |            | 7          | m             | 4             | 2          | 9             | 7        | œ ·        | on :       | 10         | 11         | 12         | 13           | 14            | 15            | 16         | 17            | 18            | 19            | 20         | 21         | 22         | 23         | 24         | 25           | 56         | 27         | 28         | 53     | 30     | 31         | 32    | 33            |

|                          | P11109 bacteriopha<br>Q10332 schizosacch |            |            |            |            |            |            |
|--------------------------|------------------------------------------|------------|------------|------------|------------|------------|------------|
| T2F1_FLAOK<br>NNP1_DROME | EXO2_BPT5<br>YBMA_SCHPO                  | KINH_MOUSE | US26_HCMVA | E4L2_HUMAN | NCR1_MOUSE | ACF7_MOUSE | PAB2_ARATH |
|                          |                                          |            | -          |            | -          | Н          | П          |
| 583<br>687               | 612<br>830                               | 963        | 603        | 1005       | 2453       | 5327       | 629        |
| 3.5<br>5.5               | 3.5<br>5.5                               | 3.5        | 9.0        | 3.4        | 3.4        | 3.4        | 3.4        |
| 98.5<br>98.5             | 8 8<br>6<br>6                            | 98         | 97.5       | 96.5       | 96.5       | 96.5       | 96         |
| 34<br>35                 | 36<br>37                                 | 38         | 40         | 42         | 43         | 44         | 45         |

## ALIGNMENTS

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 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 PPO3_HUMAN STANDARD; PRT; 533 AA.

Q9YGF1; Q9UG81;

LG-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

16-OCT-2001 (Rel. 40, Last annotation update)

Poly [ADP-ribose] polymerase-3 (EC 2.4.2.30) (PARP-3) (NAD(+) ADP-ribosyltransferase-3) (Poly(ADP-ribose] synthetase-3) (PABPRT-3)
 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 "A human poly(ADP-ribose) polymerase gene family (ADPRTL): cDNA cloning of two novel poly(ADP-ribose) polymerase homologues."; Genomics 57:442-445(1999).
 HSSP; P26446; 1A26.
InterPro; IPR001290; PARP.
InterPro; IPR004102; PARP_reg.
Pfam; PF00644; PARP; 1.
Pfam; PF00844; PARP; 1.
Transferase; Glycosyltransferase; NAD; Nuclear protein;
 K -> N (IN REF. 2).
 TISSUE-Fetal brain;
MEDLINE-99263509; PubMed=10329013;
 EMBL; AF083068; AAD29855.1; -. EMBL; AL050034; CAB43246.1; -.
 (hparē-3).
Adpril3 or parp3 or adpri3.
 30
80
 SEQUENCE FROM N.A.
 ADP-ribosylation.
 NCBI_TaxID=9606;
 Johansson M.;
 DOMAIN
RESULT 1
PPO3_HUMAN
 PAGE BARRARY AND STANDARY AND S
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us-09-701-586b-8.rsp

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EVENTS INVOLVED IN THE RECOVERY OF CELL FROM DNA DAMAGE
 +++
 á
 5;
 Ganesh A., Philips E., Thacker J., Meuth M.;

"Supression of the radiation-sensitive phenotype of hamster irsl and irs2 strains selected for resistance to 3-aminobenzamide.";
Int. J. Radiat. Biol. 77:609-616(2001).
-!- FUNCTION: POLY[ADP-RIBOSE] POLYMERASE MODIFIES VARIOUS NUCLEAR PROTEINS BY POLY(ADP-RIBOSYL)ATION. THE MODIFICATION IS DEPENDENT ON DNA AND IS INVOLVED IN THE REGULATION OF VARIOUS IMPORTANT CELLULAR PROCESSES SUCH AS DIFFERENTIATION, PROLIFERATION, AND TUMOR TRANSFORMATION AND ALSO IN THE REGULATION OF THE MOLECULAR
 235
 QVHEDYDCTLNQTNIGNNNNKFYIIQLLEEGSRFF-CWNRWGRVGEVGQSKMNHFTCLED 117
 61 QVYEDYNCTLNQTNIENNNKKFYIIQLLQDSNRFFTCWNRWGRVGEVGGSKINHFTRLED 120
 177
 234
 294
 QTLQAAPGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQTGNSYRCPN 354
 354
 LRHVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPHSGGRVGKGIY 414
 FASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQ 474
 16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Poly [ADP-ribose] polymerase-1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+)
ADP-ribosyltransferase-1) (PolyfADP-ribose] synthetase-1).
 Gaps
 1 MAPKRKASVQTEG--SKKQRQGTEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGI 58
 9
 1 MAPKPWWQTEGPEKKKGRQAGREEDPFRSTAEALKAIPAEKRIIRVDPTCPLSSNPGT
 AKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKALSPQVDSGPVRT
 V - - - VKPCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEA
 LEEAMKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELA
 Euteleostomi;
 Cricetulus griseus (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 12;
 Length 533;
 Indels
A -> G (IN REF. 2).

K -> E (IN REF. 2).

7C0AB89E64D1B9FD CRC64;
 %; Score 2229; DB 1;
%; Pred. No. 1.2e-154;
37; Mismatches 60;
 1012 AA
 SEQUENCE FROM N.A. MEDLINE-21276334; Pubmed-11382339;
 16-OCT-2001 (Rel. 40, Created)
 MM;
 Query Match
Best Local Similarity 79.8%;
Matches 430; Conservative 37
 60117
 STANDARD;
171
411
533 AA;
 NCBI_TaxID=10029;
 PPOL_CRIGR
Q9R152;
 Cricetulus.
 SEQUENCE
CONFLICT
 ADPRT.
 415
 PPOL_CRIGR
 178
 235
 118
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 295
 296
 355
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 17;
CATALYTIC ACTIVITY: NAD(+) + {ADP-D-ribosyl}(N)-acceptor = nicotinamide + {ADP-D-ribosyl}(N+1)-acceptor.

COFACTOR: ZINC, CONTAINS TWO MOLES OF ZINC PER MOLE OF PROTEIN (BY
 SIMILARITY).
SUBURT: HOMODIMER (POCENTIAL).
SUBGUELLULAR LOCATION: Nuclear.
MISCELLULAR LOCATION: Nuclear.
MISCELLULAR LOCATION: Nuclear.
MISCELLANEOUS: THE ADP-D-RIBOSYL GROUP OF NAD(+) IS TRANSFERRED TO
MISCELLANEOUS: THE ADP-D-RIBOSYL GROUP ON A HISTONE OR THE BUZYME ITSELF, AND
FURTHER ADP-RIBOSYL GROUPS ARE TRANSFERRED TO THE 2'-POSITION OF
THE TERMINAL ADENOSINE MOIETY, BUILDING UP A POLYMER WITH AN
SIMILARITY: BELONGS TO THE PARP FAMILY.
SIMILARITY: CONTAINS I BRCT DOMAIN.
 PROSITE; PS50172; BRCT; 1.

PROSITE; PS00347; PARP_ZN_FINGER_1; 2.

PROSITE; PS50064; PARP_ZN_FINGER_2; 2.

Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein; ADP-ribosylation; Zinc-finger; Zinc.

INIT_MET 0 0 BY SIMILARITY.

DNA_BIND 1 371 BY SIMILARITY.
 Gaps
 SIMILARITY)
 2 APKRKASVQTEGSKKQRQGTEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQVH 61
 NUCLEAR LOCALIZATION SIGNAL 1ST PART
 2ND PART
 49;
 Length 1012;
 AUTOMODIFICATION DOMAIN (BY
 NUCLEAR LOCALIZATION SIGNAL
 Indels
 NAD-BINDING (BY SIMILARITY)
 (POTENTIAL)
 (POTENTIAL)
 (POTENTIAL)
 (POTENTIAL)
 (POTENTIAL)
 (POTENTIAL)
 (POTENTIAL)
 (POTENTIAL)
CBOF7 CRC64
 POTENTIAL)
 (POTENTIAL)
 (POTENTIAL)
 ADP-RIBOSYLINI (POTENT)
ADP-RIBOSYLINI (POTENT)
ADP-RIBOSYLINI (POTENT)
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ADP-RIBOSYLINI (POTENT)
ADP-RIBOSYLINI (POTENT)
ADP-RIBOSYLINI (POTENT)
ADP-RI
 25.4%; Score 713.5; DB 1; 33.9%; Pred. No. 4.6e-44;
 214;
 Mismatches
 (POTENTIAL)
 Interpro; IPR001357; BRCT.
Interpro; IPR001102; PARE_reg.
Interpro; IPR001510; Znf-PARP.
Pfam; PF00533; BRCT; 1.
Pfam; PF002877; PARE_reg; 1.
Pfam; PF00645; Zf-PARP; 2.
ProDom; PD004675; Znf-PARP; 2.
 97;
 EMBL; AF168781; AAD45817.1; -. HSSP; P26446; 1A26.
 512
518
112400 M
 Conservative
 SMART; SM00292; BRCT; 1.
 371
522
475
1012
55
161
208
 4412
44434
44436
4444
44755
4483
 AA;
 Query Match
Best Local Similarity
Matches 185; Conserv
 518
1012
 4412
4434
4443
4443
4443
4470
4487
5111
 20
124
206
 220
 MOD_RES
MOD_RES
MOD_RES
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MOD_RES
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MOD_RES
SEQUENCE
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 Ame J.-C., Rolli V., Schreiber V., Niedergang C., Apiou F., Decker P., Muller S., Hoger T., Menissier-de Murcia J., de Murcia G.M.; "PARP-2, A novel mammalian DNA damage-dependent poly(ADP-ribose)
193 APKGKSAAPSKKSK----GLYKEEGVNKSEKRMKLTLKGGAAVDPDSGLEHSAHVLEKGG 548
 119 KKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKALSPQVDSGPVRTV 178
 235
 714
 407
 887
 944
 SVIARGQTEPDPAQDIELELDGQPVVVPQGPPVQCPS-FKSSSFSQSEYLIYKESQCRLR 526
 296 TLQAAPGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQ----TGNSYR 351
 RVGKGIYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFD 467
 "A bidirectional promoter connects the poly(ADP-ribose) polymerase 2 (PARP-2) gene to the gene for RNase P RNA."; J. Biol. Chem. 276:11092-11099(2001).
 62 EDYDCTLNQTNIGNNNNKFYIIQLLEEG -- SRFFCWNRWGRVGEV-GQSKMNHFTCLEDA
 179 VKP---CSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEAL
 EEAMKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQ
 829 L-EVMDIFKIEREGESQRYKPFKQLHNRRLLWHGSRTTNFAGILSQGLRIAPPEAPVTGY
 16-OCT-2001 (Rel. 40, Last sequence update)
16-MAR-2002 (Rel. 41, Last annotation update)
Poly (App-ribose) polymerase-2 (EC 2.4.2.30) (PARP-2) (NAD(+) App-ribose] (PARP-2) (PARP-2) (POly[ADP-ribose] synthetase-2) (PADPRT-2)
 549 KVFSATLGLVDIVKGTNSYYKLQLLEDDKESRYWIFRSWGRVGTVIGSNKLEQMPSKEDA
 352 CPNLRHVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGG
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
 de Murcia G.M.,
 MEDLINE-21179160; PubMed-11133988;
Ame J.-C., Schreiber V., Fraulob V., Dolle P.,
Niedergang C.P.;
 559 AA
 SEQUENCE FROM N.A., AND CHARACTERIZATION
 Biol. Chem. 274:17860-17868(1999).
 TISSUE-Embryo;
MEDLINE-99292755; PubMed-10364231;
 PPO2_MOUSE STANDARD; P
088554; Q99N29;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequol-MAR-2002 (Rel. 41, Last anno
 (mPARP-2).
ADPRTL2 OR PARP2 OR ADPRT2.
 Mus musculus (Mouse).
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 999 YLLKL 1003
 527 YLLEI 531
 STRAIN-129Sv;
 polymerase."
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 23;
 Berghammer H., Ebner M., Marksteiner R., Auer B.; "pADPRT-2: a novel mammalian polymerizing(ADP-ribosyl)transferase gene related to truncated pADPRT homologues in plants and Caenorhabditis
 FEBS Lett. 449:259-263(1999).

- FEBS LETT. A ROLE IN THE RESPONSE TO DNA DAMAGE.

- CAPALYTIC ACTIVITY: NOLE | + {ADD-D-ribosy1}(N)-acceptor = nicotinamide + {ADP-D-ribosy1}(N+1)-acceptor.

- FEBSUE SEMELLUAR LOCATION: Nuclear.

- TISSUE SPECIFICITY: Widely expressed; the highest levels were in testis followed by ovary.

- INDUCTION: By high levels of DNA-damaging agents.

- SIMILARITY: BELONGS TO THE PARP FAMILY.
 GSR--FFCWNRWGRVGEVGQSKMNHFTC---LEDAKKDFKKKFWEKTKNKWEERDRFVAQ 143
 144 PNKYTLIEVQGEAESQEAVVKALSPQVDSGPVRTVVKPCSLDPATQNLITNIFSKEMFKN 203
 AMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEAMKNPTGD-GQSLEELSSCFYTVIPH 262
 Pfam; PF00644; PARP; 1.
Pfam; PF02877; PARP_reg; 1.
Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein;
 82; Gaps
 1 MAPRRORSGSGRRVLNE-AKKVDNGNKATEDDSPPGKKMRTCORKGPMAGGKDADRTKDN 59
 R------VIRVDPSCPFSRNPG---IQVHEDYDCTLNQTNIGNNNNKFYIIQLLEE 88
 1 MAPKRKAS-----VQTEGSKKQRQGTE--EEDS--FRSTAEALRAAP------ADN 41
 PGKYDMLQMDYAASTQD-----ESKTKEEETLKPESQLDLRVQELLKLICNVQTMEE
 NUCLEAR LOCALIZATION SIGNAL 2ND PART (POTENTIAL).
 NUCLEAR LOCALIZATION SIGNAL 1ST PART
 25.2%; Score 70%; DB 1; Length 559; 34.4%; Pred. No. 5.1e-44; ive 88; Mismatches 212; Indels
 SIMILARITY)
 L -> V (IN REF. 2).
V -> I (IN REF. 2).
R -> Q (IN REF. 2).
EDAEDAEE412C1445 CRC64;
 NAD-BINDING (BY
 (POTENTIAL)
 EMBL; AJ007780; CAA07679.1; -.
EMBL; AF191547; AAK13253.1; -.
EMBL; AP072521; AAC25415.1; ALT_INIT.
HSSP; PG4446; 1A26.
MGD; MGT:1341112; AGPT2.
InterPro; IPR001290; PARP.
 POTENTIAL.
MEDLINE-99268466; PubMed-10338144;
 486 F
63396 MW;
 Query Match 25.2°
Best Local Similarity 34.4°
Matches 200; Conservative
 65
559
9
 82
177
 39
 82
177
486
559 AA;
 ADP-ribosylation.
 33
 DNA_BIND
DOMAIN
 CONFLICT
CONFLICT
SEQUENCE
 CONFLICT
 DOMAIN
 DOMAIN
 42
 89
 178
 204
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01-MAR-1989 (Rel. 10, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Poly [ADP-ribose] polymerase-1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+)
ADP-ribosyltransferase-1) (Poly[ADP-ribose] synthetase-1).
NFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAAPGEEEEKVEEVPHPLDRDYQLL 322
 288 DFGLSIPPVIRTEKELSDKVKLLEALGDIEIALKLVKS---ERQGLE---HPLDQHYRNL 341
 323 RCQLQLLDSGESEYKAIQTYLKQTGNSYRCP-----NLRHVWKVNREGEGDRFQAHSK 375
 342 HCALRPLDHESNEFKVISQYLQST----HAPTHKDYTMTLLDVFEVEKEGEKEAFR--ED 395
 376 LGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKGIYFASENSKSAGYVTTMHC 431
 MEDLINE-88068596; PubMed-2891139; Cherney B.W., McBride O.W., Chen D., Alkhatib H., Bhatia K., Hensley P., Smulson M.E.; "cDNA sequence, protein structure, and chromosomal location of the human gene for poly(Abp-ribose) polymerase."; Proc. Natl. Acad. Sci. U.S.A. 84:8370-8374(1987).
 "Primary structure of human poly(ADP-ribose) synthetase as deduced from cDNA sequence.";
 TISSUE=Fibroblast;
MEDLINE=88076933; PubMed=3120710;
MCDida K., Morita T., Sato T., Ogura T., Yamashita R., Noguchi S., Suzuki H., Nyunoya H., Miwa M., Sugimura T.;
"Nucleotide sequence of a full-length cDNA for human fibroblast poly(ADP-ribose) polymerase.";
 432 GGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQTEPDPAQDIELELDGQP
 Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
 SEQUENCE OF 440-1013 FROM N.A.
MEDLINE-87298455; PubMed-3113420;
Suzuki H., Uchida K., Shima H., Sato T., Okamoto T., Kimura T.,
 Σ.
 TISSUE-Fibrobiast;
BADLINE-80658958; PubMed-2824474;
Kurosai T., Ushiro H., Mitsuchi Y., Suzuki S., Matsuda M.
Matsuda Y., Katunuma N., Kangawa K., Matsuo H., Hirose T.,
 MEDLINE-90091744; PubMed-2513174;
Auer B., Nagl U., Herzog H., Schneider R., Schweiger M.;
Human nuclear NAD+ ADP-ribosyltransferase(polymerizing):
Organization of the gene.";
DNA 8:575-580(1989).
 492 VVVPQGPPVQCPSFKSSSF--SQSEYLIYKESQCRLRYLLEI 531
 Biochem. Biophys. Res. Commun. 148:617-622(1987)
 511 -TVPLGPASDTGILNPEGYTLNYNEFIVYSPNQVRMRYLLKI
 PRT; 1013 AA
 Biol. Chem. 262:15990-15997(1987).
 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
 STANDARD;
 Inayama S., Shizuta Y.,
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID-9606;
 PPOL_HUMAN
P09874;
 PPOL_HUMAN
563
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"The human poly(ADP-ribose) polymerase nuclear localization signal is a bipartite element functionally separate from DNA binding and caralution activity."
"Molecular cloning of cDNA for human poly(ADP-ribose) polymerase and expression of its gene during HL-60 cell differentiation."; Biochem. Biophys. Res. Commun. 146:403-409(1987).
 Simonin F., Menissier de Murcia J., Poch O., Muller S., Gradwohl G., Mollinete M., Penning C., Reith G., de Murcia G.M., "Expression and site-directed mutagenesis of the catalytic domain of human poly(ADP-ribose)polymerase in Escherichia coli. Lysine 893 is
 polymerase are
of DNA breaks and nicks
 Yokoyama Y., Kawamoto T., Mitsuuchi Y., Kurosaki T., Toda K., Ushiro H., Terashima M., Sumimoto H., Kuribayashi I., Yamamoto Y., Maeda T., Ikeda H., Sagara Y., Shizuta Y., Human poly(ADP-ribose) polymerase gene. Cloning of the promoter region.";
 "Characterization of a putative promoter region of the human poly(ADP-ribose) polymerase gene: structural similarity to that of the DNA polymerase beta gene."; Biochem. Biophys. Res. Commun. 167:701-710(1990).
 Ikelima M., Noguchi S., Yamashita R., Ogura T., Sugimura T., Gill D.M., Miwa M.; are zinc fingers of human poly(ADP-ribose) polymerase are differentially required for the recognition of DNA breaks and nic and the consequent enzyme activation. Other structures recognize
 MUTAGENESIS OF CATALYTIC DOMAIN.
MEDLINE-27461532; PubMed-9311881;
Rolli V., O'Farrell M., Menissier-de Murcia J., de Murcia G.M.;
"Random mutagenesis of the poly(ADP-ribose) polymerase catalytic
 Ogura T., Nyunoya H., Takahashi-Masutani M., Miwa M., Sugimura
Esumi H.;
 MEDLINE-90222155; PubMed-2109322; Gradwohl G., Menissier de Murcia J., Molinete M., Simonin F., Koken M.H.M., Hoeljmakers J.H.J., de Murcia G.M.; The second Zinc-finger domain of poly(ADP-ribose) polymerase determines specificity for single-stranded breaks in DNA."; Proc. Natl. Acad. Sci. U.S.A. 87:2990-2994(1990).
 Suzuki H., Uchida K., Shima H., Sato T., Okamoto T., Kimura
 SEQUENCE OF 1-39 FROM N.A.
Herzog H., Schneider R., Hirsch-Kauffmann M., Schnitzer
Schweiger M.;
 Submitted (JUL-1991) to the EMBL/GenBank/DDBJ databases
 H., de Murcia G.M.,
 Biochem. Biophys. Res. Commun. 148:1549-1550(1987)
 Biol. Chem. 265:21907-21913(1990).
 Biol. Chem. 265:19249-19256(1990).
 Eur. J. Biochem. 194:521-526(1990).
 MEDLINE=92371433; PubMed=1505517;
Schreiber V., Molinete M., Boeuf H
Menissier de Murcia J.;
 SEQUENCE OF 1-94 FROM N.A.
MEDLINE=91099327; PubMed=2125269;
 SEQUENCE OF 1-39 FROM N.A. MEDLINE=90211250; PubMed=2108670;
 MUTAGENESIS OF CATALYTIC DOMAIN.
MEDLINE=91035460; PubMed=2121735;
 ANALYSIS OF ZINC FINGERS.
MEDLINE-91072398; Pubmed-2123876;
 NUCLEAR LOCALIZATION SIGNAL.
 EMBO J. 11:3263-3269(1992).
 ANALYSIS OF ZINC FINGERS.
 for activity
 catalytic activity
 intact DNA.
 Miwa M.;
 critical
 ERRATUM.
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InterPro; IPR004102;
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 RESULT 5
PPOL_BOVIN
 ADPRT.
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 domain reveals amino acids involved in polymer branching.";
Biochemistry 36:12147-12154(1997).
-!- FUNCTION: POLY[ADP-RIBOSE] POLYMERASE MODIFIES VARIOUS NUCLEAR PROTEINS BY POLY(ADP-RIBOSCL)ATION. THE MODIFICATION IS DEPENDENT ON DAM AND IS INVOLVED IN THE REGULATION OF VARIOUS IMPORTANT CELLULAR PROCESSES SUCH AS DIFFERENTIATION, PROLIFERATION, AND TUMOR TRANSFORMATION AND ALSO IN THE REGULATION OF THE MOLECULAR
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 M17081; AAA51599.1; ALT_SEQ
 Aarhus/Ghent-2DPAGE; 1620; NEPHGE.
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 X56141; CAA39606.1; JOINED. M60436; AAA60000.1; -.
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 EMBL; X16674; CAA34663.1; -. EMBL; M18112; AAA60137.1; -.
 AAA51663.1;
AAA51663.1;
AAA51663.1;
 InterPro; IPR001357; BRCT.
InterPro; IPR001290; PARP.
 J03473; AAB59447.1;
 M29545; AAA51663.1;
 AAA51663.1;
 AAA51663.1;
AAA51663.1;
 AAA51663.1;
 AAA51663.1;
 AAA51663.1;
AAA51663.1;
 AAA51663.1;
 AAA51663.1;
AAA51663.1;
 M29544; AAA51663.1;
 AAA51663.1;
 AAA51663.1
 M32721; AAA60155.1
M29786; AAA51663.1
 AAA51663.1
 AAA51663.1
 AAA51663.
 AAA51663.
 A35635.
 A28498.
A29725.
 B33321; B33321
A39976; A39976
 S14010
 HSSP; P26446; 1A26
 EMBL; M32721;
 M29766;
 M29768;
 M29767;
 M29769:
 M29770:
 M29774;
 M29779;
 M29780;
 M29783;
 M29784;
 M29785;
 M29782;
 x56140;
 M29772:
 M29775:
 A35635;
 S14010;
 A29725;
 A33321;
 A28498;
 MIM; 173870;
 M29777
 EMBL;
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17;
 948 KGLGKTTPDPSANI--SLDG--VDVPLGTGIS-SGVNDTSLLYNEYIVYDIAQVNLKYLL 1002
 | : | | : | | | | :: | | | :: | | 609 AIEHFMKLYEEKTGNAWHSKN-FTKYPKKFYPLEID-YGQDEEAVKKL---TVNPGTKSK 663
 237
 297
 354 NLRHVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRV 409
 470 IARGQTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLL 529
 PPOL_BOVIN STANDARD; PRT; 1015 AA.
P1843; 09TS00;
01-N0V-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Poly [ADP-ribose] polymerase-1 (EC_2.4.2.30) (PARP-1) (ADPRT) (NAD(+)
 61 HEDYDCTLNQTNIGNNNNKFYIIQLLEEG--SRFFCWNRWGRVGEV-GQSKMNHFTCLED 117
 QAAPGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQ----TGNSYRCP 353
 GKGIYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSV 469
 Gaps
 1 MAPKRKASVQTEGSKKQRQGTEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQV 60
 SEQUENCE FROM N.A. MEDIAGE 119324; MEDLINE-90382673; PubMed=2119324; Saito I., Hatakeyama K., Kido T., Ohkubo H., Nakanishi S., Ueda K.; "Cloning of a full-length cDNA encoding bovine thymus poly(ADP-ribose) synthetase: evolutionarily conserved segments and
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 492 VAPRGKSGA---ALSKKSKGQVKEEGINKSEKRMKLTLKGGAAVDPDSGLEHSAHVLEKG
 178 VVKPCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEE
 238 AMKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTL
 AKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKALSPQVDSGPVRT
 40;
 Length 1013;
 Query Match 25.1%; Score 705; DB 1; Length 101
Best Local Similarity 33.8%; Pred. No. 1.9e-43;
Matches 183; Conservative 101; Mismatches 218; Indels
 ADP-ribosyltransferase-1) (Poly[ADP-ribose] synthetase-1)
PARP_reg.
Znf-PARP.
 their potential functions.";
Gene 90:249-254(1990).
 Bovidae; Bovinae; Bos.
NCBL_TaxID=9913;
 Pfam; PF00533; BRCT;
Pfam; PF00644; PARP;
 InterPro; IPR001510;
 Bos taurus (Bovine).
 1003 KL 1004
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9

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Query Match
Best Local Simi
Matches 187;
 MOD_RES
MOD_RES
SEQUENCE
 MOD_RES
MOD_RES
MOD_RES
MOD_RES
 PPO2_HUMAN
 233
 465
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 661
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 C. I. FUNCTION: POLY(ADP-RIBOSE) POLYMERASE MODIFIES VARIOUS NUCLEAR PROTEINS BY POLY(ADP-RIBOSE) POLYMERASE MODIFIESTION IS DEPENDENT OF VARIOUS INFORMATION. THE MODIFICATION IS DEPENDENT ON DNA AND IS INVOLVED IN THE RECULATION OF VARIOUS INFORMAT CELLULAR PROCESSES SUCH AS DIFFERENTIATION PROLIFERATION, AND TUMOR TRANSFORMATION AND ALSO IN THE RECULATION OF THE MOLECULAR EVENTS INVOLVED IN THE RECOVERY OF CELL FROM DNA DAMAGE.

1. CATALYTIC ACTIVITY: NAD(+) + {ADP-D-tibosy1}(N)-acceptor - I.COFACTOR: INC. CONTAINS TWO MOLES OF ZINC PER MOLE OF PROTEIN.

2. I. SUBGUITT: HOMODIMER (Potential).

3. SUBGELLAULAR LOCATION: Nuclear.

4. NA SCELLANEOUS: THE ADP-D-RIBOSYL GROUP OF NAD(+) IS TRANSFERRED TO THE 2'-POSITION OF THE TEXMINAL ADENOSINE MOLEY, BUILDING UP A POLYMER WITH AN AVERAGE CHAIN LENGTH OF 20-30 UNITS.

2. STMILARITY: BELONGS TO THE PARP FAMILY.
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 MEDLINE-88151954; PubMed-2450019; Taniquchi T., Yamauoto T., Toyoshima K., Harada N., Tanakuchi T., Yamamoto T., Toyoshima K., Harada N., Tanaka H., Takahashi S., Yamamoto H., Fujimoto S.; "Depression in gene expression for poly(ADP-ribose) synthetase during
 SMART; SM00292; BRCT; 1.
PROSITE; PS50172; BRCT; 1.
PROSITE; PS50047; PARP_ZN_FINGER_1; 2.
PROSITE; PS50064; PARP_ZN_FINGER_2; 2.
Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein;
 the interferon-gamma-induced activation process of murine macrophage
 PART.
PART.
 NUCLEAR LOCALIZATION SIGNAL 1ST PA.
NUCLEAR LOCALIZATION SIGNAL 2ND PA.
ADP-RIBOSYL[N] (POTENTIAL).
 AUTOMODIFICATION DOMAIN
 ; Zinc.
BY SIMILARITY
 647-714 AND 838-903 FROM N.A.
 PARP-TYPE.
 tumor cells.";
Eur. J. Biochem. 171:571-575(1988)
 Pfam; PF00644; PARP; I.
Pfam; PF02847; PARP; I.
Pfam; PF00845; zf-PARP; 2.
ProDom; PD0004675; Znf-PARP; 2.
 Zinc-finger;
 InterPro; IPR004102; PARP_reg.
InterPro; IPR001510; Znf-PARP.
 EMBL; D90073; BAA14114.1; -. EMBL; X06986; CAA30046.1; -. EMBL; X06987; CAA30047.1; -.
 InterPro; IPR001357; BRCT.
InterPro; IPR001290; PARP.
 525
462
1015
55
164
 PIR; JS0428; JS0428.
PIR; S00328; S00328.
HSSP; P26446; 1A26.
 Pfam; PF00533; BRCT;
 ADP-ribosylation;
 INIT_MET
DNA_BIND
DOMAIN
 DOMAIN
DOMAIN
ZN_FING
ZN_FING
 MOD_RES
MOD_RES
MOD_RES
 DOMAIN
MOD_RES
MOD_RES
MOD_RES
 MOD_RES
 DOMAIN
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20;
 115 SEVQQALSQGSSDSHIL-DLSNRFYTLIPHDFGMKKPPLLNNANSVQAKVEMLDNLLDIE 773
 LAQTLQAAPGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQ----TGN 348
 404
 464
 58 I -- QVHEDYDCTLNQTNIGNNNNKFYIIQLLEEG -- SRFFCWNRWGRVGEV - GQSKMNHF 112
 113 TCLEDAKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKALSPQVDS 172
 Gaps
 1 MAPKRKASVQTEGSKKQRQGTEEEDSFRSTAE---ALRAAPADNRVIRVDPSCPFSRNPG 57
 01-MAR-2002 (Rel. 41, Last annotation update)
Poly (ADP-ribose] polymerase-2 (EC 2.4.2.30) (PARP-2) (NAD(+) ADP-ribosyltransferase-2) (Poly[ADP-ribose] synthetase-2) (PADPRT-2)
 494 VGPKGKSGAAP--SKKSKGPVKEEGINKSEKRMKLTLKGGAA-----VDPDSGLEHNAH
 EALEEAMKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIE
 SYRCPNLRHVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----
 GFDSVIARGQTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCR
 546 VLEKGGKVFSATLGLVDIVKGTNSYYKLQLLEDDKESRYWIFRSWGRVGTVIGSNKLEQM
 GPVRTVVKPCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEAL
 SGGRVGKGIYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPP
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 50;
 Length 1015;
ADP-RIBOSYL[N] (POTENTIAL).
 Mismatches 215; Indels
 ; DB 1;
3.2e-43;
 PPO2_HUMAN STANDARD; PKI; Jos ALL. 99UGN5; Q9YGC8; Q9NUV2; Q9UMR4; D16-CCT-2001 (Rel. 40, Last sequence update) 16-CCT-2001 (Rel. 40, Last sequence update)
 Score 702;
Pred. No. 3
 25.0%; Scor
34.2%; Pred
 [1]
SEQUENCE FROM N.A. (ISOFORM 2).
TISSUE-Fetal brain;
 113355
 ADPRIL2 OR PARP2 OR ADPRIZ.
 Conservative
 472
485
485
492
514
521
 Homo sapiens (Human)
 ¥.
 Local Similarity
 1000 LKYLLKL 1006
 525 LRYLLEI 531
 485
489
492
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515
521
1015
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VARSPLIC
CONFLICT
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 Berghammer H., Ebner M., Marksteiner R., Auer B.,
"pADPRT-2: a novel mammalian polymerizing(ADP-ribosyl)transferase gene related to truncated pADPRT homologues in plants and Caenorhabditis
 <u>.</u>
 Masuho Y., Kanehori K.;
"NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: HAS DNA-DEPENDENT POLY[ADP-RIBOSE] FOLYMERASE ACTIVITY.
SEEMS TO PLAY A ROLE IN THE RESPONSE TO DNA DAMAGE (BY
 Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein; ADP-ribosylation; Alternative splicing.

DNA_BIND 1 88 POTENTIAL.
 Niedergang C., Apiou F., Decker
Murcia J., de Murcia G.M.;
 TISSUE-Placenta;
Stogal T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,
Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y.,
Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,
 (POTENTIAL).
NUCLEAR LOCALIZATION SIGNAL 2ND PART (POTENTIAL).
 NAD-BINDING (BY SIMILARITY).
NUCLEAR LOCALIZATION SIGNAL 1ST PART
 Ame J.-C., Rolli V., Schreiber V., Niedergang C., Apiou F., Decke Muller S., Hoeger T., Menissier-de Murcia J., de Murcia G.M.; "PARP-2, a novel mammalian DNA damage-dependent poly(ADP-ribose)
 "A human poly(ADP-ribose) polymerase gene family (ADPRTL): cDNA cloning of two novel poly(ADP-ribose) polymerase homologues."; Genomics 57:442-445(1999).
 -!- SIMILARITY: BELONGS TO THE PARP FAMILY.
 [3]
SEQUENCE OF 22-583 FROM N.A. (ISOFORM 1).
 SEQUENCE OF 2-583 FROM N.A. (ISOFORM 1).
 AF085734; AAD29857.1; ALT_INIT.
AJ236876; CAB41505.2; ALT_INIT.
AK001980; BAA92017.1; ALT_TERM.
 polymerase.";
J. Biol. Chem. 274:17860-17868(1999).
 MEDLINE-99292755; PubMed-10364231;
 TISSUE-Fetal brain;
MEDLINE-99263509; PubMed-10329013;
 TISSUE=Fibroblast;
MEDLINE-99268466; PubMed-10338144;
 SEQUENCE FROM N.A. (ISOFORM 1).
 InterPro; IPR004102; PARP_reg.
Pfam; PF00644; PARP; 1.
Pfam; PF02877; PARP_reg; 1.
 FEBS Lett. 449:259-263(1999).
 EMBL; AJ236912; CAB65088.1; -
 HSSP; P26446; 1A26.
InterPro; IPR001290; PARP.
 40
 86
 35
 Johansson M.;
 THYMUS
 elegans.
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 DOMAIN
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 EMBL:
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330
 PPOL_RAT
PPOL_RAT
PPOL_RAT
P27008: 035937;
01-AUG-1992 (Rel. 33, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Poly (ADP-ribose) polymerase-1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+)
ADP-LIbosyltransferase-1) (Poly[ADP-ribose] synthetase-1).
 224
 222
 281
 384
 442
 --IQVHEDYDCTLNQTNIGNNNNKFYIIQLLEEGSR--FFCWNRWGRVGEVGQSKMNHFT 113
 282 KDMLLVLADIELAQTLQAAPGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQT 341
 LRIMPH----SGGRVGKGIYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITI 454
 501 ANPKAEGLLQGKHSTKGLGKMAPSSAHFV--TLNGS--TVPLGPASDTGILNPDGYTLNY 556
 Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
 Beneke S., Meyer R., Buerkle A.;
"Isolation of cDNA encoding full-length rat (Rattus norvegicus) poly
 114 C---LEDAKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEV-----QGEAESQEAV
 165 CSGNLNKAKEIFQKKFLDXTKNNWEDREKFEKVPGKYDMLQMDYATNTQDEEETKKEESL
 273 AQIKAGYQSLKKIEDCIR--AGQHGRALMEACNEFYTRIPHDFGLRTPPLIRTQKELSEK
 331 IQLLEALGDIBIAIKL-----VKTELQSPEHPLDQHYRNLHCALRPLDHESYEFKVISQ
 163 VKALSPQVDSGPVRTVVKPCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTK
 225 KSPLKPE-----SQLDLRVQELIKLICNVQAMEEMMMEMKYNTKKAPLGKLTV
 223 QQIARGFEALEALEEAMKNPTGD-GQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAK
 342 YLKQT---GNSYRCPNLRHVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSG
 DDPSLKSPPPGFDSVIARGQTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSF--SQ
 GSKKQRQGTEEED-----SFRSTAEALRA----APADNRVIRVDPSCPFSRNPG-
 17;
 Length 583;
 Indels
 5B7AE8AE531836AF CRC64;
 5).
 Query Match 24.8%; Score 696.5; DB 1; Best Local Similarity 33.1%; Pred. No. 3.7e-43; Matches 185; Conservative 97; Mismatches 200;
 MISSING (IN ISOFORM
 P -> H (IN REF. 2).
N -> H (IN REF. 4).
 (ADP-ribose) polymerase.";
Biochem. Mol. Biol. Int. 43:755-761(1997).
 STRAIN=SPRAGUE-DAWLEY; TISSUE=Monocytes; MEDLINE-98046546; PubMed-9385436;
 66205 MW;
 :||::| :| |:||||::
NEYIVYNPNOVRMRYLLKV 575
 SEYLIYKESQCRLRYLLEI 531
80
447
481
 Rattus norvegicus (Rat)
 68
447
481
583 AA;
 SEQUENCE FROM N.A.
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4407
44313
44313
4444
4445
4444
4488
4488
4491
6318
6318
6411
 1001 LLKL 1004
 528 LLEI 531
 PPOL_CHICK
ID PPOL_CHICK
AC P26446;
DT 01-AUG-1992 (
DT 15-JUL-1998 (
 CONFLICT
 Query Match
 MOD_RES
MOD_RES
MOD_RES
MOD_RES
MOD_RES
MOD_RES
 MOD_RES
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 CONFLICT
 MOD_RES
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 MOD RES
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 663
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 PROSITE; PS50172: BRCT: 1.
PROSITE; PS50172: BRCT: 1.
PROSITE; PS50164: PARP_ZN_FINGER_1; 2.
PROSITE; PS5064: PARP_ZN_FINGER_2; 2.
Transferase; Glycosyltransferase; NaD; DNA-binding; Nuclear protein;
ADP_ribosylation; Zinc-finger; Zinc.
INIT_MET 0 0 BY SIMILARITY.
DOMAIN 385 461 BRCT.
 Potvin F., Thibodeau J., Kirkland J.B., Dandenault B., Duchaine C., Poirier G.G.; Structural analysis of the putative regulatory region of the rat gene encoding poly(App-ribose) polymerase."; FEBS Lett. 302:269-273(1992).
[2]
REVISION TO 811.
Beneke S., Meyer R., Buerkle A.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
 BRCT.
AUTOMODIFICATION DOMAIN.
ND-BINDING.
PARP-TYPE.
PARP-TYPE.
 STRAIN-SPRAGUE-DAWLEY; TISSUE-Prostate;
 EMBL; U94340; AAC53544.1; -.
EMBL; X65496; CAA46477.1; -.
EMBL; X65497; CAA46478.1; ALT_INIT.
 MEDLINE=92290013; PubMed=1601134;
 InterPro; IPR001357; BRCT.
InterPro; IPR001390; PARP.
InterPro; IPR001100; PARP.
InterPro; IPR001510; Znf-PARP.
Pfam; PF00533; BRCT; 1.
Pfam; PF00644; PARP; 1.
Pfam; PF00645; Zf-PARP; 2.
ProDom; PF00645; Zf-PARP; 2.
 523
1013
55
161
 SMART; SM00292; BRCT
 P26446; 1A26
 DOMAIN
DOMAIN
ZN_FING
ZN_FING
 HSSP;
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177 TVVKPCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALE 236
 61 HEDYDCTLNQTNIGNNNNKFYIIQLLE--EGSRFFCWNRWGRVGEV-GQSKMNHFTCLED 117
 118 AKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVK-ALSPQVDSGPVR 176
 EAMKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQT 296
 LQAAPGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQ----TGNSYRC 352
 PNLRHVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGR 408
 Gaps
 1 MAPKRKASVQTEGSKKQRQGTEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQV
 VGKGIYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPGFDS
 VIARGQTEPDPAQDIELELDGQPVVVPQGPPVQCPS-FKSSSFSQSEYLIYKESQCRLRY
 45;
 Length 1013;
 ADP-RIBOSYL[N] (POTENTIAL).
ADP-RIBOSYL[N] (POTENTIAL).
ADP-RIBOSYL[N] (POTENTIAL).
ADP-RIBOSYL[N] (POTENTIAL).
ADP-RIBOSYL[N] (POTENTIAL).
ADP-RIBOSYL[N] (POTENTIAL).
ADP-RIBOSYL[N] (POTENTIAL).
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ADP-RIBOSYL[N] (POTENTIAL).
ADP-RIBOSYL[N] (POTENTIAL).
ADP-RIBOSYL[N] (POTENTIAL).
ADP-RIBOSYL[N] (POTENTIAL).
AD (IN REF. 4).
N -> D (IN REF. 4).
NUCLEAR LOCALIZATION SIGNAL NUCLEAR LOCALIZATION SIGNAL BLOCKED (BY SIMILARITY).
 Indels
 DB 1;
 Best Local Similarity 33.5%; Pred. No. 1.1e-42;
Matches 182; Conservative 101; Mismatches 216;
 1.1e-42;
 (Rel. 23, Created)
(Rel. 36, Last sequence update)
 24.7%; Score 694.5; 33.5%; Pred. No. 1.1
 112529 MW;
 STANDARD;
 1013 AA;
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PDB; 4PAX;
PDB; 1A26;
 DOMAIN
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 DOMAIN
 DOMAIN
 181
 241
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 719
 301
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 MOL. Biol. 278:57-65(1998).

-I- FUNCTION: POLY(ADP-RIBOSE) POLYMERASE MODIFIES VARIOUS NUCLEAR PROTEINS BY POLY(ADP-RIBOSE) POLYMERASE MODIFIES VARIOUS NUCLEAR PROTEINS BY POLY(ADP-RIBOSE).

ON DNA AND IS INVOLVED IN THE REGULATION OF VARIOUS IMPORTANT CELLULAR PROCESSES SUCH AS DIFFERENTIATION, PROLIFERATION, AND TUMOR TRANSPORMATION AND ALSO IN THE REGULATION OF THE MOLECULAR EVENTS INVOLVED IN THE RECOVERY OF CELL FROM DNA DAMAGE.

-!- CATALYTIC ACTIVITY: NAD(+) + {ADP-D-ribosyl}(N)-acceptor—nicotinamide + {ADP-D-ribosyl}(N+1)-acceptor—nicotinamide + {ADP-D-ribosyl}(N+1)-acceptor + {ADP-D-ribosyl
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 Poly [ADP-ribose] polymerase-1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+) ADP-ribosyltransferase-1) (Poly[ADP-ribose] synthetase-1).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 polymerase as derived
 reaction of poly(ADP-
 MEDLINE-96353841; PubMed-8755499;
Ruf A., Mennissier de Murcia J., de Murcia G.M., Schulz G.E.;
"Structure of the catalytic fragment of poly(AD-ribose) polymerase
 Ittel M.-E., Garnier J.-M., Jeltsch J.-M., Niedergang C.; "Chicken poly(ADP-ribose) synthetase: complete deduced amino acid sequence and comparison with mammalian enzyme sequences."; Gene 102:157-164(1991)
 X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 659-1011, AND REVISION 895.
 MEDLINE-98239716; pubmed-9571033;
Wiff A., Roll1 V., de Murcla G.M., Schulz G.E.;
"The mechanism of the elongation and branching reaction of
ribose) polymerase as derived from crystal structures and
 X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 659-1011
 X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 659-1011.
 Proc. Natl. Acad. Sci. U.S.A. 93:7481-7485(1996).
 Ruf A., de Murcia G.M., Schulz G.E.;
"Inhibitor and NAD+ binding to poly(ADP-ribose)
from crystal structures and homology modeling.";
Biochemistry 37:3893-3900(1998).
 update)
 16-OCT-2001 (Rel. 40, Last annotation
 TISSUE=Oviduct;
MEDLINE=91340148; PubMed=1840535;
 MEDLINE-98191351; PubMed-9521710;
 EMBL; X52690; CAA36917.1; -.
 Gallus gallus (Chicken).
 2PAW; 27-MAY-98.
1PAX; 15-MAY-97.
 2PAX; 27-MAY-98.
3PAX; 27-MAY-98.
 JH0581; JH0581
 SEQUENCE FROM N.A.
 NCBI_TaxID=9031;
 mutagenesis.";
J. Mol. Biol. 27
-!- FUNCTION: PC
 from chicken
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549
 PGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQ----TGNSYRCPNLR 356
 64 YDCTLNQTNIGNNNKFYIIQLLEEG--SRFFCWNRWGRVGEV-GQSKMNHFTCLEDAKK 120
 550 FSATLGLVDIVKGTNSYYKLQLLEDDRESRYWVFRSWGRVGTVIGSNKLEQMPSKEDAVE 609
 121 DFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKALSPQVDSGPVRTVVK 180
 NPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAA 300
 |: :| |:| |:| :| |: | GNEDGDK----DPIDINYEKLRTDIKVVDKDSEEAKIIKQYVKNTHAATHNAYDL-KVV 831
 SMART; SM00292; BRCT; 1.
PROSITE; PS50172; BRCT; 1.
PROSITE; PS00347; PARP_ZN_FINGER_1; 2.
PROSITE; PS50064; PARR_ZN_FINGER_2; 2.
Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein;
 Gaps
 5 RKASVQTEGSKKQRQG-TEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQVHED 63
 : : | | : | | : | | : | | : | | : | | : | DGGSESQIL-DLSNRFYTLIPHDFGMKKPPLLSNLEYIQAKVQMLDNLLDIEVAYSLLRG
 PCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEAMK
 SIGNAL 2ND PART
 610 HFLNLYEEKTGNSWHSKN-FTKYPKFYPLEID-YGQDEEAVRKL---TVSAGTKSKLAK
 497 KPANMKSAGKVKEEQGPSKSEKKMKLTVKGGAAVDPDSGL--EDSAHVPEKGGKI----
 Length 1011;
 NUCLEAR LOCALIZATION SIGNAL 1ST NUCLEAR LOCALIZATION SIGNAL 2ND
 Indels
 (POTENTIAL)
 (POTENTIAL).
 261AED9383139144 CRC64;
 (POTENTIAL)
 (POTENTIAL)
 (POTENTIAL)
 (POTENTIAL)
 (POTENTIAL)
 (POTENTIAL)
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 (POTENTIAL)
 (POTENTIAL)
 (POTENTIAL)
 (POTENTIAL)
 AUTOMODIFICATION DOMAIN.
 Zinc-finger; Zinc; 3D-structure
 24.6%; Score 691.5; DB 1; 33.9%; Pred. No. 1.8e-42; ive 97; Mismatches 206;
 ADP-RIBOSYL[N]
ADP-RIBOSYL[N]
ADP-RIBOSYL[N]
ADP-RIBOSYL[N]
ADP-RIBOSYL[N]
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ADP-RIBOSYL[N]
ADP-RIBOSYL[N]
ADP-RIBOSYL[N]
ADP-RIBOSYL[N]
ADP-RIBOSYL[N]
 NAD-BINDING
 PARP-TYPE
 ۰
 InterPro; IPR004102; PARP_reg.
InterPro; IPR001510; Znf-PARP.
Pfam; PF00533; BRCT; 1
Pfam; PF00544; PARP; 1.
Pfam; PF002877; PARP_reg; 1.
Pfam; PF00645; Zf-PARP; 2.
ProDom; PD004675; Znf-PARP; 2.
 113520
InterPro; IPR001357; BRCT.
 Query Match 24.6
Best Local Similarity 33.9
Matches 185; Conservative
 488
488
509
510
517
 468
 InterPro; IPR001290;
 AA;
 ADP-ribosylation;
 MOD_RES
CONFLICT
SEQUENCE
 DNA_BIND
 ZN_FING
 MOD_RES
MOD_RES
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MOD_RES
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637 AA; 72175 MW; 527A8F464605D127 CRC64;

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 MEDLINE-95269779; Dubmed=7750552; MEDLINE-95269779; Dubmed=7750552; MEDLINE-95269779; Dubmed=7750552; MEDLINE-95269779; Dubmed=7750552; Lepiniec L., Babiychuk E., Kushnir S., van Montagu M., Inze D.; Lepiniec L., Babiychuk E., Kushnir S., van Montagu M., Inze D.; Craracterization of an Arabioopsis thaliana cDNA homologue to animal poly(ADP-ribose) polymerase...; FORCION POLY(ADP-RIBOSE) POLYMERASE MODIFIES VARIOUS NUCLEAR PROTEINS BY POLY(ADP-RIBOSYL)ATION. THE MODIFICATION IS DEPENDENT CELLULAR PROCESSES SUCH AS DIFFERENTIATION OF VARIOUS IMPORTANT CELLULAR PROCESSES SUCH AS DIFFERENTIATION OF THE MOLECULAR EVENTS INVOLVED IN THE RECULATION OF THE MOLECULAR EVENTS INVOLVED IN THE RECOVERY OF CELL FROM DNA DAMAGE.

-!- CATALYTIC ACTIVITY: NAD(+) + {ADP-D-Tibosyl}(N)-acceptor =
 01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Poly [ADP-ribose] polymerase (RC 2.4.2.30) (PARP) (ADPRT) (NAD(+) ADP-
 357 HVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKG 412
 IYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEH-----HITIDDPSLKSPPPGF 466
 892 IYFADMVSKSANYCHTSQ--ADPIGLILLGEVALGNMYELKNASHIT-----KLPKGK 942
 DSVIARGQTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLR 526
 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 POTENTIAL.
NAD-BINDING (BY SIMILARITY).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 SMART; SM00513; SAP; 2.
Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein;
ADP-ribosylation.

1 140 POTENTIAL.
 ribosyltransferase) (Poly[ADP-ribose] synthetase)
 637 AA
 SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE PARP FAMILY
 EMBL; 248243; CAA88288.1; -.
HSSP; P26446; 1A26.
InterPro; IPR0001290; PARP.
InterPro; IPR004102; PARP_reg.
InterPro; IPR003034; SAP.
Pfam; PF00644; PARP; 1.
 Pfam; PF02877; PARP_reg; 1.
Pfam; PF02037; SAP; 2.
 STANDARD;
 140
637
62
 NCBI_TaxID=3702;
 |||::
998 YLLKL 1002
 YLLEI 531
 PPOL_ARATH
Q11207;
 DOMAIN
 PPOL_ARATH
 413
 467
 527
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 PAGE BARREN BARR
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01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Poly [ADP-ribose] polymerase (EC 2.4.2.30) (PARP) (ADPRT) (NAD(+) ADP-ribosyltransferase) (Poly(ADP-ribose] synthetase) (Fragment).
Xenopus laevis (African clawed frog).
 120 KDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKALSPQVDSGPVRTVV 179
 237
 343 VIDR--YDRTRLEELSGEFYTVIPHDFGFKKMSQFVIDTPQKLKQKIEMVEALGEIELAT 400
 351
 401 KLLSVDPGLQDD------PLYYHYQQLNCGLTPVGNDSEEFSWVANYMENTHAKTHSGY 453
 64 -YDCTLNQTNIGNNNNKFYIIQLLEEGSR--FFCWNRWGRVGEVGQSKMN-HFTCLEDAK 119
 CPNLRHVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGG 407
 408 RVGKGIYFASENSKSAGYVTTMHC---GGHQVGYMFLGEVALGKEHHITIDDPSLKSPPP 464
 465 GFDSVIARGQTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCR 524
 "Isolation of cDNAs encoding the catalytic domain of poly(ADP-ribose)
 Gaps
 6 KASVQTEGSKKQRQGTEEEDSFRS--TAEALRAAPADNRVIRVDPSCPFSRNPGIQVHED 63
 228 EIFTNKFNDKTKNYWSDRKEFIPHPKSYTWLEMDYGKEENDSPVNNDIPSSSS----EV
 180 KP--CSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEE
 295 QTLQAAPGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQT---GNSYR
 238 AMKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPP--INSPDVLQAKKDMLLVLADIELA-
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
 48;
 SEQUENCE OF 742-876 FROM N.A.
MEDLINE-93277538; Pubmed-8503897;
Ozawa Y., Uchida K., Uchida M., Ami Y., Kushida S., Okada N.,
 Length 637;
24.5%; Score 690; DB 1; Length 63
34.7%; Pred. No. 1.2e-42;
.ive 90; Mismatches 219; Indels
 998 AA
 Saulier-Le Drean B.M.;
Thesis (1992), University of Rennes, France.
 PRT;
 Matches 190; Conservative
 STANDARD;
 Similarity
 SEQUENCE FROM N.A.
 525 LRYLLEI 531
 625 MRYVIQV 631
 NCBI_TaxID=8355;
 TISSUE=Ovary;
 PPOL_XENLA
P31669;
Query Match
 Miwa M.;
 Best Local
 PPOL_XENLA
 269
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STRAIN-BXSB;
 182;
 CONFLICT
 Query Match
 Huppi K
 RESULT 11
PPOL_MOUSE
 Matches
 10
 69
 246
 306
 769
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 418
 940
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 EVENTS INVOCATED IN THE RECOVERY OF CELL FROM DAMAGE.

- CATALVATIC ACTIVITY: NAD(+) + {ADP-D-ribosyl}(N)-acceptor = nicotinamide + {ADP-D-ribosyl}(N+1)-acceptor = nicotinamide + nico
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polymerase from Xenopus laevis and cherry salmon using heterologous oligonucleotide consensus sequences."; Blochem. Blophys. Res. Commun. 193:119-125(1993).

-I-FUNCTION: POLY[ADP-RIBOSE] POLYMERASE MODIFIES VARIOUS NUCLEAR PROTEINS BY POLY(ADP-RIBOSE) POLYMERASE MODIFIES VARIOUS INFORMATION ON DNA AND IS INVOLVED IN THE REGILATION OF VARIOUS IMPORTANT CELLULAR PROCESSES SUCH AS DIFFERENTIATION, PROLIFERANIOM, AND TUMOR TRANSFORMATION AND ALSO IN THE REGULATION OF THE MOLECULAR
 PROSITE; PS50172; BRCT; 1
PROSITE; PS50172; BRCT; 1
PROSITE; PS500347; PARP_ZN_FINGER_1; 2.
PROSITE; PS50064; PARP_ZN_FINGER_2; 2.
Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein;
ADP-ribosylation; Zinc-finger; Zinc.
 PART.
PART.
 NUCLEAR LOCALIZATION SIGNAL 1ST
NUCLEAR LOCALIZATION SIGNAL 2ND
 (POTENTIAL).
(POTENTIAL).
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 AUTOMODIFICATION DOMAIN.
 ADP-RIBOSYL[N]
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 NAD-BINDING.
 Pfam; PF02877; PARP_reg; 1.
Pfam; PF00645; zf-PARP; 2.
ProDom; PD004675; znf-PARP; 2.
SMART; SM00292; BRCT; 1.
 unterpro; IPR001290; PARP.
Interpro; IPR004102; PARP_reg.
Interpro; IPR001510; Znf-PARP.
Pfam; PF00533; BRCT; 1.
Pfam; PF00644; PARP; 1.
 EMBL; D13810; BAA02966.1; -. PIR; S31735; S31735. HSSP; P26446; 1A26. Interpro; IPR001357; BRCT. Interpro; IPR001290; PARP.
 EMBL; Z12139; CAA78126.1; -.
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 NQTNIGNNNNKFYIIQLLE--EGSRFFCWNRWGRVGEV-GQSKMNHFTCLEDAKKDFKKK 125
 126 FWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKALSPQVDSGPVRTVVKPCSLD 185
 651
 305
 PPOL_MOUSE STANDARD; PRT; 1012 AA.
PPILO3; Q9JUAT, 09QVQ3;
01-JUL-1989 (Rel. 11, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
16-OCT-2010 (Rel. 40, Last annotation update)
Poly [ADP-riboss] polymerase-1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+)
ADP-ribosyltransferase-1) (Poly[ADF-ribose] synthetase-1) (msPARP).
ADPRT OR ADPRT OR ADPRT.
 EKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLK----QTGNSYRCPNLRHVWKV 361
 EK----DPIDVKYEKIKTDIKVVAKDSEESRIICDYVKNTHADTHNAYDLEVL-EIFKI 822
 883 MVSKSANYCHAM--PGSPIGLILLGEVALGNMHELKAASQITKL-PKGKHSVKGLGRTAP 939
 362 NREGEGDRFQAHSKLGNRRLLMHGTNVAVVAAILTSGLRIMPH----SGGRVGKGIYFAS 417
 ENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQTEP 477
 Gaps
 Huppl K., Bhatia K., Siwarski D., Klinman D., Cherney B., Smulson M.;
Sequence and organization of the mouse poly (ADP-ribose) polymerase
 QTEGSKKQRQGT-EEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQVHEDYDCTL 68
 SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION.
STRAIN=129/SV X C57BL/6; TISSUE-Fibroblast;
MEDLINE=20270268; PubMed=10809783;
Sallmann F.R., Vodentcharov M.D., Wang Z.-Q., Poirier G.G.;
"Characterization of sparp-1. An alternative product of Parp-1 gene
 186 PATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEEAMKNPTGD
 --VQELIKLIFDVESMKKAMVEFEIDLQKMPLGKLSKRQIQSAYSILSQVQQAVSESLS
 GOSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAAPGEEE
 Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
 45;
 478 DPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEI 531
 Length 998;
 Indels
746 746 Q -> E (IN REF. 2).
998 AA; 111126 MW; F5A25E4A3366BAE7 CRC64;
 DB 1;
 24.4%; Score 686.5; DB 1
34.1%; Pred. No. 4.2e-42;
 95; Mismatches
 Nucleic Acids Res. 17:3387-3401(1989)
 MEDLINE-89263780; PubMed=2498841;
 SEQUENCE FROM N.A. (ISOFORM 1).
 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rođentia;
 Conservative
 Mus musculus (Mouse)
 Similarity
 NCBI_TaxID=10090;
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998 KYLLKL 1003
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 PROSITE; PS50172; BRCT; 1.
PROSITE; PS00347; PARP_ZN. FINGER_1; 2.
PROSITE; PS50064; PARP_ZN. FINGER_2; 2.
Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein;
with poly(ADP-ribose) polymerase activity independent of DNA strand
 POLYMERASE-1, SHORT
 ; Zinc; Alternative initiation.
BY SIMILARITY.
POLY [ADP-RIBOSE] POLYMERASE-1, LONG
 AUTOMODIFICATION DOMAIN.
 ISOFORM.
POLY [ADP-RIBOSE]
 SHORT ISOFORM
 NAD-BINDING.
PARP-TYPE.
PARP-TYPE.
 or send an email to license@isb-sib.ch)
 EMBL; X14206; CAA32421.1; -.
EMBL, AF12671; AAF61293.1; ALT_INIT
PIR; S04200; S04200
HSSP; P26446; 1A26.
 Biol. Chem. 275:15504-15511(2000)
 FOR
 Pfam; PF00533; BRCT; 1.
Pfam; PF00644; PARP; 1.
Pfam; PF02877; PARP_reg; 1.
Pfam; PF00645; zf-PARP; 2.
ProDom; PD004675; Znf-PARP; 2.
 ADP-ribosylation; Zinc-finger;
 InterPro; IPR004102; PARP_reg
InterPro; IPR001510; Znf-PARP
 IPR001290; PARP.
 MGD; MGI:1340806; Adprtl.
InterPro; IPR001357; BRCT
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 SM00292; BRCT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: NAD-LACED CLIL FOUR DIA CARACEL
CATALYTIC ACTIVITY: NAD-LACED CLIL FOR DIA CACCEPTOR -
INCOCTIONNIGE + {ADP-D-ribosy1}(N+1) - acceptor -
COFACTOR: ZINC, CONTAINS TWO MOLES OF ZINC PER MOLE OF PROTEIN.
COFACTOR: ZINC, CONTAINS TWO MOLES OF ZINC PER MOLE OF PROTEIN.
MISCELLANEOUS: THE ADP-D-RIBOSYL GROUP OF NAD(+) IS TRANSFERED TO
AN ACCEPTOR CARBOXYL GROUP ON A HISTONE OR THE BUZYME ITSELF, AND
THE TERMINAL ADP-RIBOSYL GROUP ON A HISTONE OR THE 2'-POSITION OF
THE TERMINAL ADENOSINE MOIETY, BUILDING UP A POLYMER MITH AN
AVERAGE CHAIN LENGTH OF 20-30 UNITS.
SIMILARITY: BELONGS TO THE PARP FAMILY.
SIMILARITY: CONTAINS 1 BRCT DOMAIN.
                                                                                           01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Poly (Apprince) (Poly (Po
                                                                                                                                                                                                                                                                                                                                                                                                                  Masutani M., Nozaki T., Titoni Y., Ikejima M., Nagasaki K., de Prati A.C., Kurata S., Natori S., Sugimura T., Esumi H.; de Prati A.C., Kurata S., Natori S., Sugimura T., Esumi H.; Cloning and functional expression of poly(ADP-ribose) polymerase CDNA from Sarcophaga peregrina."; Eur. J. Biochem. 220:607-614(1994).

-! FUNCTION: POLY(ADP-RIBOSE) POLYMERASE MODIFIES VARIOUS NUCLEAR PROTEINS BY POLY (ADP-RIBOSYL) ATION. THE MODIFICATION IS DEPENDENT ON DNA AND IS INVOLVED IN THE REGULATION OF VARIOUS IMPORTANT CELLULAR PROCESSES SUCH AS DIFFERENTIATION, PROLIFERRATION, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TUMOR TRANSFORMATION AND ALSO IN THE REGULATION OF THE MOLECULAR EVENTS INVOLVED IN THE RECOVERY OF CELL FROM DNA DAMAGE.
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PROSITE; PS00347; PARP_ZN_FINGER_1; FALSE_NEG.
PROSITE; PS50064; PARP_ZN_FINGER_2; 2.
Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein; ADP-ribosylation; Zinc-finger; Zinc.
DNA_BIND 1 369 SIMILARITY.
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BY SIMILARITY.
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NUCLEAR LOCALIZATION SIGNAL 1ST PART.
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                                                                     996 AA.
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. MEDLINE-94170813; Pubmed-8125121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00644; PARP; 1.
Pfam; PF02877; PARP_reg; 1.
Pfam; PF00645; zf-PARP; 2.
ProDom; PD004675; znf-PARP; 2.
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InterPro; IPR001510; Znf-PARP.
Pfam; PF00533; BRCT; 1.
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InterPro; IPR001290; PARP.
                                                                  STANDARD;
                                                                  PPOL_SARPE
011208;
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                                         PPOL_SARPE
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P35875; Q9W5O5; Q9W5S1;

01-JUN-1994 (Rel. 29, Created)

01-JUN-1994 (Rel. 29, Last sequence update)

01-MAR-2002 (Rel. 41, Last annotation update)

POLY (ADP-ribose] Polymerase (EC 2.4.2.30) (PARP) (ADPRT) (NAD(+) ADP-ribosyltransferase) (Poly[ADP-ribose] synthetase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -SVQDIIKLMFDVDSMKRTMMEFDLDMEKMPLGKLSQKQIQSAYKVLTEIYELIQG-GGT 710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : :: |||:|||||| || :: :: : || | :|| | :| | : || | :| | | :| | | :| | :| | | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGEGDREOAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKGIYFASE 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               886 VSKSANYCCTSH--HNSTGLMLLSEVALGDMMECTAAKYVTKLPNDK-HSCFGRGRTMPN 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NQTNIGNNNNKFYIIQLLEEG--SRFFCWNRWGRVG-EVGQSKMNHFTCLEDAKKDFKK 125
                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EEEDSFRSTAEALRAAPADNRV----IRVDPSCPF-----SRNPGIQVHEDYDCTL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., ALTERNATIVE SPLICING, DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQTEPD
NUCLEAR LOCALIZATION SIGNAL 2ND PART: , 690DDD36E7487298 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PATONLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEAMKNPTGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GOSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAAPGEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        604 YLEKSGNHFENRENFVKVAGRMYPIDIDYAEDS------KIDLSAEHDIKSKLPL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sugimura T., Miwa M.; "Cloning of cDNA encoding Drosophila poly(ADP-ribose) polymerase:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEIH 532
                                                                                                                                                                                                                                           Length 996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Uchida K., Hanai S., Ishikawa K.-I., Ozawa Y.-I., Uchida M.,
                                                                                                                                                                                                                                                                                                   al Similarity 32.8%; Pred. No. 4e-39;
175; Conservative 101; Mismatches 205; Indels
                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              leucine zipper in the auto-modification domain.",
Proc. Natl. Acad. Sci. U.S.A. 90:3481-3485(1993),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     994 AA
                                                                                                                                                                                                                                                 Score 645.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly)
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MEDLINE-93234521; PubMed=8475096;
                                                                    113018 MW;
                                                                                                                                                                                                                                                 22.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
            232 ;
996 AA;
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RA Adams M.D., Celniker S.E., Lip P.W., Hoskins R.A., Gocayne J.D., Ra Adams M.D., Celniker S.E., Lip P.W., Hoskins R.A., Galle R.F., Genger S. C., Scherer S.E., Lip P.W., Hoskins R.A., Galle R.F., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej K.G., Champe M., Pfeiffer B.D., Ra Mandon R.C., Baldam D., Barden G.R., Miklos G.L.G., Appayand A., Dar Held G., Nolson C.R., Miklos G.L.G., Appayand A., Dar Held G., Nolson C.R., Miklos G.L.G., Ballew R.M., Basu A., Barondale J., Bayraktaroglu L., Basakey E.M., Ballew R.M., Basu A., Barondale J., Bayraktaroglu L., Baldawin D., Ra Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Ra Carlery J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Chandra I., Ra Duckon B.D., Dew I., Dietz S.M., Dodgon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Rodgon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Rodger A., Gorne F., Garry B.S., Gelbart W.M., Glasser K., R. Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C., Jablin M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kecchum K.A., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Liu X., Mattei B., McThtoph T.C., Morieco M.P., Moshrefi A., Ralush F., Karpen G.H., Ke Z., Kennison J.A., Kecchum K.A., Rount S.M., Moy M., Murphy B., Murphy L., Murshy D.M., Noshrefi A., Ralush G.S., Pan S., Pollard J., Puri V., Realington K.A., Stunger S., Worker S., Woller E., Shen H., Spiele E., Spadling A.C., Standers R., Venter E., Wang A., Berler E., Shang X., Woodage T., Stangson M., Strong G., Zhoo O.A., Wulliams S.M., Woodage T., Stangson M., Strong S., Zhu S., 
              Genomic organization of Drosophila poly(ADP-ribose) polymerase and listribution of its mRNA during development."; Biol. Chem. 273:11881-11886(1998).
  Uchida K.;
  Miwa M.,
Uchida M., Kobayashi S.,
                                                                                                                                   MEDLINE=20196006; PubMed=10731132;
                                                                                              SEQUENCE FROM N.A. (LONG ISOFORM)
                                        distribution
```

PROTEINS BY POLY (ADP-REDSYL) ATTON. THE MODIFIES WITHOUT IS DEPRINENT ON DNA AND IS INVOLVED IN THE REGULATION OF VARIOUS IMPORTANT CELLULAR PROCESSES SUCH AS DIFFERENTIATION, PROLIEFERATION, AND TUMOR TRANSFORMATION AND ALSO IN THE REGULATION OF THE MOLECULAR EVENTS INVOLVED IN THE RECOVERY OF CELL FROM DNA DAMAGE.

-!- CATALYTIC ACTIVITY: NAD(+) + {ADP-D-TIDOSY1}(N)-acceptor - nicotinamide + {ADP-D-TIDOSY1}(N)+1)-acceptor.

-!- COFACTOR: ILMC, CONTAINS TWO MOLES OF ZINC PER MOLE OF PROTEIN.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SUBCELLULAR PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: EXPRESSED IN ADULT FEMALE OCCTIES, ANAL PLATES OF STACE 12 EMBRYOS AND IN CELLS AROUND THE CENTRAL NERVOUS SYSTEM

IN LATER EMBRYOS.

DEVELOPMENTAL STAGE: EXPRESSED BOTH MATERNALLY AND ZYGOTICALLY IN EMBRYOS, PUPAE AND ADULTS. EXPRESSION IS HIGHEST IN EMBRYOS.
MISCELLANBOUGS: THE ADP-D-RIBOSYL GROUP OF NAD(+) IS TRANSFERRED TO AN ACCEPTOR CARBOXYL GROUP ON A HISTONE OR THE ENZYME ITSELF, AND FURTHER ADP-RIBOSYL GROUP ON A HISTONE OF THE ZYME ITSELF, AND FURTHER ADP-RIBOSYL GROUPS ARE TRANSFERRED TO THE 2'-POSITION OF THE TERMINAL ADBROSYLE MOIETY, BUILDING UP A POLYMER WITH AN AVERAGE CAIN LENGTH OF 20-30 UNITS.
SIMILARITY: BELONGS TO THE PARP FAMILY.

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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). 17; 821 68 LNQTNIGNNNNKFYIIQLL--EEGSRFFCWNRWGRVG-EVGQSKMNHFTCLEDAKKDFKK 124 125 KFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKALSPQVDSGPVRTVVKPCSL 184 DGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAAPGEE 304 Gaps PROSITE; PS50172; BRCT; 1.
PROSITE; PS00147; PRPE_ZN_FINGER_1; 1.
PROSITE; PS50064; PARP_ZN_FINGER_2; 2.
Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein; KOROGTEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQ----VHED----YDCT 67 NUCLEAR LOCALIZATION SIGNAL 1ST PART. NUCLEAR LOCALIZATION SIGNAL 2ND PART. DPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEAMKNPTG EEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQT-GNSYRCPNLR--HVWKV 44; Score 619; DB 1; Length 994; Pred. No. 3.4e-37; ADP-ribosylation; Zinc-finger; Zinc; Alternative splicing Matches 168; Conservative 100; Mismatches 222; Indels MISSING (IN SHORT ISOFORM)
WW; ACA85A270DD29E08 CRC64; AUTOMODIFICATION DOMAIN NAD-BINDING PARP-TYPE. PARP-TYPE. AE002666; -; NOT_ANNOTATED_CDS AE002892; AAF45445.2; ALT_SEQ. Pfam; PF02877; PARP_reg; 1. Pfam; PF00645; zf-PARP; 2. ProDom; PD004675; Znf-PARP; 2. InterPro; IPR004102; PARP_reg. InterPro; IPR001510; Znf-PARP. Pfam; PF00533; BRCT; 1. Pfam; PF00644; PARP; 1. 22.0%; 113791 Flybase; FBgn0010247; Parp InterPro; IPR001357; BRCT. InterPro; IPR001290; PARP. 454 994 54 161 A47474; A47474. SMART; SM00292; BRCT 994 AA; Similarity P26446; Query Match DNA_BIND VARSPLIC SEQUENCE Best Local ZN_FING ZN_FING DOMAIN DOMAIN DOMAIN DOMAIN HSSP; 1 DOMAIN EMBL; 481 540 245 16 708 185 648 305 762 ð g ŏ Dp δ g Qγ g ŏ g Qγ a

448

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PPOV.HUMAN STANDARD; PRT; 1724 AA.

QUUKKS; 075903; Q9H1M6; Q14682;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Vault poly(AbP-ribose) polymerase (EC 2.4.2.30) (VPARP) (193-kDa vault protein) (PARP-related/Ialphal-related H5/proline-rich) (PH5P).
                                                                                             ---IYQRLYERLPCHLEPVSE------EIAGKIGDCLAMRGPTHCYKLSLIDA 339
 255 CFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVL----ADIELAQTLQAAPGEEEEKVE 309
                                                                                                                                       -- REGEGDRFQAHSKLG------ NRRLLWHGINVAVVAAILIS 397
                                                                                                                                                                                                                                               400 GLQFPVGDRCGLMFGNGVYFANVPTKSANYC----CPEASKRV-FMLLCEVETANPLVLY 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nagase T., Seki N., Ishikawa K.-I., Tanaka A., Nomura N.;
"Prediction of the coding sequences of unidentified human genes. V.
The coding sequences of 40 new genes (KIAA0161-KIAA0200) deduced by
analysis of cDNA clones from human cell line KG-1.";
                                                                                                                                                               GLR--IMPHSGGRVGKGIYFASENSKSAGYVTTMHC--GGHQVGYMFLGEVALGK----
                                                                                                                                                                                                                                                                                  EHHITIDDPSLKSPPPGFDSVIARGQTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                     310 EVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQTGNSYRCPNLR---HVWKVN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 306-319.
MEDLINE=99408776; PubMed=10477748;
Kickhoefer V.A., Siva A.C., Kedersha N.L., Inman E.M., Ruland C Streuli M., Rome L.H.;
"The 193 kb vault protein, VPARP, is a novel poly(ADP-ribose)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Still I.H., Vince P., Cowell J.K.;
Identification of a novel gene (ADPRTLI) encoding a potential
poly(ADP-ribosyl)transferase protein.";
Genomics 62:533-536(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISCUSSION OF SEQUENCE.
MEDILINE-99198702; PubMed=10100603;
Jean L., Risler J.-L., Nagase T., Coulouarn C., Nomura N.,
Salier J.-P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                    -----SSFSQSEYLIYKESQCRLRYLLEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Thymus;
MEDLINE=20112770; PubMed=10644454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96281124; PubMed=8724849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell Biol. 146:917-928(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 94-1724 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                         496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 GIQVHEDYDCTLNQTNIGNNNNKFYIIQLLEEGSRFFCWNRWGRVGEVGQSKMNHFTCLE 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 DAKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKALSPQ----VDS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173 GPV-----RTVVKPCSLDPATQNLITNIFSKEMFKNAMTL-----MNLDVKKM----- 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |: |: |: |: || :|| :1
182 GRPIDCLSLAQLTTGYEILSKIEESIGGKSARRSTRGRPRVADRVLAVKSDGPSLHDINK 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --PLGKLTKQQIARGFEALEALEEAMKNPT---------GDGQSLEELSS 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                  :|:|| ||: || ||: ||||: ||||| SRQGEARREKPFKKLHNRKLLWHGSRLTNFVGILSHGLRIAPPEAPPTGYMFGKGIYFAD
                                                                                         MVSKSANYCCTSQ--QNSTGLMLLSEVALGDMMECT-SARYINKLSNNKHSCFGRGRTMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 KNTRGRKKRGIVKEKKEIKKEEEPVEEV--NEKLKELMKCICDEDVHLGLLKQLKFNEAF
362 NREGEGGRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRI----MPHSGGRVGKGIYFAS
                                                                 ENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQTEP
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                                                                                                                                       DPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEI 531
                                                                                                                                                           Indels 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: SOME, TO THE MIDDLE PART OF NAD(+) ADP-RIBOSYLTRANSFERASE (EC 2.4.2.30).
                                                                                                                                                                                                                                                                                             01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Hypothetical 61.3 kDa protein E02H1.4 in chromosome II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .l protein.
538 Aa; 61268 MW; 3144E25465FC7341 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.1%; Score 396.5; DB 1; 26.1%; Pred. No. 2.1e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87; Mismatches 184;
                                                                                                                                                                                                                                                                538 A.A.
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InterPro; IPR001290; PARP.
InterPro; IPR004102; PARP_reg.
Pfam; PF00644; PARP, 1.
Pfam; PF02877; PARP_reg; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; 247075; CAA87379.1; -. HSSP; P26446; 1A26.
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                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
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Q09525;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERACTION WITH THE MAJOR VAULT PROTEIN. NUCLEAR LOCALIZATION SIGNAL 1ST PART
"The nuclear protein PH5P of the inter-alpha-inhibitor superfamily: missing link between poly(ADP-ribose)polymerase and the inter-alpha-inhibitor family and a novel actor of DNA repair?"; FEBS Lett. 446:6-8(1999).
-!- CATALYTIC ACTIVITY: NAD(+) + {ADP-D-ribosyl}(N)-acceptor = nicotinamide + {ADP-D-ribosyl}(N+1)-acceptor.
-!- SUBGUNIT: BINDS TO THE MAJOR VAULT PROTEIN (MPV). THE VAULT, A LARGE RIBONUCLEOPROTEIN COMPLEX, CONTAINS THE 100-kDA MPV AND 2
                                                                                                                                                                                                 PROTEINS OF 193 AND 240-KbA.
SUBCELLULAR LOCATION: CYTOPLASMIC, BUT IS ALSO FOUND IN THE NUCLEUS, ASSOCIATED WITH MITOTIC SPINDLES.
TISSUE SPECIFICITY: WIDELY EXPRESSED; THE HIGHEST LEVELS ARE IN THE KIDNEY; ALSO DEFECTED IN HEBRY, PLACEWINA, LUNG, LIVER, SKELETAL MUSCLE, SPLEEN, LEUKOCYTES AND PANCREAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEAR LOCALIZATION SIGNAL 2ND PART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAD-BINDING (BY SIMILARITY).
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EMBL; AF057160; AAC62491.1; --
EMBL; A1539763; CAC21562.1; --
EMBL; D79999; BAA11494.1; --
HSSP; P26446; 1A26.
InterPro; IPR001357; BRCT.
InterPro; IPR001390; PARP.
InterPro; IPR001290; PARP.
InterPro; IPR00293; WFA.
Pfam; PF00633; BRCT; 1.
Pfam; PF00692; VWa; 1.
SMART; SM00322; WRA; 1.
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PROSITE; PS50234; VWFA; 1.
Transferase; Glycosyltrans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               287 VLAD-IELAQTLQAAPGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQ 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :: | : : : | : | : | 352 LIRDMVNVCETNLSKPNP------PSLAKYRALRCKIEHVEQNTEEFLRVRKEVLQ 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              346 TGNSYRCPNLRHVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGL---RIM 402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               460 EDRGYQRTDVGNLGSGIYFSDSLSTSIKYSHPGETDGTRL--LLICDVALGKCMDLHEKD 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSLKSPPPGFDSVIARGQTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYL 516
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                                                                                                                                               104 PDQKASSSEVKTEGLCPD-SATEEEDTVELTEFGMQNVEIPHLPQDFEVAKYNT----LE 158
                                                                                                                                                                                                   55 NPGIQVHEDYDCTLNQTNIGNNNNKFYIIQ--LLEEG---SRFFCWNRWGRVGEVGQSKM 109
                                                                                                                                                                                                                                                                                                                                                209 -----EDASEYFENYIEELKKQGFLLREHFTPE---------ATQLASEQ 244
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                                                                                                 3 PKRKAS---VQTEGSKKQRQCTEEEDSFRSTAEALRAA-----PADNRVIRVDPSCPFSR 54
                                                                                                                                                                                                                                                                                                                                                                                                 170 VDSGPVRTVVKPCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGF
                                                                                                                                                                                                                                              159 KVGMEGGQEAVVVELQCSRDSRDCPFLISSHFLLDDGMETRRQFAIKKTS-----
                                                213; Indels 120;
Length 1724;
  9.8%; Score 275; DB 1;
11.7%; Pred. No. 7.4e-12;
                         Best Local Similarity 21.7%; Pred. No. 7.4e
Matches 121; Conservative 103; Mismatches
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       Query Match
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PCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEAMK
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC014260; AAH14260.1; ...
Hypothetical protein.
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 60.1 KAA PROTEIN.
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Kofler B., Schweiger M., Wagner E.F.;
"On the biological role of the nuclear polymerizing NAD+: protein(ADP-
ribosyl, transferase (ADPRT): ADPRT from Dictyostellum discoideum and
inactivation of the ADPRT gene in the mouse.";
Biochimie 77:444-449(1995).
HSSP: P26446; 1AA5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --YDCTLNQTHIGNNNNKFYIIQLLE--EGSRFFCWNRWGRVGEVGQSKMNHF--TCLED 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                   FASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 DVYDATLNQTEISQNNNKXYIIQLLEADDGSSYSVWNRWGREGLKGQSSRKDFGKGGLNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 AKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKALSPQVDSGPVRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QTLQAAPGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQTGNSYRCPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNIIKDSESDESNI-----LELHYAKLKTDIQPLDENSCEYKNILLYVKNTYQGGKKPT
LRHVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPHSGGRVGKGIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 KASVQTEGSKKQRQGTEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQVHED--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 VV---KPCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEEAMKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELA
                                                                                                                                                                                                                      475 TEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEIHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NAD+:PROTEIN(ADP-RIBOSYL)-TRANSFERASE (EC 2.4.2.30)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        077; PARP_reg; 1.
612 AA; 69241 MW; CB340F7A88FF2364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.2%; Score 822.5; DB 5
38.3%; Pred. No. 3.6e-58;
ive 79; Mismatches 207
                                                                                                                                                                                                                                                                                                                                                                                                                   612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida;
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 38.39
Watches 209; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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468
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                                                                 532
                                                                                                                                                                                                       587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 VVKP---CSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QTLQAAPGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQ----TGNSY 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEDYDCTLNQTNIGNNNNKFYIIQLLEEG--SRFFCWNRWGRVGEV-GQSKMNHFTCLED 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 AKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKALSPQVDSGPVRT 177
RHVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGK 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAPKRKASVQTEGSKKQRQGTEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQV 60
                                    GYYFADMFSKSANY----CYASEACRSGVLLICEVALGDMNELLNADYDANNLPKGKLR
                                                                                                                                                                                                                                                                            469 VIARGQTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKVFSATLGLVDIVKGTNSYYKLQLLEDDKESRYWIFRSWGRVGTVIGSNKLEQMPSKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 LEEAMKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RCPNLRHVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GIYFASENSKSAGYVTTMHCGGHQV - - - GYMFLGEVALGKEHHITIDDPSLKSPPPGFDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 11; Length 1014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
1-DEC-2001 (TrEMBLREL.)
1-DEC-2001 (TrEMBLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 24.9%; Score 700.5; DB 11; Length Best Local Similarity 33.3%; Pred. No. 6.2e-48; Matches 182; Conservative 100; Mismatches 215; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5DCE68E4CB3F46EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC012041; AAH12041.1; -.
Transferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                  529 LEIH 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   644 LHVN 647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQ-GEAESQEAVVKALSPQVDSGPVRTVVK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |: || || || :| | :| || :| || || 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 AAPGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQT---GNSYRCPNL 355
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KGIYFASENSKSAGYVTTMHCGGHQVGY-MFLGEVALGKEHHITID---DPSLKSPPPGF 466
                                                                                                                                                                             DCTLNQTNIGNNNNKFYIIQLLEE--GSRFFCWNRWGRVGEVGOSKMNHFTCLED-AKKD 121
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                                    467 DSVIARGQTEPDPAQDIELELDGQPVVVPQGPPVQCPS-FKSSSFSQSEYLIYKESQCRL
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01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
POLY(ADP-RIBOSE) POLYMERASE.
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; Pred. No. 1.5e-49;
91; Mismatches 205;
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Pfam; PF02877; PARP_reg; 1.
Pfam; PF02037; SAP; 2.
SMART; SM00513; SAP; 2.
SEQUENCE 653 AA; 72995 MW;
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SEQUENCE FROM N.A.
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KYLLQL 610
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Pfam; PF02877; PARP_reg; 1.
PROSITE; PS50172; BRCT; 1.
SEQUENCE 607 AA; 67496 MW;
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InterPro; IPR001290; PARP.
InterPro; IPR004102; PARP_reg.
Pfam; PF00533; BRCT; 1.
Pfam; PF00644; PARP; 1.
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                                                                                                                                                                                                                                                                  527 YLLEI 531
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01-MAY-2000
01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 YDCTLNQTNIGNNNNKFYIIQLLEEG--SRFFCWNRWGRVGEV-GQSKMNHFTCLEDAKK 120
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889 YMFGKGIYFADMVSKSANYCHTSQ--GDPIGLILLGEVALGNMYELK-HASHISKLPKGK
                                                467 DSVIARGQTEPDPAQDIELELDGQPVVVPQGPPVQCPS-FKSSSFSQSEYLIYKESQCRL
                                                                         946 HSVKGLGKTTPDDPSASITLE---GVEVPLGTGI--PSGVNDTCLLYNEYIVYDIAQVNL
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                                                                                                                                                                                                                                                                                                                       607 AA.
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68033 MW;
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InterPro; IPR001357; BRCT.
InterPro; IPR001290; PARP.
InterPro; IPR004102; PARP_reg.
Pfam; PF00533; BRCT; 1.
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1000 KYLLKL 1005
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                                                                                                                                                RYLLEI 531
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SEQUENCE FROM N.A.

MEDLINE=96007847; PubMed=7578427;

MEDLINE=96007847; PubMed=7578427;

Auer B., Filck K., Wang Z.Q., Haidacher D., Jager S., Berghammer H.,

Kofler B., Schweiger M., Magner E.F.;

"On the biological role of the nuclear polymerizing NAD+: protein(ADP-
ribosyl) transferase (ADPRT): ADPRT from Dictyostelium discoideum and
inactivation of the ADPRT gene in the mouse.";

Blochimie 77:444-449(1995).

HSSP; P26446; 1A26.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 FWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKALSPQVDSGPVRTVVKPCSLD 185
                          487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 QTEGSKKQRQGT-EEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQVHEDYDCTL
488 IYFRDMVSKSANYCHTSQ--ADPIGLILLGEVALGNMYELKNASHIT------KLPKGK
                                                                                                                                                                                                 DSVIARGOTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLR
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                                                                                  IYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEH-----HITIDDPSLKSPPPGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 19, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAD+:PROTEIN(ADP-RIBOSYL)-TRANSFERASE, ADPRT.
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19;

Gaps

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Mismatches 220; Indels

90;

Conservative

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Matches 190;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-2998 (TrEMBLrel. 19, Last annotation update)
01-DEC-2010 (TrEMBLrel. 19, Last annotation update)
T14P8.19 PROTEIN (NAD+ ADP-RIBOSYLTRANSFERASE).
T14P8.19 OR AT4G02390.
Arabidopsis thallana (Mouse-ear cress).
Bukaryota; ViridIplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                             :|||| |:: :| ||:|||||| DREGEYQRYKPFKQLHNRQLLWHGSRTINFAGILSOGLRIAPPEAPVIGYMFGKGIYFAD 491
                                                                                                                                                                        ENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQTEP 477
EKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLK----QTGNSYRCPNLRHVWKV 361
                                                                                     362 NREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRVGKGIYFAS
                                                                                                                                                                                                                                                           DPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEI 531
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STRAIN=CV. COLUMBIA;
Kalicki J., Elliott G., Cloud J.;
"The sequence of A. thaliana T14P8.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Sequencing Project.";
998) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF065298; AAC19283.1; -.
EMBL; AL161494; CAB80732.1; -.
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InterPro; IPR001290; PARP.
InterPro; IPR004102; PARP_reg.
InterPro; IPR003034; SAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00644; PARP; 1.
Pfam; PF02877; PARP_reg; 1.
Pfam; PF02037; SAP; 2.
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Transferase.
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Submitted (JUN-1998)
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NCBI_TaxID=3702;
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Mayer K.F.X.
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Length 635;

Score 683.5; DB 10; Pred. No. 7.3e-47;

24.3%;

Query Match Best Local Similarity

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21;
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                                                                                                                        RTVVKP--CSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALE 233
                                                                                                                                                                                                                                                                                                                                       --EVKPEQSKLDTRVAKFISLICNVSMMAQHMMEIGYNANKLPLGKISKSTISKGYEVLK 336
                                                                                                                                                                                                                                                                                                                                                                                       291
                                                                                                                                                                                                                                                                                                                                                                                                                   ELA-QTLQAAPGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQT---G 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               461 SPPPGFDSVIARGQTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKE 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                               109 APVKSSNDEAE---DDNNGFEEEKKEEKIVTATKKGAAVLDQWI----PDEIKSQYHVLQ 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
APKRKASVQTEGSKKQRQGTEEEDSFRS--TAEALRAAPADNRVIRVDPSCPFSRNPGIQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDAKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKALSPQVDSGPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234 ALEEAMKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPP--INSPDVLQAKKDMLLVLADI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     348 NSYRCPNLRHVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH---
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STRAIN-CV. LANDSBERG ERECTA;
Doucet-chabeaud G., Kazmaier M.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ131705; CAA10482.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Last sequence update) POLY(ADP-RIBOSE) POLYMERASE (EC 2.4.2.30).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                983 AA
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Transferase; Glycosyltransferase; NAD
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Best Local Similarity 32.7
Matches 179; Conservative
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Length 1009;

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498 KKQRKLPFDKYKIEDTSESLVTVKVKGRSAVHEAS------GLQEHCHILEDGNSIYNT 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     296 TLQAAPGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQTGNSYRCP-- 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGFDSVIARGOTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQC 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     718 TESDPQPTMKESLLVDASNRFFTMIP----SIHPHIIRDEDDFKSKVKMLEALQDIEIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 KKQRQGTEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQVH----ED----YDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        659 -SSNLAPSLIELMKMLFDVETYRSAMMEFEINMSEMPLGKLSKHNIQKGFEALTEIQRLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----NLRHVWKVNREGEGDRFQAH-SKLGNRRLLWHGTNVAVVAAILTSGLRI----MP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 KPCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEAL----EAL
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NAD+:PROTEIN(ADP-RIBOSYL)
Drosophila sp. (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 22.1%; Score 621.5; DB 10; Length Best Local Similarity 32.7%; Pred. No. 1.6e-41; Matches 179; Conservative 87; Mismatches 209; Indels
                                                                                                                                                                                                                                                                            SMART; SM00292; BRCT; 1.
PROSITE; PS50172; BRCT; 1.
PROSITE; PS50064; PARP_ZN_FINGER_2; 2.
SEQUENCE 1009 AA: 114133 MW; CDE6E41CC2A3A2DB CRC64;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC006593; AAD20677.1; -.
HSSP; P26446; 1A26.
                                                                                                                                                                                                      Pfam; PF02877; PARP_reg; 1.
Pfam; PF00645; zf-PARP; 2.
ProDom; PD004675; Znf-PARP; 2.
                                                                                                               IPR004102; PARP_reg
IPR001510; Znf-PARP
                                                                 IPR001357; BRCT
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                                                                                                                                                                                        PF00644; PARP; 1.
                                                                                                                                                           Pfam; PF00533; BRCT;
                                                                                            InterPro; IPR001290;
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996 KLQFLLKV 1003
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                                                                                                               InterPro;
InterPro;
                                                                   InterPro;
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MEDLINE-20083487; Pubbed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                               235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 KKKFWEKTKN----KWEERDRFVAQPNKYTLIEVQGEAESQEAVVKALSPQVDSGPVRTVV 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                  15 KKQRQGTEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQVH----ED----YDC
                                                                                         TLNQINIGNNNNKFYIIQLLEE--GSRFFCWNRWGRVG--EVGQSKMNHFICLEDAKKDF
                                                                                                                 180 KPCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEAL----EAL
                                                                                                                                                                                                                                                                                                                                                                      EEAMKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                296 TLQAAPGEEEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQTGNSYRCP--
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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PUTATIVE POLY (ADP-RIBOSE) POLYMERASE
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970 KLQFLLKV 977
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Q92SV1
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                                                                                                         MEDLINE-96007847; PubMed=7578427;
Auer B., Flick K., Wang Z.Q., Haidacher D., Jager S., Berghammer H.,
Kofler B., Schweiger M., Wagner E.F.;
"On the biological role of the nuclear polymerizing NAD+: protein(ADP-
ribosyl) transferase (ADPRT): ADPRT from Diccyostelium discoideum and
lnactivation of the ADPRT gene in the mouse.";
Blochimie 77:444449(1995).
HSSP: P26446; 1A36.
InterPro; IPR001357; BRCT.
InterPro; IPR001309; PARP.
InterPro; IPR004102; PARP.
Pfam; PF00533; BRCT; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        245 DGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAAPGEE 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        481 MVSKSANYCCTSQ--QNSTGLMLLSEVALGDMMECT-SAKYINKLSNNKHSCFGRGRTMP
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Pred. No. 6.1e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223; Indels
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
POLY (ADP-RIBOSE) POLYMERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167; Conservative 100; Mismatches
Pterygota; Neoptera; Endopterygota; Dip
Ephydroidea; Drosophilidae; Drosophila.
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PROSITE; PS50172; BRCT; 1.
SEQUENCE 593 AA; 68018 MW;
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31.3%;
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                                                                                      SEQUENCE FROM N.A.
                                            NCBI_TaxID=7242;
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Zea mays (Maize).
Eukaryots, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae, Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 DRFVAOPNKYTLIEVQGEAESQEAVVKALSPQVDSGPVRTVVKPCSLDPATONLITNIFS 197
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| :: || :: :| :: :||||||: :: :|:
635 VETYRAAMMEFEINMSEMPLGKLSKENIEKGFEALTEIQNLLKDTADQALAVRESLIVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 ALRAAPADNRVIRVDPSCPFSRNPGIQ----VHED----YDCTLNQTNIGNNNKFYIIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10; Length 969;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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PROSITE; PS50064; PARP_ZN_FINGER_2; 2.
CERCHENCE: 969 AA: 109128 MW; EB23AC62EEC14009 CRC64;
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InterPro; IPR003034; SAP.
InterPro; IPR001510; Znf-PARP.
Pfam; PF00533; BRCT; 1.
Pfam; PF00644; PARP; 1.
Pfam; PF00464; PARP; 1.
Pfam; PF00465; Zf-PARP; 2.
ProDom; P0004675; Znf-PARP; 2.
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Best Local Similarity 31.5% Matches 156; Conservative
                                                                           PRELIMINARY;
                                                                                                                                               Y71F9AL.18.
Caenorhabditis elegans.
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Mahajan P.B., Zuo Z.;
Mahajan P.B., Zuo Z.;
"Purification and cDNA cloning of maize Poly(ADP)-ribose polymerase.";
Plant Physiol. 118:895-905(1998).
EMBL; AF093627; AAC79704.1; -.
HSSP; P26446; 1A26.
                                                                       Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            479 ALESSKGSTVTVKVKGRSAVHESSGLQDTAHILEDGKSIYNATLNMSDLALGVNSYYVLQ 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --LDDKYMKLHCDITPLAHDSEDYKLIEQYLLNT----HAPTHKDWSLELEEVFSLDRDG 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAAPGEEEEKVEEVP 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLE--EGSRFFCWNRWGRVG--EVGQSKMNHFTCLEDAKKDFKKKFWEKTKNKWEE---R 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 DRFVAQPNKYTLIEVQGEAESQEAVVKALSPQVDSGPVRTVVKPCSLDPATQNLITNIFS 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 ALRAAPADNRVIRVDPSCPFSRNPGIQ ---- VHED ----YDCTLNQTNIGNNNKFYIIQ 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               198 KEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEAMKNPTGDGQSLEE----L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             478 DPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKESQCRLRYLLEI 531
                                                                                                                                                                                                                                                                                                                                                                                                                                        20.8%; Score 584.5; DB 10; Length 980; 30.7%; Pred. No. 1.6e-38; ive 98; Mismatches 199; Indels 73;
                                                                                                                                                                                                                                                                                                                                                                                                      9D8AED26BC37E5C1 CRC64;
           01.MAY-1999 (TrEMBLrel. 10, Created)
01.MAY-1999 (TrEMBLrel. 10, Last sequence update)
01.DEC-2001 (TrEMBLrel. 19, Last annotation update)
POLY(ADP)-RIBOSE POLYMERASE (EC 2.4.2.30).
                                                                                                                                                                                                                                                                                                                                                      SMART; SM00292; BRCT; 1.
PROSITE; PS50172; BRCT; 1.
PROSITE; PS50064; PARP_ZN_FINGER_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                            Glycosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                       110475 MW;
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InterPro; IPR003034; SAP.
InterPro; IPR001510; Znf-PARP.
Pfam: PF00533; BRCT; 1.
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Pfam; PF00645; zf-PARP; 2.
ProDom; PD004675; znf-PARP; 2.
                                                                                                                                                                                                                                 IPR001357; BRCT. IPR001290; PARP.
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Q9ZSV1;
01-MAY-1999 (TrEMBLrel.
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                                                                                                                        NCBI_TaxID=4577;
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SEOUENCE 1
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 YDCTLNQTNIGNNNNKFYIIQLLEEGSR -- FFCWNRWGRVG - EVGQSKMNHFTCLEDAKK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              643 LLVKLPIDASRILDFSNKFYTIIPHNFGMRVPEPIDSFHKIKEKNNMLNALLDIKFAYD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 537 KFQDVFHEKTKNDWIYRKHFRKMPGMFSYVETDYSEFAQ------ITDTEIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 PCS---LDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 AMKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTL
                          974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 945;
925 LESEFVKWRDD---VVVPCGKPVP-SSIRSSELMYNEYIVYNTSQVKMQFLLKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of the nematode C. elegans: a platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
REMBL; ACC1200; AAF36011.1; -.
RHSSP, P26446; 1A26.
RICHEPTO; IPR001510; DARP.
RICHEPTO; IPR001510; Znf-PARP.
RICHEPTO; IPR001510; Znf-PARP.
RPfam; PF00644; PARP; 1.
RPCDOm; PD004675; Znf-PARP; 1.
RPCSTITE; PS5064; PARP_ZN_FINGER_2; 1.
RPCSTITE; PS5064; PARP_ZN_FINGER_2; 1.
RPCSTITE; PS5064; PARP_ZN_FINGER_2; 1.
RPCDCHCE 945 AA; 108006 MW; 1D0A62C954BC6AD9 CRC64;
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80; Mismatches 201; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bradshaw-Cordum H., Scott K., Graves T.; "The sequence of C. elegans cosmid Y71F9AL."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 108.0 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.2%; Score 569.5; DB 5; 31.5%; Pred. No. 2.4e-37;
                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99069613; PubMed=9851916;
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ò	RHVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPHSGGRVGK 41	
a		
oy Oy	412 GIYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHLITID-DPSLKSPPGEDSVI 470	
ογ	471 ARGQTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLI 517	
qq	:	
δ	518 YKESQCRLRYLLEIHL 533	
QQ	924 YDVDQIQLKYLVRVKM 939	-
RESULT 09XHA5	ULT 15 11A5	
G S	OSTUAS PRELIMINARY; PRT; 727 AA.	
2 2 2	EMBLrel. 12, Creat	
D B	C-2001 (TrEMBLrel. 19, Last annotation PROTEIN.	
N SO	AC8.1. Caenorhabditis elegans.	
888	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. NCRT maxTD-6234.	
N. C	CENTER OF STATE OF ST	
Z Z Z	SEQUENCE FROM N.A. MCMUITED A.A. Submitted ANOVE-1006, to the must Access Another description	
Z.	of the many delibativy uppor	
8 X 8	SEQUENCE FROM N.A.	
RT	none; "Genome sequence of the nematode C.elegans: A platform for	
RŢ		
1 2 E	EMBL; 283097; CAB05448.1; HSSP: D26448.1;	
n n	Interpro; IPR001290; PARP.	
Z Z	InterPro; IPR004102; PARP_reg. InterPro; IPR001510; 2nf-PARP.	
Z C	Pfam; PF00644; PARP; 1. Dfam: DF00877: DADD roc: 1	
22 22	Pfam; PF00645; zf-PARP; 1. ProDom; PD004675; znf-PARP; 1.	
% %	PROSITE; PS50064; PARP ZN FINGER 2; 1. SEQUENCE 727 AA; 82884 MW; 530ABA8E991FFEFD CRC64;	
M B O	Query Match 16.9%; Score 475.5; DB 5; Length 727; Best Local Similarity 30.2%; Pred. No. 7e-30; Matches 134; Conservative 68; Mismatches 170; Indels 71; Gaps. 13;	
ογ	126 FWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKALSPQVDSGPVRTVVKPCS 183	
g	315 FHEKTKNDWIYRKHFRKMPGMFSYVETDYSEFVGTNNGHKKKITPGSKITPGSKTLLPKS 374	
δy	184 LDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIARGFEALEALEEAMKNPT 243	
С	375 VKEVVMSIFDVENMKSALKSFEIDVNKMPLGRLSHNQINLAFEVLNDISDLLVKLP 430	•
δ		
g	431 IDASKILDFSNKFYTIIPHNFGMRVPEPIDSFHKIKEKNNMLNALLDIKFAYD-QISGGD 489	
٥y	304 EEEKVEEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQT-GNSYRCP-NLRHVWKV 361	
යු	490 VPASTSLSIDPVDINYRKLKCIMEPLQQGCDDWNMIHQYLKNTHGATHDLKVELIDILKV 549	_

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	GenCore Version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
OM protein - pro	OM protein - protein search, using sw model
Run on:	August 29, 2002, 07:59:24; Search time 69.02 Seconds (without alignments) 742.040 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-701-586B-4 2823 1 MAPKPKPWVQTEGPEKKKGREYLIYQESQCRLRYLLEVHL 533
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched:	283138 seqs, 96089334 residues

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000 pirl:* pir2:* pir3:* pir4:* PIR_71:* Database

283138

Total number of hits satisfying chosen parameters:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Gaps

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Length 459; Indels

85.7%; Score 2419; DB 2; 99.8%; Pred. No. 6.3e-162;

Query Match
Best Local Similarity 99.8
Matches 458; Conservative

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1; Mismatches

9

75 IENNNNKFYIIQLLQDSNRFFTCWNRWGRVGEVGQSKINHFTRLEDAKKDFEKKFREKTK 134

1 IENNNNKFYIIQLLQDSNRFFTCWNRWGRVGEVGQSKINHFTRLEDAKKDFEKKFREKTK

135 NNWAERDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGPVRTVTKRVQPCSLDPATQKLIT 194

61

	Description	NAD+ ADP-ribosyltr	_		ADP-		NAD+ ADP-ribosyltr	NAD+ ADP-ribosyltr		NAD+ ADP-ribosyltr	NAD+ ADP-ribosyltr			probable poly (ADP		hypothetical prote	hypothetical prote	NAD+ ADP-ribosyltr	protein ZK1005.1 (chromosome assembl	protein B0361.3 [i	probable peptidogl	myosin heavy chain	regulatory protein	NAD+ ADP-ribosyltr	IgA Fc receptor pr	IgA Fc receptor pr	cytoplasmic dynein	hypothetical prote	ribosome receptor,
SUMMARIES	ED CI	Ö	T01311	JS0428	S42208	T03656	JH0581	A29725	S26057	S31735	S04200	A47474	T51353	C84719	T03657	T18600	T20414	PN0494	D88948	B70356	C88504	AB1180	A40997	S69632	T03058	A60234	FCSOAG	T30838	T25400	A56734
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ď	Query Match	85.7	24.6	24.0	23.9	23.8	23.7	23.6	23.3	23.1	23.0	22.6	21.2	21.2		•	•	6.7	5.8		4.5	4.3	4.3	4.1	4.0	4.0	4.0	٠.	3.9	9.8
	Score	2419	694	677	674.5	670.5	669.5	6.999	657	653	649.5	638	598.5	598.5	578	534	393.5	190.5	164.5	134	126	120.5	N		113.5				٠.	110
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SHFYTVIPHNEGHSQPPPINSPELLQAKKDMLLVLADIELAQALQAVSEQEKTVEEVPHP 314

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315 241 375

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KLGNRKLLWHGTNMAVVAAILTSGLRIMPHSGGRVGKGIYFASENSKSAGYVIGMKCGAH

LDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQTGSNHRCPTLQHIWKVNQEGEEDRFQAHS

PQGQPVPCPEFSSSTFSQSEYLIYQESQCRLRYLLEVHL 533

HVGYMFLGEVALGREHHINTDNPSLKSPPPGFDSVIARGHTEPDPTQDTELELDGQQVVV

hypothetical prote gag polyprotein - transforming prote chromosome segrega hypothetical prote hypothetical prote carbamoyl-phosphat giantin - human giantin - human hypothetical prote chromosome segrega hypothetical prote protoplast regener hypothetical prote hyaluronan recepto protoplast regener hypothetical prote toucan gene protei	RESULT 1 T0813 NAD+ ADP-ribosyltransferase homolog DKFZp566G0224.1 - human (fragment) C;5pecies asplans (man) C;5pecies (man) C;6pecies (man)
729999 7000335 700034 700034 700034 711375 711375 712910 713906 713906 713906	ALIC LOG DKF7 Log DKF7 3, H.W.; 5 Databa dey; clc
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2288 446 446 1233 1871 1871 1092 725 726 726 728 728 7199	sferase he ens (man) #sequence cer, U.; Me er, U.; Me tein Sequence Z16472 ANS EMBL:ALO56 e: fetal } 4.1
$\overset{\circ}{\circ}{\circ}\overset{\circ}$	transf. sapies 399) #sn 3713 7713 Alrkner oer: Z1 067: Z1 3713 5713 5713 5713 5713 5713 5713
110 108.5 108.5 108.5 108.5 108.5 108.5 108.5 108.5 106.5 106.5 106.5	RESULT 1 T08713 NAD- ADP-ribosyltransferase homolog DKFZp566 C;Species: Homo saptens (man) C;Accession: T08713 R;Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gas submitted to the Protein Sequence Database, A;Reference number: 216472 A;Accession: T08713 A;Molecule type: mRNA A;Residues: 1.459 cANS> A;Residues: 1.459 cANS> A;Residues: 1.459 cANS> A;Residues: EMBL:ALO50034 A;Residues: BRDL:ALO50034 A;Residues: EMBL:ALO50034 A;Residues: EMBL:ALO50034 A;Residues: EMBL:ALO50034 A;Residues: BADP-ribosyltransferase C;Superfamily: NAD+ ADP-ribosyltransferase
	RESULT 1 T0813 NAD+ ADP-ri C.Species: C.Date: 11-C; Accession R; Ansorge, supmitted A; Reference A, Accession A, Accession A, Accession A, Accession A, Accession C, Genetics: A, Cross-ref A, Residues: A, Accession C, Genetics: A, Note: DKF

С

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A; Experimental source: thymus
R; Taniguchi, T.; Yamauchi, K.; Yamamoto, T.; Toyoshima, K.; Harada, N.; Tanaka, H.; T
Eur. J. Blochem. 171, 571-575, 1988
A; Title: Depression in gene expression for poly(ADP-ribose) synthetase during the int
A; Reference number: $00328; MUID:88151954
A; Accession: $00328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Residues: 658-685;689-665;893-901 <TA2>
C;Superfamily: NAD+ ADP-ribosyltransferase
C;Keywords: DNA binding; glycosyltransferase; NAD; nucleotide binding; nucleus; P-loo F;21-51/Region: zinc finger
                                                                                                                                                                                                                                                                                                      NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - bovine
NAD+ ADP-ribosyltransferase (polymerizing); poly(adenosine diphosphate C; Species: Bos primigenius taurus (cattle)
C; Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001
C; Accession: JS0428; S00328; A30458
R; Saito, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
                                                         111 KINHFTRLEDAKKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQ-AEDEAQEAVVKVD 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  289 LADIELAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT-G 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GHTEPDPTQDTELELDGQQVVVPQGQPV - - PCPEFSSSTFSQSEYLIYQESQCRLRYLLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 NPGTQVYED----YNCTLNQTNIENNNNKFYIIQLLQDSNRF-FTCWNRWGRVGEV-GQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 RGPVRTVTKRVQPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             230 FEALEALEEAL-KGPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99; Mismatches 205; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;128-165/Region: zinc finger
F;200-220/Region: helix turn-helix motif
F;204-231/Region: nuclear location signal
F;250-270/Region: helix-turn-helix motif
F;494-501/Region: nucleotide-binding motif A (P-loop)
F;890-903/Region: nucleotide binding #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.0%; Score 677; DB 1; 33.8%; Pred. No. 2.8e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to JIPID, February 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 648714;838-904 <TAN
A;Cross-references: EMBL:X06986
A;Accession: A30458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 187; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: JS0428
A; Accession: JS0428
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A; Residues: 1-1016 <SAI>
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A Accession: T01311
A Accession: T01311
A Status: translated from GB/EMBL/DDBJ
A Status: 1635 <ALL>
A Cross-references: EMBL:AF069288: NID:g3193282; PID:g3193299
A Cross-references: EMBL:AF069288: NID:g3193282; PID:g3193299
A Status: Status: Columbia
A Status: Status: Status of an Arabidopsis thaliana cDNA homologue to animal poly(ADP-rA)
A Status: nucleic acid sequence not shown
A Status: nucleic acid sequence not shown
A Status: NED:B C CLEP>
A Residues: 1-115, GT', 116-635 <LEP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 4
A;Introns: 28/3; 116/1; 162/3; 190/1; 268/3; 312/1; 330/3; 355/2; 371/1; 387/3; 408/3;
A;Note: T14P8.19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: T14P8.19
Keywords: DNA binding; glycosyltransferase; NAD; pentosyltransferase; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                    NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - Arabidopsis thaliana NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - Arabidopsis thaliana (SADF-ribose) polymerase; protein 714P8.19 (SPecies: Arabidopsis thaliana (mouse-ear cress) (C.) atte: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 21-Jul-2000 (C.) Accession: T01311; S65662 (R.) Allicki, J.; Elliott, G.; Cloud, J. Submitted to the EMBL Data Library, May 1998 (A.) Description: The sequence of A. thaliana T14P8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: EMBL:Z48243; NID:q853721; PIDN:CAA88288.1; PID:g853722 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNAPVKSSNDEAEDDNNGFEEEKKEEKIVTATKKGAAVLDQWIPDEIKSQYHVLQRGDDV 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGPVRTVTKRVQP- 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -CSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALEEALK 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPTDGGQSLEELSSHFYTVIPHNFGHSQPPP--INSPELLQAKKDMLLVLADIELAQALQ 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT-GSNHRCPTLQ-- 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :| : |:| | |:: :: |:| | |:: SVDPGLQ-----DDPLYYHYQQLNCGLTPVGNDSEEFSMVANYMENTHAKTHSGYTVEIA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YNCTLNQTNIENNNNKFYIIQLLQ-DSNRFFTCWNRWGRVGEVGQSKIN-HFTRLEDAKK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IYFASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSLKSPPPGFDSVIAR 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 TEGPEKKKGRQAGREEDPFRSTAEALKAIPAEKRIIRV-DPTCPLSSNPGTQVYED---- 65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OLFRASRAVEADRFQQFSSSKNRMLLWHGSRLTNWAGILSQGLRIAPPEAPVTGYMFGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                357 HIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPH----SGGRVGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.6%; Score 694; DB 2; Length 635 ilarity 34.2%; Pred. No. 9.3e-41; Conservative 97; Mismatches 221; Indels
POGQPVPCPEFSSSTFSQSEYLIYQESQCRLRYLLEVHL 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 185;
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Best Local 9
                        421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242
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Db 829 EARRYKPFKKLHNRRLLWHGSRLTNFAGILSHGLKIAPPEAPVTGYMFCKGIYFADMVSK 888 Qy 422 SAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNFSLKSPPDGFDSVIARGHTEPDP 479	Cy Genetics: A; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Genetics: C; Keywords: DNA binding; glycosyltransferase; NAD; pentosyltransferase C; Keywords: DNA binding; glycosyltransferase; NAD; pentosyltransferase C; Keywords: DNA binding; glycosyltransferase; NAD; DB 2; Length 653; Best Local Similarity 35.4%; Pred: No. 4.3e-39; Matches 170; Conservative 93; Mismatches 186; Indels 31; Gaps 14; Cy 64 EDYNCTLNQTNIENNINKEYIIOLLQ-DSNRFFTCWNRWGRVGEVGOKINHFTRLED-A 121 Db 188 EIYDATLANGTNYONNINKEYIIOLLG-DSNRFFTCWNRWGRVGVRGOKLHGFSPTROA 247 Cy 122 KRDFEKRFREKTRNNWARRDHFVSHFGKYTLIEVQAEDEAQEAVVKVDRGPKTVTTRVQ 181 C	OY 242 GPTDGGOSLEELSSHFYTVIPHNFCHSQPPPINSPELLQAKKDMLLVLADIELAQALQ 299 361KADRRHLEQLTGEFYTVIPHDFGFRKMREFIIDTPQKLKAKLEMVEALGEIEIATKL- 417 OY 300 AVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT-GSNHRCPTLQ 356 10	RESULT 6 JH0581 NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - chicken N;Alternate names: poly(ADP-ribose) synthase C;Species: Gallus gallus (chicken)
Oy 348 SNHRCPTLQHIWKVNOEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPH- 404	A; Title: Cloning and functional expression of poly(ADP-ribose) polymerase cDNA from Sard A; Reference number: \$42208; MUID:94170813 A; Accession: \$42208 A; Maccession: \$42208 A; Molecule type: mRNA A; Residues: 1-996 cMaS> A; Cross-references: EMBL:D16482; NID:9473742; PIDN:BAA03943.1; PID:9538248 A; Accession: \$71496 A; Molecule type: protein A; Residues: 170-188;721-736;813-819;879-885 cMaX> C; Superfamily: NAD+ ADP-ribosyltransferase; NAD; pentosyltransferase; Zinc finger C; Superfamily: NAD+ ADP-ribosyltransferase; NAD; pentosyltransferase; C; Keywords: DNA binding; 91ycosyltransferase; NAD; pentosyltransferase; S; 1-369/Domain: DNA binding; #status predicted cDNA> F; 370-507/Domain: auto-modification #status predicted cAMO> F; 508-996/Domain: NAD binding #status Page S	Qy 25 EEDPFRSTAEALKAIPAEKRIIRVDPTCPLSSNPGTQVYEDYNCTLNQTN 74 1	Oy 309 EEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT-GSNHRCPTLQHIWKVNQEG 365 1:1:1:1:1:1:1:1:1:1:1 Db 773NPIDKHYEQLKTKLEPLDKNSEEYILLQKYVKNTHAETHKLYDLEVVDIFKVARQG 828 Oy 366 EEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPHSGGRVGKGIYFASENSK 421 : : : : : :

4

from cDNA Katu

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A; Modecule type: mRNA
A; Residues: 1-16, F', 18-211, 'K', 213-236, 'R', 238-366, 'H', 369-1014 <KUR>
A; Residues: 1-16, E', 18-2103473
A; Crosz-references: GB: J03473
B; Cherney, B.W.; McBride, O.W.; Chen, D.; Alkhatib, H.; Bhatia, K.; Hensley, P.; Smul
Proc. Natl. Acad. Sci. U.S.A. 84, 8370-8374, 1987
A; Title: CDNA sequence, protein structure, and chromosomal location of the human gene
A; Reference number: A39976; MUID: 88068596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-49, D', 51-612, Q', 614-907, Y', 909-939, 'R', 941-979, 'I', 981-1014 <CHE>
A; Residues: 1-49, D', 51-612, Q', 614-907, Y', 909-939, 'R', 941-979, 'I', 981-1014 <CHE>
A; Cross-references: GB:J03030
A; Note: the authors translated the codon ATA for residue 980 as Asn
R; Suzuki, H.; Uchida, K.; Shima, H.; Sato, T.; Okamoto, T.; Kimura, T.; Miwa, M.
Biochem: Biochbyys. Res. Commun. 146, 403-409, 1987
A; Title: Molecular cloning of cDNA for human poly(ADP-ribose) polymerase and expressi
A; Reference number: A26901; MUID:87298455
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A; Residues: 38 -43;93-137;204-209;237-242;276-281;335-340;384-389;431-436;512-5
A; Cross-references: GB:M29544; GB:M2953
A; Note: the authors translated the codon GTG for residue 54 as Glu
A; Note: these fragments represent intron-exon boundaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 441-610, N',612-880;921-1014 <SUZ>
A; Note: the sequence figure has an omission of forty residues
A; Note: the sequence figure has an omission of forty residues
R; Ogura, T.; Nyunoya, H.; Takahashi Masufani, M.; Miwa, M.; Sugimura, T.; Esumi, H.
Biochem. Biophys. Res. Commun. 167, 701-710, 1990
A; Title: Characterization of a putative promoter region of the human poly(ADP-ribose)
A; Reference number: 138096; MUID:90211250
A; Accession: 138096
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A; Note: these fragments represent a zinc finger-containing DNA-binding region R; Gradwohl, G.; Menissier de Murcia, J.; Molinete, M.; Simonin, F.; Koken, M.; Hoeijm Proc. Natl. Acad. Sci. U.S.A. 87, 2990-2994, 1990
A; Title: The second zinc-finger domain of poly(ADP-ribose) polymerase determines spec A; Reference number: A33635; MUID:90222155
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A; Residues: 12-26, 47, 28-66, 116-166 < GRA>
A; Residues: 12-26, 47, 28-66, 116-166 < GRA>
R; Schneider, R; Auer, B.; Kuehne, C.; Herzog, H.; Klocker, H.; Burtscher, H.J.; Hirs
Eur. J. Cell Biol. 44, 302-307, 1987
A; Title: Isolation of a CDNA clone for human NAD (+): protein ADP-ribosyltransferase.
A; Reference number: A61559; MUID:88082900
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R;Residues: 81-420;882-710 <SCH>
R;Yokoyama, Y.; Kawamoto, T.; Mitsuuchi, Y.; Kurosaki, T.; Toda, K.; Ushiro, H.; Eur. J. Blochem. 194, 521-526, 1990
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Eur. J. Blochem. 194, 521-526, 1990
A;Title: Human poly(ADP-ribose) polymerase gene. Cloning of the promoter region. A;Reference number: $14010; MUID:91099327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Human nuclear NAD(+) ADP-ribosyltransferase(polymerizing): organization A;Reference number: A33321; MUID:90091744
       A;Molecule type: mRNA
A;Residues: 1-69, 0, 71-1014 <UCH>-
A;Residues: 1-69, 0, 71-1014 <UCH>-
A;Cross-references: GB:M18112; NID:9190166; PIDN:AAA60137.1; PID:9190167
B;Rurosaki, T.; Ushiro, H.; Mitsuuchi, Y.; Suzuki, S.; Matsuda, M.; Matsuda,
J. Biol. Chem. 26., 15997-15997
J. Biol. Chem. 26., 15997-15997
A;Title: Primary Structure of human poly (ADP-ribose) synthetase as deduced
A;Reference number: A28499; MUID:88058958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-40 < RES>
A; Cross-references: EMBL:X16674; NID:9510112; PIDN:CAA34663.1; PID:91017423
R; Auer B.; Nagl, U.; Herzog, H.; Schneider, R.; Schweiger, M.
DNA 8, 575-580, 1989
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NAD+ ADP-ribosyltransferase (EC 2.4.2.30), nuclear - human
NA1 transferase (EC 2.4.2.30), nuclear - human
NA1 transferase; poly (ADP-ribose) polymerase; poly (ADP-ribose) synthetase; poly (ADP)
C; Species: Homo sapiens (man)
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Accession: A29725; A28498; A39976; A26901; I38096; B33321; A33321; A35635; A61559; S14
R; Uchida, K.; Morita, T.; Sato, T.; Yamashita, R.; Noguchi, S.; Suzuki, H.; N
Blochem: Biophys. Res. Commun. 148, 617-622, 1987
A; Title: Nucleotide sequence of a full-length cDNA for human fibroblast poly(ADP-ribose)
A; Reference number: A29725; MUID:88076933
                                                                                                                               A:Title: Chicken poly(ADP-ribose) synthetase: complete deduced amino acid sequence and A;Reference number: JH0581; MUID:91340148
A;Reference number: JH0581; MUID:91340148
A;Recasion: JH0581
A;Recalle type: MRNA
A;Residues: 1-1011 <TTT>
A;Cross-references: EMBL:X52690; NID:963742; PIDN:CAA36917.1; PID:963743
C;Comment: This protein is a chromatin-bound enzyme.
C;Comment: This sorzyme catalyzes DNA-dependent post-translational modifications of var C;Superfamily: NAD+ ADP-ribosyltransferase; C;Keywords: DNA binding: 91ycosyltransferase; NAD; nucleus; pentosyltransferase; zinc
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Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          534 SGLEDS--AHVFEKGGKIFSATLGLVDIVKGTNSYYKLQLLEDDRESRYWV-FRSWGRVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EV-GOSKINHFTRLEDAKKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQ-AEDEAQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QQIARGFEALEALEEALKGPTDGGQSLE--ELSSHFYTVIPHNFGHSQPPPINSPELLQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKDMLLVLADIELAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YLEQT-GSNHRCPTLQ--HIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_C;Accession: JH0581
K;Ittel, M.E.; Garnier, J.M.; Jeltsch, J.M.; Niedergang, Gene 102, 157-164, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.7%; Score 669.5; DB 1
llarity 33.2%; Pred. No. 9.5e-39;
Conservative 100; Mismatches 205
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Matches 186; Conserv
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A;Accession: S78453
A;Molecule type: mRNA
A;Residues: 1-124,'H',126-127,'A',129-238,'D',240-500 <POT>
A;Cross-references: EMBL:X65497
C;Superfamily: NAD+ ADP-ribosyltransferase
C;Keywords: DNA binding; DNA repair; glycosyltransferase; NAD; nucleus; pentosyltrans
                                                                                                                                                                                                        Conservative
A; Reference number: S78453
                                                                                                                                                                                   Similarity
                                                                                                                                                                 Query Match
Best Local Simi
Matches 177;
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                                                                                                                                                                   Keywords: DNA binding; DNA repair; glycosyltransferase; NAD; nucleus; pentosyltransfer
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 18-Jun-1999
C;Accession: S26657; S78453; 152331
R;Thibodeau, J.; Gradwohl, G.; Dumas, C.; Clairoux-Moreau, S.; Brunet, G.; Penning, C.; Biochem. Cell Biol. 67, 653-660, 1989
A;Title: Cloning of rodent cDNA encoding the poly(ADP-ribose) polymerase catalytic domain A;Accession: S26657
                                                                                                                                                                                                                                                            24;
                                A.Cross-references: EMBL.X56140; NID:g35286; PIDN:CAA39606.1; PID:g825702
C.Comment: This protein can ADP-ribosylate itself as well as other proteins.
C.Genetics:
A.Gene: GDB:ADPRT; PPOL
A.Cross-references: GDB:119508; OMIM:173870
A.S.Map position: 1941-1942
C.Superfamily: NAD+ ADP-ribosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               935 AS-HISKLPKGKHSVKGLGKTTPDPS--ANISLDG--VDVPLGTGI-SSGVNDTSLLIYNE 988
                                                                                                                                                                                                                                                                                                                      PLSSNPGTQVYED----YNCTLNQTNIENNNNKFYIIQLLQD--SNRFFTCWNRWGRVGE 106
                                                                                                                                                                                                                                                                                                                                                                                             | : | | : : | | : | | | GLEHS--AHVLEKGGKVFSATLGLVDIVKGTNSYKLQLLEDDKENRYW-IFRSWGRVGT 594
                                                                                                                                                                                                                                                                                                                                                                                                                                               V-GOSKINHFTRLEDAKKDFEKKFREKTKNNWAERDHFVSHPCKYTLIEVQ-AEDEAQEA 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MLLVLADIELAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLE 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QT-GSNHRCPTLQ--HIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRI 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MPH----SGGRVGKGIYFASENSKSAGYVIGMKCGAHH---VGYMFLGEVALGREHHINT 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QIARGFEALEALEEALKGPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKD 284
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                PW-----VQTEGPEKKKGRQAGR-----EEDPFRSTAEALKAIPAEKRIIRVDPTC 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Cross references: EMBL:X65497; NID:g56849; PIDN:CAA46478.1; PID:g56850 R;Potvin, F. submitted to the EMBL Data Library, March 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VVKVDRGPVRTVTKRVQPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNPSLKSPPPGFDSVIARGHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSE
                                                                                                                                                                                                                                                            63;
                                                                                                                                                                                                                         Length 1014;
                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                     Query Match 23.6%; Score 666.5; DB 1; Best Local Similarity 33.4%; Pred. No. 1.5e-38; Matches 186; Conservative 101; Mismatches 207;
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989 XIVYDIAQVNLKYLLKL 1005
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A; Residues: 1-500 <THI>
                   1-95 <YOK>
A; Molecule type:
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NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - African clawed frog (fragment)
N.Alternate names: poly ADP-ribose polymerase
C.Species: Xenopus laevis (African clawed frog)
C.Species: Xenopus laevis (African clawed frog)
C.Satcession: S31735; PN0495
R.Saulier-le Drean, B.M.
Submitted to the EMBL Dia Library, May 1992
A.Reference number: S31735
A.Accession: S31735
A.Accession: S31735
A.Molecule type: mRNA
A.Residues: 1-988 <SAD.
A.Residues: 1-988 <SAD.
A.Storos-references: EMBL:212139; NID:g64967; PIDN:CAA78126.1; PID:g1334661
R.Ozawa, Y.; Uchida, K.; Uchida, M.; Ami, Y.; Kushida, S.; Okada, N.; Miwa, M.
Biochem: Biophys. Res. Commun. 193, 119-125, 1993
A.Reference number: PN0494; MUID:93277538
A.Accession: PN0495.
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A;Residues: 742-745, Er,747-876 <02A>
C;Comment: This sinc-finger protein plays a role in DNA repair, cell growth, and diff
C;Superfamily: NAD+ ADP-ribosyltransferase
                                                                 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  347
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                                                                                                                                                                                                                                                                                            SDKESRYWIFRSWGRVGTVIGSNKLEQMPSKEDAVEHFWKLYEEKTGNAWHSK-NFTKYP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                122 KKFYPLEIDYGQDE--EAVKKL---AVKPGTK----SKLPKPVQELVGMIFDVESMKKAL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267 HSQPPPINSPELLQAKKDMLLVIADIELAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQL 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HGTNMAVVAAILTSGLRIMPH----SGGRVGKGIYFASENSKSAGYVIGMKCGAHH---V 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GYMFLGEVALGREHHINTDNPSLKSPPPGFDSVIARGHTEPDPTQDTELELDGQQVVVPQ 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -DSNRFFTCWNRWGRVGEV-GQSKINHFTRLEDAKKDFEKKFREKTKNNWAERDHFVSHP 147
                                                                                                                                                                                                                                                                                                                                                                                     GKYTLIEVQ-AEDEAQEAVVKVDRGPVRTVTKRVQPCSLDPATQKLITNIFSKEMFKNTM 206
                                                                                                                                                                41 AEKRI-----IRVDPTCPLSSNPGTQVYED----YNCTLNQTNIENNNNFYIIQLLQ 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QLLDSGAPEYKVIQTYLEQT-GSNHRCPTLQ--HIWKVNQEGEEDRFQAHSKLGNRKLLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207 ALMDLDVKKMPLGKLSKQQIARGFEALEALEEALKGPTDGGQSLEELSSHFYTVIPHNFG
                                                                    52;
23.3%; Score 657; DB 2; Length 50
34.4%; Pred. No. 2.6e-38;
Live 96; Mismatches 190; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GQPVPCPEFSSSTFSQSEYLIYQESQCRLRYLLEV 531
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-----EKRMKLTLKGGAAVDPDSG

346 820 403

652 226 705 286 764

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A47474
NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Drosophila melanogaster
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: A47474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H----SGGRVGKGIYFASENSKSAGYVIGMKCGAHH----VGYMFLGEVALGREHHINTDN 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GOSKINHFTRLEDAKKDFEKKFREKTKNNWAERDHFVSHPCKYTLIEVQ-AEDEAQEAVV
                                                                                                                                                                                                                                                                                                                                                     287 LVLADIELAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSNKLEOMPSKEEAVEOFMKLYEEKTGNAWHSK-NFTKYPKKFYPLEIDYGODE--EAVK
                                                                                                                                                                                                                                                                                                                                                                                                                                227 ARGFEALEALEEALKGPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          457 PSLKSPPPGFDSVIARGHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYL
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                                                                                          LSSNPGTQVYED - - - - YNCTLNQTNIENNNNKFYIIQLLQDSNRF - FTCWNRWGRVGEV -
        :||: | :|: | :| | 493 VAPRGK----SAAPSKKSKGCFKEEGVNKS-
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990 VYDIAQVNLKYLLKL 1004
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C;Keywords: DNA binding; glycosyltransferase; hexosyltransferase; NAD; nucleus; pentosyl
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Cispedies: Mus musculus (house mouse)
Cispedies: Mus musculus (house mouse)
Cispedies: Mus musculus (solution of the mouse)
Cispedies: Musculus (solution of the mouse poly (hop-ribose)
R; Huppl, K.; Bhatia, K.; Siwarski, D.; Kilinman, D.; Cherney, B.; Smulson, M.
Nucleic Acids Res. 17, 3387-3401, 1989
A; Title: Sequence and organization of the mouse poly (ADP-ribose) polymerase gene.
A; Reference number: Solution;
A; Reference number: Solution;
A; Residues: 1-1013 (HUP>
A; Residues: 1-1013 (HUP>
A; Cross references: EMBL:X14206; NID:949893; PIDN:CAA32421.1; PID:949894
C; Genetics:
C; Genetics:
C; Superfamily: NaD+ ADP-ribosyltransferase
C; Keywords: DNA binding; glycosyltransferase; zinc
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-KIFSATLGLVDITRGINSYYKLQLIEHDRDSRYWVFRSWGRVGTVIGSKKLEEMSSKED
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Best Local Similarity 32.4%; Pred. No. 2.4e-37;
Matches 180; Conservative 103; Mismatches 205;
                                                                                    Score 653; DB 2;
Pred. No. 1.3e-37;
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32.5%;
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A;Molecule type: mRNA
A;Residues: 1-994 <UCH>
A;Cross-references: GB:D13806; GB:D13807; GB:D13808; NID:g303545; PIDN:BAA02964.1;
A;Cross-reference extracted from NCBI backbone (NCBIN:129703, NCBIP:129704)
C;Genetics:
R;Uchida, K.; Hanai, S.; Ishikawa, K.; Ozawa, Y.; Uchida, M.; Sugimura, T.; Miwa, Proc. Natl. Acad. Sci. U.S.A. 90, 3481-3485, 1993
A;Title: Cloning of cDNA encoding Drosophila poly(ADP-ribose) polymerase: leucine A;Reference number: A47474; MUID:93234521
                                                                                                                                                                                                                                                                                                                                               A,Gene: Flybase:Parp
A,Cross-references: Flybase:FBgn0010247
C;Superfamily: NAD+ ADP-ribosyltransferase
C;Keywords: DNA binding; glycosyltransferase; NAD; nucleus; pentosyltransferase
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Matches 168; Conservative 100; Mismatches 195;
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968 QVKLQFLLKV 977
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAD+ ADP-ribosyltransferase (EC 2.4.2.30) [imported] - Arabidopsis thaliana NA1ternate names: poly(ADP-ribose) polymerase (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Spacession: T51353 (Spoucet-chabeaud, G.; Kazmaier, M. Submitted to the EMBL Data Library, December 1998 A.Reference number: 225379 A.Reference number:
                                                                                                                                                                                                                                                                                   GHSQPPPINSPELLQAKKDMLLVLADIELAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQ 325
                                                                                                                                                                                                                                                                                                                                                                                                                                         LQLLDSGAPEYKVIQTYLEQT-GSNHRCPTLQ--HIWKVNQEGEEDRFQAHSKLGNRKLL 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WHGTNMAVVAAILTSGLRI----MPHSGGRVGKGIYFASENSKSAGYVIGMKCGAHHVGY 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WFLGEVALG-----REHHIN--TDNPSLKSPPPGFDSVIARGHTEPDPTQDTELELDGQ 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |::||||| :| :| :: :| |||: :: || ||: || :|| :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||
LKADKKEKYWIFRSWGRIGTNIGNSKLEEFDTSESAKRNFKEIYADKTGNEYEQRDNFVK 617
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                                                                                                                                                                                                                                     MALMDLDVKKMPLGKLSKQQIARGFEALEALEEALKGPTDGGQSLEELSSHFYTVIPHNF
                                                                           HPGKYTLIEVQAEDEAQEAVVKVDRGPVRTVTKRVQPCSLDPATQKLITNIFSKEMFKNT
                                                                                                                    Description: ADP-ribose polymer synthesis
Superfamily: NAD+ ADP-ribosyltransferase
Keywords: DNA binding; glycosyltransferase; NAD; pentosyltransferase
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C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Species: Or-Feb-2001 #sequence_revision 02-Feb-2001
C'Accession: C64719
K;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Reference condent type: DNA
A;Residues: 1-1009 <STO>
A;Cross-references: GB:AE002093; NID:94432827; PIDN:AAD20677.1; GSPDB:GN00139
A;Genetics:
A;Genetics:
C;Genetics:
C;Genetics:
C;Genetics:
C;Superfamily: NAD+ ADP-ribosyltransferase
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                                                                                                                                                                                                                                                                                                                                           401
                                                                                                                                                                                                                                                                                                                                                                                  521
                                                                                                                                                                                                        294 LAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQTGSNHRCP 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MPHSGGRVGKGIYFASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSLKS 461
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FKRLFLEKTGNTWESWEQKTNFQKQPGKFLPLD------IDYGVNKQVAKK-E 654
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PFQTSSNLAPSLIELMKMLFDVETYRSAMMEFEINMSEMPLGKLSKHNIQKGFEALTEIQ 688
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                                                                      EAL----KGPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIE
                                                                                                      462 PPPGFDSVIARGHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYLIYQES
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Submitted to the EMBL Data Library, November 1996
A;Reference number: 218996
A;Accession: T18600
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-727 <WHL>
A;Cross-references: EMBL:283097; PIDN:CAB05448.1; GSPDB:GN00023; CESP:AC8.1
A;Experimental source: clone AC8
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
T18600
hypothetical protein AC8.1 - Caenorhabditis elegans
c;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T18600
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                                                                                                                                                                                                                  905 TKGLGKTVP---LESEFVKWRDDVVVPCGKPVP-SSIRSSELMYNEYIVYNTSQVKMQFL 960
EVFSLDRDGELNKYSRYKNNLHNKMLLWHGSRLTNFVGILSQGLRIAPPEAPVTGYMFGK 850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ::| | ::|: |:
182 KATGEYVBALAAKGG--STEPATPASASP-TPPEAETPVLSAEGSPESSNKRPASAEIIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 VRTVT--KRVQPCS---LDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              287 LVLADIELAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EAPVSGYMFGKGVYFADMFSKSFFY---CRANAKEEAYLLLCDVALGNVQQLMASKNVSR
                                                                                        469 VIARGHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYLIYQESQCRLRYL
                                                   GIYFASENSKSAGYVIGMKCGA---HHVGYMFLGEVALGREHHINTDNPSLKSPPPGFDS
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A;Introns: 31/3; 271/3; 312/3; 348/1; 466/3; 545/3; 617/3; 702/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 18.9%; Score 534; DB 2; Length 72' Best Local Similarity 28.6%; Pred. No. 1.9e-29; Matches 162; Conservative 104; Mismatches 211; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------DSNRFF--TCWNRWGRVGEVGQSKI-------
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Pred. No. 1.9e-29;
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R; Bablychuk, E.; Cottrill, P.; Storozhenko, S.; Fuangthong, M.; O'Farrell, M.; Van Monta Bublychuk, E.; Cottrill, P.; Storozhenko, S.; Fuangthong, M.; O'Farrell, M.; Van Monta Bublitche to the EMBL Data Library, November 1997
A; Reference number: 214992
A; Reference number: 214992
A; Recession: T03657
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Mesidues: 1-969 - EMBLA
A; Residues: 1-960 - 
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C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 20-Jun-2000
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                                                                                                                                           T-----LQHIWKVNQEGEEDRFQAH-SKLGNRKLLWHGTNMAVVAAILTSGLRI---- 401
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                                                                                                                                                                                                                                                       MPHSGGRVGKGIYFASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSLKS 461
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                                                                                                                                                                                LAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQTGSNHRCP
                                                                                                                                                                                                                                                                                                                                                                    PPPGFDSVIARGHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYLIYQES
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C;Superfamily: NAD+ ADP-ribosyltransferase
C;Keywords: DNA binding; glycosyltransferase; NAD; pentosyltransferase
                                                                                  771 IASRI -- VGFDVDSTES----LDDKYKKLHCDISPLPHDSEDYRLIEKYLNTT----HAP
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C; Genetics:
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507 SSTFSQSEYLIYQESQCRLRYLLEVHL 533 :|:::| |:|| |: 695 DYHLLYNEFIVYDVDQIQLKYLVRVKM 721

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Search completed: August 29, 2002, 07:59:29 Job time: 276 sec

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Sequence 2, Application US/08860886

Patent No. 6335009

GENERAL INFORMATION:
APPLICANT: Burkle, Alexander
APPLICANT: Jaur Hausen, Harald
APPLICANT: Jaur Heiner, Kupper
TITLE OF INVENTION: IN GENE THERAPY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
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US-09-308-375-2
US-08-035-818-14
US-08-235-838-14
US-08-923-992A-2
US-08-923-992A-2
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US-08-839-425-11
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: SYSTEM: Windows
SOFTWARE: FastSEQ for Windows
SOFTWARE: FastSEQ for Windows
CURRENT APPLICATION DATA:
FILLING DATE: 03-0CT-1997
                                                                                                                                                                                                                                                                                                                                                                    US-08-533-306A-6
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APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/POCKET NUMBER: 8484-
TELECOMMUNICATION INFORMATION:
TELECHONE: 650-493-5556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1013 amino acids
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-860-886-2
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STATE: NI
COUNTRY: USA
TO: 10036-2811
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      Query Match
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278.240 Million cell updates/sec
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Sequence 1, Al
Sequence 1, Al
Sequence 31, 1
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Sequence 1,
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1: /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*
4: /cgn2_6/ptodata/2/laa/6A_COMB.pep:*
5: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*
6: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*
6: /cgn2_6/ptodata/2/laa/pep:*
                        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-196-387-2
US-08-328-254-6
US-08-461-234-1
US-08-463-480-1
US-08-463-480-1
US-08-225-224-1
US-08-72-258-1
US-08-12-258-1
US-08-12-258-1
US-08-12-258-1
US-08-336-4468-1
US-08-336-4468-1
US-08-336-447A-15
US-08-811-485-4
US-08-811-485-4
US-08-811-485-4
US-08-811-485-4
US-08-811-653A-4
US-08-817-053A-4
US-08-817-053A-4
US-08-817-053A-4
US-08-353-700-1
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PCT-US94-09143-31
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US-08-125-077-5
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                   August 29, 2002, 07:58:18
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Gapop 10.0 , Gapext 0.5
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2813
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833 VIDIFKIEREGECQRYKPFKQLHNRRLLWHGSRTTNFAGILSQGLRIAPPEAPVIGYMFG 892
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                                                                                                                                                                                                                                                                                                                                                                          493 VAPRGKSGA---ALSKKSKGQVKEEGINKSEKRMKLTLKGGAAVDPDSGLEHSAHVLEKG 549
                                                                                                                                                                                                                                                                                                                                                                                                                                             665 LPKP-----VQDLIKMIFDVESMKKANVEYEIDLQKMPLGKLSKRQIQAAYSILSEVQQ 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298 QAAPGEEEEKVEEVPHPLDRDYQLLRCOLQLLDSGESEYKAIQTYLKQT-GNSYRCPNLR 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         357 --HVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH---SGGRVG 410
                                                                                                                                                                                                                                                                                                                                                                                                                          61 HEDYDCTLNQTNIGNNNNKFYIIQLLEEG--SRFFCWNRWGRVGEV-GQSKMNHFTCLED 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEAVVKALSPQVDSGPVRT 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTL 297
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                                                                                                                                                                                                                                                                          Length 1014;
                                                                                                                                                                                                                                                                        24.9%; Score 700; DB 4; Length 10 illarity 33.6%; Pred. No. 5.3e-60; Conservative 102; Mismatches 219; Indels
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411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09196387
Patent No. 6277613
GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
UMBER OF SEQUENCES: 12
32,837
ER: UALB-03283
                   REFERENCE/DOCKET NUMBER: UA TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410
                                              TELEPHONE: (415) 705-8110
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                   not relevant
                                                                                                                            LENGTH: 1014 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS: ADDRESSE:
                                                                                                                                                                                                 MOLECULE TYPE: protein
REGISTRATION NUMBER:
                                                                                                                                                                                unknown
                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 182; Conserv
                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: unk
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                                                                                                                              61 HEDYDCTLNQTNIGNNNNKFYIIQLLEEG--SRFFCWNRWGRVGEV-GQSKMNHFTCLED 117
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                     Gaps
                                                       1 MAPKRKASVQTEGSKKQRQGTEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQV 60
                                                                                                                                                       178 VVKPCSLDPATQNLITNIFSKEMFKNAMTLANLDVKKMPLGKLTKQQIARGFEALEALEE
                                                                                                                                                                                                                                                                                                 238 AMKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTL
                                                                                                                                                                                                                                                                                                                                                                          354 NLRHVWKVNREGEGDRFQAHSKLGNRRLLWHGTNVAVVAAILTSGLRIMPH----SGGRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKGIYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3. Application US/09078347A
Patent No. 6132968
GENERAL INFORMATION:
APPLICANT: Le, Xiao-Chun
APPLICANT: Wenfeld, Michael
APPLICANT: Xing, James Z.
TITLE OF INVENTION: Methods for Quantitating Low Level
TITLE OF INVENTION: Modifications of Nucleotide Sequences
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                   Matches 183; Conservative 101; Mismatches 218;
   No. 1.7e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/078,347A FILING DATE: 13-MAY-1998 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
 33.8%;
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NAME: Carroll, Peter G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
   Local Similarity
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1003 KL 1004
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1212 IYFAENSSKSNQYVYGIGGGTGCPTHKDRSCYICHRQMLFCRVTLGKS-FLQFSTMKMAH 1270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              269 ELEFPEGGSLAALTAHQACHLPLETFTRHRQPRGWEQLEQCGYPVQRLVALYLAARLSWN 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----ALEEAMKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLA 289
                                                     462 PPPGFDSVIARGQTEPDPAQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEYLIYKES
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3.8%; Score 105.5; DB 4; Length 635;
Best Local Similarity 19.7%; Pred. No. 0.13;
Matches 78; Conservative 48; Mismatches 143; Indels 127;
                                                                                                                                                                                                                                                                                                                  ACCOURT OF 6-992-2

Sequence 2, Application US/09046992

Sequence 2, Application US/09046992

Patent No. 6140066

BENERAL INFORMATION:

APPLICANT: Lorberboum-Galski, Haya

APPLICANT: Larkoni, Shal

APPLICANT: Ben-Yehidah, Ahmi

TITLE OF INVENTION: METHODS OF CANCER DIAGNOSIS

TITLE OF INVENTION: USING A CHIMERIC TOXIN

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds, LLP

STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKetter
COMPUTER: IRM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FRAESEQ for Windows
SOFTWARE: FRAESEQ for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/046,992
FILING DATE: 24-MAR-1998
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTONNEY/AGENT INFORMATION:
NAME: POISSANT, BIANN
NAME: POISSANT, BIANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----KMPLGKLTKQQIARGFEALE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Polssant, Brian M
RECISTRATION NUMBER: 28,462
REFERENCE-POCKET NUMBER: 9457-0013-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-556
TELEFAX: 650-493-556
TELERAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                ----GRPSV---
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; FRAGMENT TYPE: internal
US-09-046-992-2
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                                                                                                        1271 APPGHHSVI----
                                                                                                                                                              522 QCRLRYLL 529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY:
STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    990 SSIDNL---TGPLAELAVGGASNAGDGAAGTE----RKEGEVAGLDMNISOFLKSLGLEH 1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1043 LR-----DIFETEQITLDVLADMGHEELKEIGINAYGHRHKLIKGVERLLGGQQGT 1093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 TPLDLATADDIRALLIDAMPPEALPTCFKRQATVVSASLISPAS------TPSCLSAA 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265 GRSRPPPINSPDVLQAKKDMLLVLADI---ELAQTLQAAPGEEEEKVEEVPHPL----D 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NREGEGDRF-----QAHSKLGNRRLLWHGTNVAVVAAILTSGL-RIMPHSGGRVGKG 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                777 TKKNRDGNTPLDLVKEGDTDIQDLLKGDAALLDAA-KKGCLARVQKLC-----TPE 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 DYDCTLNQTNIGNNNKFYII------QLLEEGSRFFCWNRWGRVG------ 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 EVGOSKMNHFTCLEDAKKDFKKKFWEKT-----KNKWEERDRFVAQPNKYTLIEVQGE 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         884 DIAALLIKYNTCVNATDK-----WAFTPLHEAAQKGRTQLCALLLAHGADPTMKNQEGQ 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 A-----ESQEAVVKALSPQ---VDSGPVRTVVKPCSLDPATQNLITNIFSKEMFKNA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 205 MILMNLDVKKMPLGKLTKQQIARGFEALEALEAMKNPTGDGQSLEELSSCFYTVIPHNF 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     317 RDYQLLRCQLQ---LLDSG--ESEYKAIQTYLKQT------GNSYRCPNLRHVWKV 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IYFASENSKSAGYVTTM----HCGGHQ-----VGYMFLGEVALGKEHHITIDDPSLKS 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 SKKQRQG------TEEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPGIQVHE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.2%; Score 146; DB 4; Length 1327; Best Local Similarity 20.2%; Pred. No. 4.2e-05; Matches 123; Conservative 83; Mismatches 232; Indels 170;
                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/196,387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        600-1-230 CIP1
                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-2:
TELECOMMUNICATION:
                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1327 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .: protein
NO
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TOPOLOGY: linear
                            New Jersey
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
  Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                               07601
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                                                   COUNTRY:
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us-09-701-586b-8.rai

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                                                                                                                                                                                          1986 ETELQREMHE-MAQKTAELQ--EELSG------EKNRLAGELQLLLEEIKSSKDQLKE 2034
                                                                                                                                                                                                                                                                                                                           ---PNLRHVWKVN 362
                                                                  168 PQVDSGPVRTVVKPCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLTKQQIAR
                                                                                                                                                  228 GFEALEALEEAMKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDML--
                                                                                                                                                                                                                                      286 LVLADIELAQTLQAAPGEEEEKVEEVPHPLDRDYQL-----LRCQLQLLDSGESEYKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08405615
Patent No. 5602095
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: FitzGerald, David J.
TITLE OF INVENTION: Recombinant Pseudomonas Exotoxin with
TITLE OF INVENTION: Increased Activity
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ellen L. Weber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Ellen L. Weber
One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OFEWATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.7%; Score 103.5; DB 1;
19.7%; Pred. No. 0.19;
tive 47; Mismatches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15280-36
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/901,709
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/405,615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 613 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       415-543-5043
                                                                                                                                                                                                                                                                                                                                                                                                          363 REGEGDRFQAHSKL 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-405-615-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: One Market P
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                        340 QTYLKQTGNSYRC-
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US-08-405-615-1
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329 QVDQVIRNALASP-GSGGDLGEAI------REQPE-----QAR--LALTLA 365
                                                           290 DIELAQTLQAAPGEEEEKVEEVPHPLDRDYQLLRCQLQL-----LDSG----ESEYKAI 339
                                                                                                      366 AAESERFVRQGTGNDEAGA-----ANADVVSLTCPVAAGECAGPADSGDALLEANYPTG 419
                                                                                                                                                340 QTYLKQIGNSYRCPNLRHVWKVNREGEGDRFQAHSKLGNRRLL---WHGTNVAVVAAILT 396
                                                                                                                                                                                                                                                                 60 VHEDYD-CTLNQTNIGN----NNNKFYIIQLLEEGSRFFCWNRWGRVGEVGQSKMNHFT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 C-LEDAKKDFKKKFWE--KTKNKWEERDRFVAQPNKYTLIEVQGEAE---SQEAVVKALS 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Zhu, Xueliang
APPLICANT: Lee, Wen-Hwa
TITLE OF INVENTION: A No. 5710022el Nuclear Mitotic Phosphoprotein
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                             SGLRIMPHSGGRVGKGIYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.7%; Score 104; DB 1; I
21.4%; Pred. No. 1.6;
tive 65; Mismatches 139;
                                                                                                                                                                                                                                                                                                                    457 PSLKSPPPGFDSVIARGQTEPDPAQDIELELDGQPV 492
                                                                                                                                                                                                                                                                                                                                              PAPLICATION NUMBER: US/08/328,254
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/141,239
FILING DATE: 22-OCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CJ 1191
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08328254
Patent No. 5710022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2482 amino acids
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Best Local Similarity 21.4<sup>1</sup>
Matches 80; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-328-254-6
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STREET: 43/v...
CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                78; Conservative
               TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-461-234-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                       Query Match
Best Local Similarity
Matches 78; Conserva
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STRANDEDNESS
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                                                                                                                   234 ----ALEEAMKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLA 289
                                                                                                                                                                                                                                                                                                                                                                                             SGLRIMPHSGGRVGKGIYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDD 456
                                                                                                                                                                                                                                                                                                                                                                                                                     307 QVDQVIRNALASP-GSGGDLGEAI------REQPE-----QAR--LALTLA 343
                                                                                                                                                                                                                                            DIELAQTLQAAPGEEEEKVEEVPHPLDRDYQLLRCQLQL-----LDSG----ESEYKAI 339
                                                                                                                                                                                                                                                                              344 AAESERFVROGTGNDEAGA----ANADVVSLTCPVAAGECAGPADSGDALLERNYPTG 397
                                                                                                                                                                                                                                                                                                                                                        398 AEFLGDGGDVSFSTRGTQNWTVER-----LLQAHRQLEERGYVFVGYHGTFLEAAQSIVF 452
                                     340 QTYLKQTGNSYRCPNLRHVWKVNREGEGDRFQAHSKLGNRRLL---WHGTNVAVVAAILT
                   -----CSLDPATQNLITNIFSKEMFKNAMTLMNLDVK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Pastan, Ira H.
APPLICANT: FitzGerald, David J.
APPLICANT: FitzGerald, David J.
TITLE OF INVENTION: Recombinant Pseudomonas Exotoxin with
TITLE OF INVENTION: Increased Activity
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,234
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Townsend and Townsend and Crew STREET: One Market Plaza, Steuart Street Tower CITY: San Francisco STATE: California
                                                                                           ----KMPLGKLTKQQIARGFEALE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               457 PSLKSPPPGFDSVIARGQTEPDPAQDIELELDGQPV 492
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TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/405,615
FILING DATE: 15-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/901,709
FILING DATE: 18-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405,615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08461234 Patent No. 5821238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 613 amino acids
TYPE: amino acid
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                 SGPVRTVVKP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307 QVDQVIRNALASP-GSGGDLGEAI------REQPE-----QAR--LALTLA 343
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                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :|| || || 247 RIHFPEGGSLAALTAHQACHLPLETFTRHRQPRGWEQLEQCGYPVQRLVALYLAARLSWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---ALEEAMKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            340 QTYLKQTGNSYRCPNLRHVWKVNREGEGDRFQAHSKLGNRRLL---WHGTNVAVVAAILT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :| |: :|||: :|||: :||| :: :||| :: :|||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :|: :||: :||: :||: :||: :||: :||: :||: :||: :||: :|: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :|:
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                                                                                                                                     Indels 127;
       Length 613;
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APPLICANT: FitzGerald, David J.

TITLE OF INVENTION: Recombinant Pseudomonas Exotoxin with TITLE OF INVENTION: Increased Activity

WINDER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,480 FILING DATE: 05-JUN-1995 CLASSIFICATION: 435
       DB 2;
                                                                                                                                     47; Mismatches 144;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          457 PSLKSPPPGFDSVIARGQTEPDPAQDIELELDGQPV 492
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                                                                             0.19;
3.7%; Score 103.5; 19.7%; Pred. No. 0.19
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APPLICATION NUMBER: US 07/901,709
FILING DATE: 18-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405,615
FILING DATE: 15-MAR-1995
ATTORNEY/AGENT INFORMATION:
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340 QTYLKQTGNSYRCPNLRHVWKVNREGEGDRFQAHSKLGNRRLL---WHGTNVAVVAAILT 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|| : ||:| || || 307
248 RLHFPEGGSLAALTAHQACHLPLETFTRHRQPRGWEQLEQCGYPVQRLVALYLAARLSWN 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 ----ALEEAMKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLA 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       345 AAESERFVROGTGNDEAGA----ANADVVSLTCPVAAGECAGPADSGDALLERNYPTG 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               399 AEFLGDGGDVSFSTRGTQNWTVER-----LLQAHRQLEERGYVFVGYHGTFLEAAQSIVF 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Circularly Permuted Ligands and TITLE OF INVENTION: Circularly Permuted Chimeric Molecules NUMBER OF SEQUENCES: 72 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 -----EADLGKLTKQQIARGFEALE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 457 PSLKSPPPGFDSVIARGQTEPDPAQDIELELDGQPV 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.7%; Score 103.5; DI Best Local Similarity 19.7%; Pred. No. 0.19; Matches 78; Conservative 47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: 1..614
; OTHER INFORMATION: /label= native-PE
US-08-225-224-1
          APPLICATION NUMBER: US/08/225,224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 1, Application US/08722258
; Patent No. 6011002
                                                                                                          NAME: Weber, Ellen L.
REGIGSTRATION UNDERE: 1526
REFERENCE/DOCKET NUMBER: 1526
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 543-9600:
TELEPAX: (415) 543-5643
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Pastan, Ira
APPLICANT: Kreitman, Robert J.
APPLICANT: Puri, Raj K.
                                                          CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                         614 amino acids
                                  8-APR-1994
                                                                                                                                                                                                                                                                                                                                                                        unknown
                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                              unknown
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STRANDEDNESS: unl
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US-08-722-258-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: PASTAN, ITA
APPLICANT: KREITMAN, Robert J.
TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND
TITLE OF INVENTION: CIRCULARLY PERMUTED FUSION PROTEINS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214 -------KMPLGKLTKQQIARGFEALE----
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 3.7%; Score 103.5; DB 2; Best Local Similarity 19.7%; Pred. No. 0.19; Matches 78; Conservative 47; Mismatches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               453 GGVRARSQDLDAIWRGFYIAGDPALAYGYAQDQEPDAR--
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NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15280-36-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                    613 amino acids
                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            340 QTYLKQTGNSYRCPNLRHVWKVNREGEGDRFQAHSKLGNRRLL---WHGTNVAVVAAILT 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234 ----ALEEAMKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLA 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  399 AEFLGDGGDVSFSTRGTQNWTVER----LLQAHRQLEERGYVFVGYHGTFLEAAQSIVF 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "native Pseudomonas exotoxin
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: BATTER: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,258
FILING DATE: 08-JAN-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 3.7%; Score 103.5; DB 3; Best Local Similarity 19.7%; Pred. No. 0.19; Matches 78; Conservative 47; Mismatches 144;
                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US95/04468
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/225,224
FILING DATE: 08-APR-1994
ATTORNEY/AGBNT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-193100US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    || ||| ||| SSL----PGFYRT-SLTLAAPEAAGEVE-RLIGHPL 536
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                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 614 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                    CIRCULARLY PERMUTATED LIGANDS AND CIRCULARLY PERMUTED FUSION PROTEINS
                                                                                                 APPLICANT:
TITLE OF INVENTION:
CIRCULARLY PERMUTATED LIGANDS AN
TITLE OF INVENTION:
CIRCULARLY PERMUTATED LIGANDS AN
TITLE OF INVENTION:
CIRCULARLY PERMUTADE FUSION PROTE
NUMBER OF SEQUENCES: 59
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04468
FILING DATE: 07-APR-1995
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19.7%; Pred. No. 0.19;
tive 47; Mismatches 144;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/225,224
FILING DATE: 08-APR-1994
ATTORNEY,AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
TELEPHONE: (415) 543-9600
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , LUCATION: 1..614
; OTHER INFORMATION: /label= native-PE
PCT-US95-04468-1
Sequence 1, Application PC/TUS9504468 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 614 amino acids
TYPE: amino acids
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Best Local Similarity 19.74
Matches 78; Conservative
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----ALEEAMKNPTGDGQSL 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360 KVNREGEGDRFQAHSKLGNRRLL---WHGTNVAVVAAILTSGLRIMPHSGGRVGKGIYFA 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225 TVER----LLQAHRQLEERGYVFVGYHGTFLEAAQSIVFGGVRARSQDLDAIWRGFYIA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           417 SENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQTE 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 ----ANADVVSLTCPVAAGECAGPADSGDALLERNYPTEAEFLGDGGDVSFSTRGTQNW 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 3.6%; Score 100.5; DB 1; Length 4 Best Local Similarity 21.2%; Pred. No. 0.21; Matches 67; Conservative 38; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                      457 PSLKSPPPGFDSVIARGQTEPDPAQDIELELDGQPV 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/120,698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: APPLICATION NUMBER: US/07/879,037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/391,259
                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Riemen, Mark W
APPLICANT: Stiemen, Steven M
TITLE OF INVENTION: Modified PE40
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Grassler, Frank P
REGISTRATION NUMBER: 31,164
REFERENCE/DOCKET NUMBER: 17879
TELECOMMUNICATION INFORMATION:
TELEFONE: (908) 594-3462
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                 ; Sequence 7, Application US/08391259
; Patent No. 5621078
                                                                                                                                                                                                                                                                                                                             Merck & Co., Inc.
                                                                                                                                                                                                                                                                                                                                             126 Lincoln Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                215 MPLGKLTKQQIARGFEALE----
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-08-391-259-7
                                                                                                                                                                                                                                                                                                                                                          SINLL: Rahway
STATE: New Jersey
COUNTRY: U.S.
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                                                                                                         RESULT 13
US-08-391-259-7
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                                                                                                    ROCKford
METHODS AND COMPOSITIONS FOR USING
MEMBRANE-PENETRATING PROTEINS TO CARRY MATERIALS ACROSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217 SGKVLCLLDPLDGVYNYLAQQRCNLDDTWEGKIYRVLAGNPAKH-----DLDIKPTVISH 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|| |: ||:| ||
272 RLHFPEGGSLAALTAHQACHLPLETFTRHRQPRGWEQLEQCGYPVQRLVALYLAARLSWN 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234 ----ALEEAMKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290 DIELAQTLQAAPGEEEEKVEEVPHPLDRDYQLLRCQLQL-----LDSG----ESEYKAI 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 369 AAESERFVRQGTGNDEAGA----ANADVVSLTCPVAAGECAGPADSGDALLERNYPTG 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            340 QTYLKQTGNSYRCPNLRHVWKVNREGEGDRFQAHSKLGNRRLL---WHGTNVAVVAAILT 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       397 SGLRIMPHSGGRVGKGIYFASENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDD 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 638;
                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/047,148
FILING DATE: Concurrently Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.7%; Score ... 0.2;
19.7%; Pred. No. 0.2;
...o 47; Mismatches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REPERBENGE/ZDOCKET NUMBER: UTSF:072
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/042,056
FILING DATE: 26-WAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                        Arnold, White & Durkee
                                                                                                                                                                   CELL MEMBRANES
                                   Sequence 2, Application US/09047148
Patent No. 6086900
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 638 amino acids
TYPE: amino acid
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Best Local Similarity 19.7%
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                         United States
                                                                                                  APPLICANT: Draper, Rockf
TITLE OF INVENTION: METH
TITLE OF INVENTION: MEM
TITLE OF INVENTION: CELL
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                              13
                                                                                                                                                                                                                                                          STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                 Houston
                                                                                                                                                                                                                                                                                                         Texas
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                                                                                                                                                                                                                                        ADDRESSEE:
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                 -09-047-148-2
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Gaps

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GENERAL INFORMATION:
APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: MACIVER, ISSUEL
APPLICANT: MACIVER, ISSUEL
APPLICANT: MACIVER, ISSUEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMC: 1024
CURRENT APPLICATION NUMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    526 QQQDQHSSDIKTLKKNVEE-------GLLELSGHLIDQKADLTK 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        || :|| ::|
423 SVGSEGKERQIVHVGAGRISNDSTDAVNGSQLYALAAAVDDNQY------DIE 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 VHEDYDCTLNQTNIGNNNNKFYIIQLLEEGSRFFCWNRWGR--------VGEVG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    470 KNQD-DIAKNQADIAKNQAD--IQTLENDVGKELLNLSGRLIDQKADIDNNINHIYELA 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    607 DQYAQKQTEAIDALNKASSENT---QNIEDLAA--YNELQDAYAKQQTEAIDALNKASSE 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              321 LIRCQLQLLD-------SGESEYKAIQTYLKQTGNSYRCPNLRHVW 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            722 LTKNQNTLIEKDKEHDKLITANKTAIDANKASADTKFAATADAITKNGNAI-TKNAKSIT 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360 KVNREGEG--------DRFQA-HSKLGNRRLLWHGTNVAVVAAILTSGLRIM 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 DLGTKVDGFDGRVTALDTKVNAFDGRITALDSKVEN------GMAAQAAL--SGL-FQ 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QSKMNHFTCLEDAKKDFKKKFWEKTKNKWEERDRFVAQPNKYTLIEVQGEAESQEA---- 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 VVKALSPQVDSGPVRTVVKPCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKKMPLGKLT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                662 NTONIAKNOADIANNINNIYELAQQODQHSSDIKTLAKASAANTDRIAKNKADADASFET 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 SVQTEGSKKQ------RQGTEEEDSFR-STAEALRAAPADNRVIRVDPSCPFSRNPGIQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222 KQQIARGFEALEALEEAMKNPTGDGQSLEELSSCFYTVIPHNFGRSRPPPI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  273 NSPDVLQAKKDMLLVLADI-ELAQ------TLQAAPGEEEEKVEEVPHPLDRDYQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.6%; Score 100.5; DB 4;
Similarity 19.9%; Pred. No. 0.69;
01; Conservative 78; Mismatches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: August 29, 2002, 07:58:21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYSVGKFNATAALGGYGSKSAVAIGAGY 857
                                                                                                                                                                                  ; Sequence 15, Application US/09336447A; Patent No. 6310190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Moraxella catarrhalis
                            477 PDPAQDIELELDGQPV 492
                                                       |: | ::| | |:
328 PEAAGEVE-RLIGHPL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 3.6
Best Local Similarity 19.9
Matches 101; Conservative
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280 GDPALAYGYAQDQEPDAR-----GRIRNGALLRVYVPRSSL----PGFYRT-SLTLAA 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----ALEEAMKNPTGDGQSL 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 LPLETLTRHROPRGWEQLEQAGYPVQRLVALYLAARLSWNQVDQVIRNALASP-GSGGDL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250 EELSSCFYTVIPHNFGRSRPPPINSPDVLQAKKDMLLVLADIELAQTLQAAPGEEEEKVE 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    310 EVPHPLDRDYQLLRCQLQL-----LDSG----ESEYKAIQTYLKQTGNSYRCPNLRHVW 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 ----ANADVVSLTCPVAAGECAGPADSGDALLERNYPTEAEFLGDGGDVSFSTRGTQNW 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225 TVER----LLQAHROLEERGYVFVGYHGTFLEAAQSIVFGGVRARSQDLDAIWRGFYIA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SENSKSAGYVTTMHCGGHQVGYMFLGEVALGKEHHITIDDPSLKSPPPGFDSVIARGQTE 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280 GDPALAYGYAQDQEPDAR-----GRIRNGALLRVYVPRSSL----PGFYRT-SLTLAA 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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21.2%; Pred. No. 0.21;
Live 38; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Power Macintosh 6.0.1
SOFTWARE: Microsoftword 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Grasler, Frank P
REGISTRATION NUMBER: 31,164
REFERENCE/DOCKET NUMBER: 178791A
TELECOMMUNICATION INFORMATION:
TELEPAN: (908) 594-4720
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Riemen, Mark W
APPLICANT: Stiemen, Steven M
TITLE OF INVENTION: Modified PE40
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                             Sequence 7, Application US/08839425
Patent No. 5912322
                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Merck & Co., Inc. STREET: 126 Lincoln Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 420 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 21.29
Matches 67; Conservative
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328 PEAAGEVE-RLIGHPL 342
                                                                   477 PDPAQDIELELDGQPV 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New Jersey COUNTRY: U.S.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Human brain PARP2	Human brain poly-A	hPARP2. Homo sapi	Human poly(ADP-rib	Human ORFX ORF2673	Human PARP-2 prote	Human PARP-2 prote	Human protein segu	Mouse PARP-2 prote	Fusion protein PAR	Novel human neopla
	ID	AAY51174	AAB11480	AAB47029	AAB60693	AAB42909	AAU29023	AAU29020	AAB93513	AAU29022	AAB47032	AAU21687
	DB	21	22	22	22	21	22	22	22	22	22	22
	Query Match Length DB	570	570	583	521	534	534	534	531	522	1063	379
æ	Query Match	100.0	100.0	99.4	91.7	91.1	91.1	8.06	83.8	82.3	68.2	9.59
	Score	2998	2998	2981.5	2749	2732.5	2732.5	2723.5	2693.5	2468	2043.5	1966
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N-terminal fragmen C-terminal fragmen Human DNA repair a Novel human neopla The poly(ADP-riboss) A poly(ADP-riboss)	Human DNA repair a Novel human neopla Poly(ADP-ribose) p Human poly(ADP-rib Human poly (ADP-rib	Human PARP-1 prote Human tankyrase2 r Human uuclear NAD+ Drosophila melanog A poly(ADP-ribose)	A poly(ADP-ribose) Novel human neopla Maize poly ADP-rib Human brain PARP3 Human uterus type Human PARP3 prote	PARFI PARPI Secrete protei	tankyr SPANK. human human
AAB47030 AAB47031 AAU20129 AAU21810 AAY68835 AAY68834	AAU20130 AAU21811 AAR99642 AAY33699 AAY58043	AAU29019 AAB66296 AAY49939 ABB66431 AAY68833	AAY68839 AAU21688 AAY51464 AAY51175 AAU29021	AAY51170 AAY51177 AAG01000 AAY54373 AAB51022 AAU33242	AAB66301 AAB47023 ABG10624 ABG25601 ABG10631
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59.7 50.6 488.6 399.4		33.6 33.6 32.7	32.1 28.3 24.2 24.2 24.0	23.3 21.2 10.2 10.2	
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113 114 115 116	18 20 21 22	23 26 27 27	335 335 335 335 335 335 335 335 335 335	4 W W W W W 4 0 O B A O W 4	44444 114643

ALIGNMENTS

RESULT

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PARP; poly(ADP-ribose) polymerase; human; murine; detection; sepsis; diagnosis; therapy; necrosis; apoptosis; neurodegenerative illness; ischemic tissue damage.
                                                                                                                                                                                                                                                                                                                                Novel genes and proteins, antibodies and binding partners useful in diagnosis and therapy of energy deficiency associated disease
                                                                                                                                                                                                                                                                             Lemaire
                                                                                                                                                                                                                                                                            Lubisch W,
                                                                                                                                                                                                                                                                            Kroeger B, Otterbach B,
       AAY51174 standard; Protein; 570 AA
                                                                                                                                                                                                                       98DE-1025213.
99DE-1008837.
                                                                                                                                                                                                    99WO-EP03889
                                                  (first entry)
                                                                       Human brain PARP2 protein.
                                                                                                                                                                                                                                                                                                 WPI; 2000-087218/07.
N-PSDB; AAZ44287.
                                                                                                                                                                                                                                                                            Kock M, Hoeger T,
                                                                                                                                                                                                                                                        (BADI ) BASF AG.
                                                                                                                                      Homo sapiens
                                                                                                                                                        WO9964572-A2
                                                                                                                                                                                                   04-JUN-1999;
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                                                  31-MAR-2000
                                                                                                                                                                              16-DEC-1999.
                             AAY51174;
AAY51174
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Human brain poly-ADP-ribose-polymerase protein.

(first entry)

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This invention describes novel human and murine poly(ADP-ribose)
polymerase (PARP) homologues, which are characterised by an amino acid
sequence with a functional NDP<sup>+</sup>-binding site and no zinc finger
sequence motif, of general formula CX_2CX_ZMHX_2C (I). The nucleic acid
sequences, PARP homologues and antibodies are useful for analytic
detection of PARP homologues and for identifying PARP effectors or
binding partners, as well as for determining their effectiveness.
PARP-binding partners are useful for the diagnosis or therapy of a
disease condition, which is the result of a PARP protein, especially an
energy deficiency, which may comprise tissue damage from call death
following necrosis or apoptosis. The disease condition may be chosen
from a neurodegenerative illness, or sepsis or ischemic tissue damage,
in particular neurotoxic disturbances, etc. This sequence represents the
human PARP2 protein used in the method of the invention.
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                              Claim 4; Page 52-54; 96pp; German
                                                                                                                                                                                                                                                                                            570 AA;
 conditions
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AAB11480 standard; Protein; 570

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RESULT

AAB11480;

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This invention describes novel 4-substituted 2H-phthalazin-1-one derivatives (I) which are used for the treatment or prophylaxis of diseases associated with elevated poly-ADP-Tibose)-polymerase (PARP): CC diseases associated with elevated poly-ADP-Tibose)-polymerase (PARP): EC 2.4.2.30) activity. The products of the invention have nootropic, neuroprotective, carciant, vasciropic, anticonvulsant, vascoring, antibacterial, immunosuppressive, antinflammatory, antithemmatic, antibacterial, immunosuppressive, antinflammatory, antithemmatic, antibacterial, immunosuppressive, antinflammatory, antithemmatic, antibacterial, antidiabetic. (I) are especially used for treating or preventing controlly rehalf and an assive bleeding, especially apoplexy or spinal-cranial trauma; or Alzheimer's disease, Huntington's disease or parknison's disease or preventing ischemic damage after renal ischemia or during and after (specifically renal damage after renal ischemia or during and after complex parantation or heart damage after cardiac ischemia), treating confically generalized epileptic attacks (e.g. temporal lope of tonic-clonic attacks) or partial epileptic attacks (e.g. temporal lope and complex partial attacks), treating microinfarction (e.g. during and after heart valve replacement, aneurysm rescentioning and heart cardial attacks), after PCTA or by pass operations) or peripheral arteries (e.g. after PCTA or by pass operations) or peripheral arteries (e.g. after PCTA or by pass operations) or peripheral arteries or after its mechanical or drug-induced lysis and treating tumors and context metastasis, sepsis and septic shock, inflammatory and strongly and septic shock, inflammatory and strongly inhibit PARP homologs, specifically contivity (e.g. with K_I values of 1-20 M) and high selectivity for PARPI (generally by a factor of more than 5).
                                                                                      Human; poly ADP-ribose polymerase; PARP; neuroprotective; nootropic; creebzoprotective; antiparkinsonian; nephrotropic; cardiant; vasotropic; anticonvulsant; cytostatic; antibacterial; immunosuppressive; treatment; antinflammatory; antirheumatic; antiarthritic; antidiabetic; epilepsy; 2H-phthalazin-1-one derivative; neurodegenerative disease; tumor; neuronal damage; Alzheimer's disease; mioridiquoton's disease; metastasis; parkinson's disease; ischemic damage; nicrolnfarction; sepsis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drugs for inhibiting PARP or especially homologous enzymes comprising 4-substituted phthalazinone derivatives, useful e.g. for treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4-substituted phthalazinone derivatives, useful e.g. for treati
neurodegenerative disease, ischemic damage, tumors or diabetes
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100.0%; Pred. No. 2.6e-275;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example A; Page 12-13; 14pp; German.
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Best Local Similarity 100.
Matches 570; Conservative
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                                                                                                                                                                                                                                                        diabetes mellitus.
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                                                                                                                                                                                                                                                                                                      Homo sapiens
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Homo sapiens.

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Human; poly(ADP-ribose) polymerase; hPARP2; oxidative stress; ARDS; inflammation; ischemic stroke; hemorrhagic shock; myocardial ischemia; finflammation; ecrebral vasospasm; rhemunatoid arthritis; osteoarthritis; will inflammation cerebral vasospasm; rhemuatoid arthritis; septic shock; gram negative sepsis; gram positive sepsis; septic shock; myotaxic shock; gram negative sepsis; gram positive sepsis; trauma; toxic shock syndrome; matchiple organ injury syndrome; vasoulitis; hemorrhage; conjunctivitis; uveitis; thyroid-associated ophthalmopathy; chronic obstructive pulmonary disease; slincosis; peperfusion injury; whenchiectasis; pulmonary disease; slincosis; peperfusion injury; pronchiectasis; pulmonary dyagen toxicity; keloid formation; brain; scar tissue formation; alterosclerosis; seynaud's syndrome; autoimmune thyroiditis; multiple sclerosis; Reynaud's syndrome; autoimmune thyroiditis; multiple sclerosis; Reynaud's syndrome; confictis; inflammatory dermatosis; contact dermatitis; atopic dermatitis; hoporolemic shock; Type I diabetes mellitus; hypersensitivity; slowel disease; alcoholic hepatitis; hypersensitivity; helmonia; hypersensitivity; helmonia; hypersensitivity; helmonia; hypersensitivity;
                                                                                                                                                 FEKVPGKYDMLQMDYATNTQDEEETKKEESLKSPLKPESQLDLRVQELIKLICNVQAMEE 240
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                                                                               IQLLEDDAQRNFSVWMRWGRVGKMGQHSLVACSGNLNKAKEIFQKKFLDKTKNNWEDREK 180
                                                                                                                                                                                                                                                           MMMEMKYNTKKAPLGKLTVAQIKAGYQSLKKIEDCIRAGQHGRALMEACNEFYTRIPHDF 300
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 MAARRRSTGGGRARALNESKRVNNGNTAPEDSSPAKKTRRCOROESKKMPVAGGKANKD
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This sequence represents human poly(ADP-ribose) polymerase (hPARP2).

This protein causes the covalent addition of polymers of ADP-ribose construction causes the covalent addition of polymers of ADP-ribose to protein targets. HPARP2 activity is induced in many instances of oxidative stress or during inflammation where there is direct damage considerive stress and the part of a construction of the DMA. HPARP2 may be used, to identify antagonists which can be used to treat a human having a disorder mediated by PARP2 activity, such as, inflammatory, neurological, cardiovascular, or neoplastic tissue growth disorders, e.g. ischemic stroke, hemorrhagic shock, myocardial ischemia or infarction, carebral vasospasm: rheumatoid, osteo- or gouty carthritis, spondylitis; Behcef's disease; sepsis, septic or endotoxic shock, gram negative or positive sepsis, toxic shock syndrome; multiple or gran injury syndrome secondary to septicemia, trauma, or hemorrhage; allergic or vernal conjunctivitis, uveitis, thyroid-associated ophthalmopathy; eosinophilic granuloma; asthma, chronic bronchitis, ophthalmopathy; eosinophilic granuloma; asthma, chronic bronchic obstructive pulmonary disease, silicosis, plumonary sarcoidosis, pleurisy, alveolitis, vasculitis, neinforme; graft versus host disease, content or anothic dermation; atherosclerosis; systemic lupus of formation, scar tissue formation; atherosclerosis; systemic lupus crythematosus, autoimmune thyroiditis, multiple sclerosis; Reynaud's sydneriul comphritis; inflammatory dermatose contect or atopic dematitis, portasis, unliquatis, inflammatory dermatose contect or atopic dematitis, portasis, unliquatis, inflammatory dermatose contect or atopic dematitis, portasis, unliquation due to infection; meningitis, encephalitis, and brain and myalajas contents and papedesis; alcoholic hepatitis; and brain and myalajas contents and inspedence or and dispedesis alcoholic hepatitis; bacterial penance or and myalajas contents and dispedesis alcoholic hepates, button and myalajas contents and 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antigen-antibody complex mediated diseases; hypovolemic shock; Type 1 diabetes mellitus; acute and delayed hypersensitivity; disease states due to leukocyte dyscrasia and metastasis; thermal injury; garanulocyte transfusion associated syndromes; and cytokine-induced toxicity. hPARP2 and antibodies to it, can also be used to diagnose these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RTEDKQD------ESVKALLLKGKAPVDPECTAKVGKAHVYCEGNDVYDVMLN 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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97.8%; Pred. No. 1e-273;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                    Goldman PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Page 94-95; 129pp; English.
                                                                                                                                                                                                                                                                                    Christenson E, Demaggio AJ,
                                                                                                                                       16-JUN-2000; 2000WO-US16629
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                                              WO200077179-A2.
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                                                                                           21-DEC-2000.
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New human polypeptide of the polyADPribose synthetase family for use in diagnostic assays and for screening modulators used for preventing and treating inflammation, autoimmune disease and Alzheimers disease
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           HYRNLHCALRPLDHESYEFKVISQYLQSTHAPTHSDYTWTLLDLFEVEKDGEKEAFREDL
                                                                                                                                                                                                                                                                                      LIKLICNVQAMEEMMMEMKYNTKKAPLGKLTVAQIKAGYQSLKKIEDCIRAGQHGRALME
                                                                                                     NTGLLLLSEVALGQCNELLEANPKAEGLLQGKHSTKGLGKMAPSSAHFVTLNGSTVPLGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; poly(ADP-ribose) synthetase; sbhPARS2; vaccine; drug screen ischaemic disorder; cerebral ischaemia; cardiac ischaemia; mycardial infarction; stroke; inflammation; autoimmune disease; diabetes; multiple sclerosis; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; chromosome localisation.
QTNLQFNNNKYYLIQLLEDDAQRNFSVWMRWGRVGKMGQHSLVACSGNLNKAKEIFQKKF
                                                                                                                                      ACNEFYTRIPHDFGLRTPPLIRTQKELSEKIQLLEALGDIEIAIKLVKTELQSPEHPLDO
                                                                                                                                                                                                                               HNRMLLWHGSRMSNWVGILSHGLRIAPPEAPITGYMFGKGIYFADMSSKSANYCFASRLK
                                             LDKTKNNWEDREKFEKVPGKYDMLQMDYATNTQDEEETKKEESLKSPLKPESQLDLRVQE
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                                                                                                                                                                                                                                                                                                                       ASDIGILNPDGYTLNYNEYIVYNPNQVRMRYLLKVQFNFLQLW 570
                                                                                                                                                                                                                                                                                                                                   Human poly(ADP-ribose) synthetase sbhPARS2
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                                                                                                                                                                                                                                                                                                                                                                                                    AAB60693 standard; Protein; 521
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This sequence represents a novel human poly(ADP-ribose)
synthetase, sbhPARS2. The invention also relates to fragments,
variants and sequences with at least 95% identify to the sbhPARS2
comprising an sbhPARS2 nucleic acid sequence; the recombinant expression
comprising an sbhPARS2 nucleic acid sequence; the recombinant expression
comprising an sbhPARS2 nucleic acid sequence; the recombinant expression
compounds which in this part as vaccines for inducing an immunological
response in a mammal. The sbhPARS2 protein is useful for identifying
compounds which inhibit or stimulate its activity or expression level.
Such agonists and antagonists of sbhPARS2 are useful for treating human
diseases including ischaemia and ischaemic tissue injury (e.g., cerebral
and cardiac ischaemia, myocardial infarction, stroke), inflammation,
autoimmune disease (e.g., diabetes, multiple sclerosis) and
cutoimmune disease (e.g., diabetes, multiple sclerosis) and
cutoimmune disease (e.g., diabetes, multiple sclerosis) and
cutoimmune disease (e.g., diabetes, multiple sclerosis) and
cletecting mutations in the associated gene; as hybridisation probes
to isolate full-length sbhPARS2 conds and sbhPARS2 genomic clones; and
for chromosome localisation studies. The sbhPARS2 genomic clones; and
condice and immunogen to produce antibodies for therapeutic use. sbhPARS2
proteins, nucleotides and antibodies are also useful in screening methods
contents.
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100.0%; Pred. No. 9.9e-252;
tive 0; Mismatches 0;
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nes 521; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     521 AA;
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                                                                                                                                                                          vulnerary; antipsoriatic; antiarthritic; immunosuppressant; arguatory, vulnerary; antipsoriatic; antiarthritic; immunosuppressant; cardiant; immunosuppressant; cardiant; immunosuppressive; antidiabatic; hypotensive; dermatological; immunosuppressive; antidiafammatory; antiariammatory; antidiabatic; antidiammatory; antidiammatory; antidiammatory; antidiammatory; antidiammatory; antidiammatory; cancer; proliferative disorder; hypertension; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; burne damage; cartilage damage; antinflammatory disease; coagulation;
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                                                                                                                                                   open reading frame; ORFX; detection; cytostatic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                     Human ORFX ORF2673 polypeptide sequence SEQ ID NO:5346.
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99US-0127636.
99US-0127728.
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   (first entry)
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08-FEB-2001
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Human; PARP; Poly (ADP-ribose) polymerase; antisense oligonucleotide; cytostatic; nootropic; neuroprotective; antiinflammatory; antidiabetic; immunosuppressant; hyperproliferative disorder; cancer; cellular injury; oxidative stress; neurological disorder; parkinsonism; apoptosis; meningitis-associated intracranial complication; ischaemia; inflammatory disorder; autoimmune disorder; arthritis; diabetes.
                                                                            ESVKALLLKGKAPVDPECTAKVGKAHVYC
                EGNDVYDVMLNQTNLQFNNNKYYLIQLLEDDAQRNFSVWMRWGRVGKMGQHSLVACSGNL
                                                                                                                       157 NKAKEIFOKKFLDKTKNNWEDREKFEKVPGKYDMLOMDYATNTODEEETKKEESLKSPLK
                                                                                                                                                                                                      SANYCFASRLKNTGLLLLSEVALGOCNELLEANPKAEGLLOGKHSTKGLGKMAPSSAHFV
                                                                                                                                                                                                                                                      RAGQHGRALMEACNEFYTRIPHDFGLRTPPLIRTQKELSEKIQLLEALGDIEIAIKLVKT
                                                                                                                                                                                        PESQLDLRVQELIKLICNVQAMEEMMMEMKYNTKKAPLGKLTVAQIKAGYQSLKKIEDCI
                                                                                                                                                                                                                                                                                                                     ELQSPEHPLDQHYRNLHCALRPLDHESYEFKVISQYLQSTHAPTHSDYTMTLLDLFEVEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               517 TLNGSTVPLGPASDTGILNPDGYTLNYNEYIVYNPNQVRMRYLLKVQFNFLQLW 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense compound useful for treating hyperproliferative,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU29023 standard; Protein; 534 AA.
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MPVAGGKANKDRTEDKQD
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Gaps

13;

0; Indels

Score 2732.5; DB 2 Pred. No. 3.8e-250; 0; Mismatches 0;

91.18; 97.68;

Ouery Match Best Local Similarity 97.6 Matches 521; Conservative

21; Length 534;

PARP; Poly (ADP-ribose)

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                                                                      The invention relates to antisense oligonucleotides targeted to human PARP nucleic acid and inhibiting expression of human PARP. PARP (POI) (ADD-ribose) polymerase plays an important role in chromatin decondensation, DNA replication, DNA repair, gene expression, mailgnant transformation, cellular differentiation and apoptosis. The antisense oligonucleotide inhibitors are useful for inhibiting the expression of PARP in human cells or tissues. They are also useful for treating a human with a disease associated with PARP especially hyperproliferative disorders (e.g. cancer), cellular injury resulting from oxidative stress, mentological (e.g parkinsonism, meningities-associated intracranial complications and isohaemia), inflammatory and autoimmune disorders (e.g arthritis) and diabetes. The present sequence is a PARP protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGNDVYDVMLNQTNLQFNNNKYYLIQLLEDDAQRNFSVWMRWGRVGKMGQHSLVACSGNL 156
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                                                                                                                                                                                                                                                                                                                                                                                          13;
                                                                                                                                                                                                                                                                                                                                                           DB 22; Length 534;
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Pred. No. 3.8e-250;
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                                             Example 16; Page 125-127; 168pp; English.
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97.6%;
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The invention relates to antisense oligonucleotides targeted to human PARP nucleic acid and inhibiting expression of human PARP. PARP PARP PARP PARP TO A CALL THE AUTHORIST A CALL TO A CALL THE AUTHORIST. THE AUTHORIST A CALL TO A CALL THE AUTHORIST. THE AUTHORIST A CALL TO A CALL THE AUTHORIST. THE AUTHORIST A CALL TO A CALL THE AUTHORIST AND AUTHORIST A CALL THE AUTHORIST AND 
                                         cytostatic; nootropic; neuroprotective; antiinflammatory; antidiabetic; immunosuppressant; hyperproliferative disorder; cancer; cellular injury; oxidative stress; neurological disorder; parkinsonism; apoptosis; mentingitis-associated intracranial complication; ischaemia; inflammatory disorder; autoimmune disorder; arthritis; diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 2723.5; DB 22; Length 534;
Pred. No. 2.7e-249;
0; Mismatches 1; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 13; Page 102-104; 168pp; English.
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                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001; 2001WO-US06572
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                                                                                                                                                                                                           Homo sapiens
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Matches 520;
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standard; Protein; 534

AAU29020 AAU29020;

AAU29020

(first entry)

18-DEC-2001

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Human PARP-2 protein #1.

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[10] The present invention describes primer sets for synthesising 5602

[10] The present invention in the specification. Where a primer set

[10] The complementary strand of a polynucleotide which comprises one of

[11] The 5602 nucleotide sequences defined in the specification, where the

[12] Oligonucleotide comprising a sequence complementary to the

[13] Complementary strand of a polynucleotide which comprises a 5'-end

[13] Sequence and an oligonucleotide comprising a sequence complementary to a complementary strand of a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence which comprises a 1-east 15 nucleotides and the complementary to a complementary strand of a polynucleotide which comprises a 1-east 15 nucleotides and the complementary to a ligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for the particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by
                                                                             456
                                                                                                                                                         516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                    360
                                                                                                                  420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                    ELQSPEHPLDQHYRNLHCALRPLDHESYEFKVISQYLQSTHAPTHSDYTMTLLDLFEVEK
                                                                           DGEKEAFREDLHNRMLLWHGSRMSNWVGILSHGLRIAPPEAPITGYMFGKGIYFADMSSK
                                                                                                                                                         SANYCFASRLKNTGLLLLSEVALGQCNELLEANPKAEGLLQGKHSTKGLGKMAPSSAHFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamamoto
                                                                                                                                                                                                                                                       517 TLNGSTVPLGPASDTGILNPDGYTLNYNEYIVYNPNQVRMRYLLKVQFNFLQLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saito K,
Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; SEQ ID 12844; 2537pp + CD ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein sequence SEQ ID NO:12844.
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T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                          AAB93513 standard; Protein; 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JUL-2000; 2000EP-0116126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sugiyama
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09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP1074617-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JUN-2001
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the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAH13639 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; PARP; Poly (ADP-ribose) polymerase; antisense oligonucleotide; cytostatic; nootropic; neuroprotective; antiinflammatory; antidiabetic; immunosuppressant, hyperprobliferative disorder; cancer; cellular injury; oxidative stress; neurological disorder; parkinsonism; apoptosis; meningitis-associated intracranial complication; ischaemia; inflammatory disorder; autoimmune disorder; arthritis; diabetes.
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                                                                                                                                                                                                                                                                                                             1 MAARRRSTGGGRARALNESKRVNNGNTAPEDSSPAKKTRRCQRQESKKMPVAGGKANKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                   QTNLQFNNNKYYLIQLLEDDAQRNFSVWMRWGRVGKMGQHSLVACSGNLNKAKEIFQKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDKTKNNWEDREKFEKVPGKYDMLQMDYATNTQDEEETKKEESLKSPLKPESQLDLRVQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACNEFYTRIPHDFGLRTPPLIRTQKELSEKIQLLEALGDIEIAIKLVKTELQSPEHPLDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYRNLHCALRPLDHESYEFKVISQYLQSTHAPTHSDYTMTLLDLFEVEKDGEKEAFREDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HNRMLLWHGSRMSNWVGILSHGLRIAPPEAPITGYMFGKGIYFADMSSKSANYCFASRLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hnrmllwhgsrmsnwvgilshglriappeapitgymfgkgiyfadmssksanycfasrlk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NTGLLLLSEVALGQCNELLEANPKAEGLLQGKHSTKGLGKMAPSSAHFVTL 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                       22;
                                                                                                                                                                                                     Score 2693.5; DB 22
Pred. No. 1.9e-246;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ä.
                                                                                                                                                                                                     89.8%;
ilarity 97.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU29022 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                        the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse PARP-2 protein.
                                                                                                                                                                                                                            Best Local Similarity
Matches 517; Conserv
                                                                                                                                                A);
                                                                                                                                              531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200164955-A1.
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                                                                                                                                              Sequence
                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
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(Poly (ADP-ribose) polymerase plays an important role in chromatin decondensation, DNA replication, DNA repair, gene expression, malignant transformation, DNA replication, DNA repair, gene expression, malignant transformation, cellular differentiation and apoptosis. The antisense oligonucleotide inhibitors are useful for inhibiting the expression of PARP in human cells or tissues. They are also useful for treating a discorders (e.g. cancer), cellular injury resulting from oxidative stress, neurological (e.g parkinsonism, meningitis-associated intracranial arthritis) and diabetes. The present sequence is a PARP protein, the cdNA encoding which was used to design the antisense
                                                                                                                                                                                                                                                                                                                  The invention relates to antisense oligonucleotides targeted to human PARP nucleic acid and inhibiting expression of human PARP. PARP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 DVYDVMLNQTNLQFNNNKYYLIQLLEDDAQRNFSVWMRWGRVGKMGQHSLVACSGNLNKA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              340 SPEHPLDQHYRNLHCALRPLDHESYEFKVISQYLQSTHAPTHSDYTMTLLDLFEVEKDGE 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  400 KEAFREDLHNRMLLWHGSRMSNWVGILSHGLRIAPPEAPITGYMFGKGIYFADMSSKSAN 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 RRCQRQESKKMPVAGGKANKDRTEDKQDESVKALLLKGKAPVDPECTAKVGKAHVYCEGN 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QLDLRVQELIKLICNVQAMEEMMMEMKYNTKKAPLGKLTVAQIKAGYQSLKKIEDCIRAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEIFQKKFLDKTKNNWEDREKFEKVPGKYDMLQMDYATNTQDEEETKKEESLKSPLKPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          280 QHGRALMEACNEFYTRIPHDFGLRTPPLIRTQKELSEKIQLLEALGDIEIAIKLVKTELQ
                                                                                                                                                                                                            bound useful for treating hyperproliferative, inflammatory and autoimmune disorders and diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.3%; Score 2468; DB 22; Length 522;
87.6%; Pred. No. 4.7e-225;
ive 35; Mismatches 21; Indels 10.
                                                                                                                                                                                                                                                                                 Example 13; Page 109-111; 168pp; English.
              01-MAR-2001; 2001WO-US06572.
                                                 02-MAR-2000; 2000US-0517467
                                                                                                                                                                                                            Antisense compound useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 67.0
Matches 465; Conservative
                                                                                  (ISIS-) ISIS PHARM INC.
                                                                                                                      Popoff I, Cowsert LM;
                                                                                                                                                       2001-602570/68.
                                                                                                                                                                                                                              neurological, inflam
inhibits human PARP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    522 AA;
                                                                                                                                                                       N-PSDB; AAS45597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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KW inflammation; ischaemic stroke; hemorrhagic shock; myocardial ischemia; tinglammation; ischaemic stroke; hemorrhagic shock; myocardial ischemia; inflammation; cerebral vasospasm; rheumatoid arthritis; osteoarthritis; world; arthritis; species of sisease; sepsis; strauma; modotoxic shock; gram negative sepsis; species shock; modotoxic shock; gram negative sepsis; gram positive sepsis; trauma; toxic shock syndrome; multiple organ injury syndrome; vasculitis; hemorrhage; conjunctivitis; uveitis; thyroid-associated ophthalmopathy; hemorrhage; conjunctivitis; uveitis; thyroid-associated ophthalmopathy; chronic obstructive pulmonary disease; sllicosis; reperfusion injury; pulmonary sarcoidosis; pleurisy; alveolitis; neumonia; myocardium; bronchiectasis; pulmonary oxygen toxicity; keloid formation; brain; soar tissue formation; atheroscierosis; systemic lupus erythematosus; contect dermaticis; syndrome; watto in thyroiditis; multiple sclerosis; systemic lupus erythematosus; contect dermatitis; atopic dermatitis; pronic glomerulomephritis; inflammatory bowel disease; ulcerative colitis; necorpialitis; encephalitis; portice dyscrasis; thermal injury; cytokine-induced toxicity; when persessed sequence tag; RACE; PCR; amplify; primer; we perpessed sequence tag; RACE; PCR; amplify; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents the fusion protein PARPIA/PARP2B. This protein contains amino acids 1-662 of hPARPI fused upstream of amino acids 230-583 of hPARP2. The CDNA encoding this sequence was amplified using the primer sequences given in AAC85312-40 and AAC85342-51. The fusion protein coding sequence was cloned in a baculovirus expression vector for the expression of the fusion protein coding sequence was cloned in a polymers of ADP-ribose to protein targets. hPARP2 activity is induced in many instances of oxidative stress or during inflammation where there is direct damage to the DNA. hPARP2 may be used to identify antagonists which may be used to treat a human having a disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human poly(ADP-ribose) polymerase for treating inflammatory, neurological, cardiovascular, or neoplastic tissue growth disorders, such as, arthritis, encephalitis, myocardial ischemia, and leukocyte metastasis
                                                                                                                                                                                                                                                                                        poly(ADP-ribose) polymerase; hPARP2; oxidative stress; ARDS;
McElligott DL;
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                                                                                                                     AAB47032 standard; Protein; 1063
                                                                                                                                                                                                                                               Fusion protein PARP1A/PARP2B.
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GSTVPLGPASDTGILNPDGYTLNYNEYIVYNPNQVRMRYLLKVQFNFLQLW 570

YCFASRLKNTGLLLLSEVALGQCNELLEANPKAEGLLQGKHSTKGLGKMAPSSAHFVTLN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 VGKAHVYCEGNDVYDVMLNQTNLQFNNNKYYLIQLLEDDAQRNFSVWMRWGRVGKMGQHS 148
                                                                                                                                                                                                                              207
                                                                                                                                                                                                                                                      691
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; neoplastic disease associated polypeptide; cancer; hyperproliferative disorder: neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder; neuroprotective; cytostatic; anti inflammatory; vasotropic.
                                                                                 68.2%; Score 2043.5; DB 22; Length 1063; 75.7%; Pred. No. 3.1e-184; Live 32; Mismatches 81; Indels 19; Gaps
                                                                                                                                 29 APEDSSPAKKTRRCQRQESKKMPVAGGKANKDRTEDKQDESVKALLLKGKAPVDPECTAK 88
mediated by PARP2 activity, such as, inflammatory, neurological, cardiovascular, or neoplastic tissue growth disorders. hPARP2 and antibodies to it, can also be used to diagnose these conditions.
                                                                                                                                                                                                                                                                           ||| :| || || :- | || :|||||| : : : ||||| : 576 ehsahvlekggkvfsatlglvdivkgtnsyyklqlleddkenrywifrswgrvgtvigsn
                                                                                                                                                                                                                                                                                                                                                                       149 LVACSGNLNKAKEIFQKKFLDKTKNNWEDREKFEKVPGKYDMLQMDYATNTQDEEETKK-
                                                                                                                                                                                                                                                                                                                            SLKKIEDCIRAGQHGRALMEACNEFYTRIPHDFGLRTPPLIRTQKELSEKIQLLEALGDI
                                                                                                                                                                                                                                                                                                                                        388 LLDLFEVEKDGEKEAFREDLHNRMLLWHGSRMSNWVGILSHGLRIAPPEAPITGYMFGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      448 IYFADMSSKSANYCFASRLKNTGLLLLSEVALGQCNELLEANPKAEGLLQGKHSTKGLGK
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                                                                                                                                                                                                                                         Novel human neoplastic disease associated polypeptide #120
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                                                                                              Best Local Similarity 75.7%
Matches 411; Conservative
                                                1063 AA;
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                                                 Sequence
                                                                                   Query Match
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Novel polypeptides and polynucleotides useful as diagnostic reagents to diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, and for treating cancers, rheumatoid arthritis

Claim 11; SEQ ID No 414; 687pp; English.

The present invention relates to the isolation of novel human neoplastic disease associated polypeptides, and CDNA (AAS34767-AAS35050) and DNA sequences encoding for these polypeptides. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of disorders involving neoplastic disease such as hyperproliferative disorders involving neoplastic disease such as concer, brain stem glioma, adult liver cancer, childhood cerebellar cancer, brain stem glioma, adult liver cancer, childhood cerebellar astrocytoma, or Hodgkin's lymphoma). The sequences of the invention may astrocytoma, or Hodgkin's lymphoma). The sequences of the invention may astrocytoma, the polypucledrisk sequences of the invention are cancer and disorders, pulmonary disorders, reproductive disorders, and renal disorders. The polypucleotide sequences of the invention are also useful in gene therapy. AAU21861 represent the novel human coplastic disease associated polypeptides of the invention.

CC also useful in gene therapy. AAU21861 represent the novel human coplastic disease associated polypeptides of the invention.

CC also useful in was obtained in electronic format directly from WIPO cc at ftp.wipo.int/pub/published_pct_sequences.

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379 AA;

Sequence

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Ruben SM;
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2000US-0246610
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                                02-0CT-2000; 20-0CT-2000; 20-0C
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192 QMDYATNTQDEEETKKEESLKSPLKPESQLDLRVQELIKLICNVQAMEEMMMEMKYNTKK 251
                                                                                                252 APLGKLTVAQIKAGYQSLKKIEDCIRAGQHGRALMEACNEFYTRIPHDFGLRTPPLIRTQ 311
                                                                                                                                                             431
                                                                                                                                                                                                                                             491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; poly(ADP-ribose) polymerase; hPARP2; oxidative stress; ARDS;
                                                                                                                                                                                                        312 KELSEKIQLLEALGDIEIAIKLVKTELQSPEHPLDQHYRNLHCALRPLDHESYEFKVISQ
                                                                                                                                                                                             YLQSTHAPTHSDYTWTLLDLFEVEKDGEKEAFREDLHNRMLLWHGSRMSNWVGILSHGLR
                                                                                                                                                                                                                                             IAPPEAPITGYMFGKGIYFADMSSKSANYCFASRLKNTGLLLLSEVALGQCNELLEANPK
                                                                                                                                                                                                                                                                                            492 AEGLLQGKHSTKGLGKMAPSSAHFVTLNGSTVPLGPASDTGILNPDGYTLNYNEYIVYNP
  Length 379;
Score 1966; DB 22;
Pred. No. 1.3e-177;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                            AAB47030 standard; Protein; 360 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-terminal fragment of hPARP2
  Query Match 65.6%;
Best Local Similarity 98.9%;
Matches 375; Conservative 1
                                                                                                                                                                                                                                                                                                                                           552 NOVRMRYLLKVQFNFLQLW 570
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WPI; 2001-465558/50. N-PSDB; AAS34886.

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hemorrhagic shock; myocardial ischemia;
rheumatoid arthritis; osteoarthritis;
      inflammation; ischaemic stroke; hemorrhagic shock;
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Synthetic.

WO200077179-A2.

21-DEC-2000.

16-JUN-2000; 2000WO-US16629

99US-0139543 16-JUN-1999;

(ICOS-) ICOS CORP.

Christenson E, Demaggio AJ,

Goldman PS, McElligott DL;

2001-025335/03. N-PSDB; AAC85314. New human poly(ADP-ribose) polymerase for treating inflammatory, neurological, cardiovascular, or neoplastic tissue growth disorders, such as, arthritis, encephalitis, myocardial ischemia, and leukocyte metastasis

Example 2; Page 100-01; 129pp; English.

This sequence is encoded by the 5' fragment of the human parp2 (poly(ADP-ribose) polymerase) cDNA. The cDNA sequence was amplified using the primers given in AAC85307-13. DNA derived from spleen and testis cDNA libraries were used as templates. The primers given in AAC85315-17 were used to confirm the sequence of the 5'-IPPARP2 in AAC85318-17 were used to confirm the sequence of the 5'-IPPARP2 closed to help determine that hPARP2 has an open reading frame of closed to help determine that hPARP2 as no open reading frame of 1080 nucleotides. The protein of the invention, hPARP2 causes the covalent addition of polymers of AADP-ribose to protein targets. The hPARP2 activity is induced in many instances of oxidative stress or during inflammation where there is direct damage to the DNA. The APARP2 may be used to identify antagonists which may be used to treat a human having a disorder mediated by PARP2 activity, such as, inflammatory, neurological, cardiovascular, or neoplastic tissue growth disorders. hPARP2 and antibodies to it, can also be used to to dispanse these conditions.

360 AA; Sequence

ij Gaps DB 22; Length 360; 0; Indels Score 1790.5; DB 2 Pred. No. 5.4e-161; 0; Mismatches 0; 59.78; Conservative Query Match Best Local Similarity Matches 347; Conserv

1 MAARRRSTGGGRARALNESKRVNNGNTAPEDSSPAKKTRRCQRQESKKMPVAGGKANKD 60

KW inflammation; ischaemic stroke; hPARP2; oxidative stress; ARDS; inflammation; ischaemic stroke; hemorrhagic shock; myocardial ischemia; inflammation; carebral vasospasm; rheumatoid arthritis; osteoarthritis; guotty arthritis; spondylltis; Behcef's disease; sepsis; septic shock; gram negative sepsis; gram positive sepsis; trauma; toxic shock syndrome; multiple organ injury syndrome; vasculitis; wendotoxic shock syndrome; multiple organ injury syndrome; vasculitis; hemorrhage; conjunctivitis; uveitis; thyroid-associated ophthalmopathy; conjunctivitis; uveitis; thyroid-associated ophthalmopathy; stronic obstructive pulmonary disease; silicosis; reperfusion injury; wulmonary sarcoidosis; pleurisy; neuemonia; myocardium; who pulmonary sarcoidosis; pulmonary oxygen toxicity; keloid formation; brain; scar tissue formation; atherosclerosis; systemic lupus erythematosus; warefulmment thyroiditis; multiple sclerosis; Reynaud's syndrome; matchimmune thyroiditis; unliammatory bowel disease; allograft rejection; cystic fibrosis; crohar's disease; ulcerative colitis; necrotizing enterocolitis; prorior glomerulonephritis; inflammatory bowel disease; contact dermatitis; atopic dermatitis; prorior syndrome; alcoholic hepatitis; atopic dermatitis; proriorsis; syndrome; alcoholic hepatitis; bacterial pneumonia; hyporolemic shock; Type I diabetes mellitus; hyporolemic shock; Type I diabetes mellitus; hyporolemic dermaticity; kW leukocyte dyscrasia; thermal injury; cytokine-induced toxicity; wexpressed sequence tag; EST; RACE; PCR; amplify; primer; -----ESVKALLLKGKAPVDPECTAKVGKAHVYCEGNDVYDVMLN 107 ||||||||| rtedkqdgmpgrswaskrvsesvkalllkgkapvdpectakvgkahvycegndvydvmln 120 167 227 LIKLICNVQAMEEMMMEMKYNTKKAPLGKLTVAQIKAGYQSLKKIEDCIRAGQHGRALME 287 288 ACNEFYTRIPHDFGLRTPPLIRTQKELSEKIQLLEALGDIEIAIKLVKTELQSPEHPLDQ 347 QTNLQFNNNKYYLIQLLEDDAQRNFSVWMRWGRVGKMGQHSLVACSGNLNKAKE1FQKKF LDKTKNNWEDREKFEKVPGKYDMLQMDYATNTQDEEETKKEESLKSPLKPESQLDLRVQE 1 maarrrrstgggraralneskrvnngntapedsspakktrrcgrqeskkmpvaggkankd AAB47031 standard; Protein; 287 AA. C-terminal fragment of hPARP2. 29-MAR-2001 (first entry) RTEDKOD-----WO200077179-A2. 21-DEC-2000 Synthetic. AAB47031; 13 108 121 228 61 61 168 RESULT 1 õ g å g ò 셤 g ò 셤

Goldman PS, McElligott DL; Christenson E, Demaggio AJ, 16-JUN-2000; 2000WO-US16629. 99US-0139543 (ICOS-) ICOS CORP. .6-JUN-1999;

WPI; 2001-025335/03. N-PSDB; AAC85320.

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17-JAN-2001; 2001WO-US01336
WO200155204-A1.
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14-AUG-2000;
14-AUG-2000;
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06-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (poly(ADP-ribose) polymerase) cond. The cond sequence was amplified using the primers given in AAGB315-17. DNA derived from a testis cDNA library was used as a template. The protein of the invention, hPARP2, causes the covalent addition of polymers of ADP-ribose to protein targets. hPARP2 activity is induced in many instances of oxidative stress or during inflammation where there is direct admage to the DNA. hPARP2 may be used to identify antaqonists which may be used to treat a human having a disorder mediated by PARP2 activity, such as, inflammatory, neurological, cardiovascular, or neoplastic tissue growth disorders. hPARP2 and antibodies to it, can also be used to diagnose these conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              284 ALMEACNEFYTRIPHDFGLRTPPLIRTQKELSEKIQLLEALGDIEIAIKLVKTELQSPEH 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344 PLDQHYRNLHCALRPLDHESYEFKVISQYLQSTHAPTHSDYTWTLLDLFEVEKDGEKEAF 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SRLKNTGLLLLSEVALGQCNELLEANPKAEGLLQGKHSTKGLGKMAPSSAHFVTLNGSTV 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human poly(ADP-ribose) polymerase for treating inflammatory, neurological, cardiovascular, or neoplastic tissue growth disorders, such as, arthritis, encephalitis, myocardial ischemia, and leukocyte metastasis
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                                                                                                                                                                                                                                                                                                                          Example 2; Page 101-02; 129pp; English.
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Homo sapiens

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(HUMA-) HUMAN GENOME SCI INC.
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Rosen CA, Barash SC, Ruben SM;

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Sequences AAU20116-AAU20147 represent the DNA repair and processing polypeptides of the invention. DNA repair and processing polypeptides and their associated polymoutectides are useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by detecting the presence or absence of a mutation in a DNA repair and processing polymoutlectide. The treatable disorders include autoimmune diseases such as rheumatoid arthritis, hyperproliferative disorders such as neoplasms of the breast or liver, cardiovascular disorders such as cardiac arrest, cerebrovascular disorders such as cardiac arrest, cerebrovascular clisorders such as conneal infection, endocrine disorders such as corneal infection, endocrine disorders such as corneal infection, endocrine disorders such as corneal infection, endocrine disorders such as Crohn's disease, renal disorders such as allomerulonephritis and creapiratory disorders such as asthma and pleurisy. The polypeptides can also be used to aid wound healing, to prevent skin aging due to subburn, and the processing and the contract of the contrac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to maintain organs before transplantation, to regenerate tissues and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hyperproliferative disorder; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder; neuroprotective; cytostatic; anti inflammatory; vasotropic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       372 YLQSTHAPTHSDYTMTLLDLFEVEKDGEKEAFREDLHNRMLLWHGSRMSNWVGILSHGLR 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252 APLGKLTVAQIKAGYQSLKKIEDCIRAGQHGRALMEACNEFYTRIPHDFGLRTPPLIRTQ
                                                                                                               Nucleic acids encoding human polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy -
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Pred. No. 2.2e-129;
1; Mismatches 5;
                                                                                                                                                                                                                                  Claim 11; SEQ ID No 56; 460pp; English.
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Matches 280; Conservative
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PR 29-SEP-2000; 2000US-0235836.

PR 29-SEP-2000; 2000US-0235637.

PR 29-SEP-2000; 2000US-0235636.

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PR 29-SEP-2000; 2000US-0235637.

PR 29-SEP-2000; 2000US-0235637.

PR 29-SEP-2000; 2000US-0236935.

PR 20-CCT-2000; 2000US-0236935.

PR 20-CCT-2000; 2000US-0236935.

PR 20-CCT-2000; 2000US-0236475.

PR 20-CCT-2000; 2000US-0246477.

PR 20-CCT-2000; 2000US-0246527.

PR 20-CCT-2000; 2000US-0246227.

PR 20-CCT-2000; 2000US-024921.

PR 20-CCT-2000; 2000US-

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HUMA-) HUMA-) HUMAN GENOME SCI INC.

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WPI; 2001-465558/50.

BR PSDB: AAS35009.

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Novel polypeptides and polynuclectides useful as diagnostic reagents to diagnose diseases or disorders associated with aberrant expression or arthritis of polypeptides, and for treating cancers, rheumatoid concers of the arthritis of disorders disorders and cDNA (AAS34767-AAS35050) and DNA (AAS34767-AAS35050) and CAAS34767-AAS35050) and CAAS34767-AAS35050) and CAAS34767-AAS35050

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                                Gaps
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Ouery Match 48.6%; Score 1456; DB 22; Length 294; Best Local Similarity 97.9%; Pred. No. 2.2e-129; Matches 280; Conservative 1; Mismatches 5; Indels 0
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GENERAL INFORMATION:
APPLICANT: Burkle, Alexander
APPLICANT: Burkle, Alexander
APPLICANT: Jur Hausen, Harald
APPLICANT: Jur Hausen, Harald
APPLICANT: Jan-Heiner, Kupper
TITLE OF INVENTION: VECTORS AND VIRUSES FOR USE
TITLE OF INVENTION: IN GENE THERAPY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
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                         COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
FILLING DATE: 03-0CT-1997
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FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: COLUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8484.
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-493-556
TELEFAX: 66141 PENNIE
INFORMATION FOR SED ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08860886
Patent No. 6335009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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FRAGMENT TYPE: internal
US-08-860-886-2
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RY: USA
10036-2811
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Sequence 1, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 22, Appli
Sequence 21, Appli
Sequence 27, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 66, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 148, Appli
Sequence 148, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 18, Appli
Sequence 18, Appli
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297.555 Million cell updates/sec
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Sequence 3,
Sequence 2,
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1 MAARRRSTGGGRARALNES......PNOVRMRYLLKVQFNFLQLM
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
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                                                            Compugen Ltd.
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                         GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                 - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Length 1013;

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REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: UALB-03283
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
INFORMATION FOR SEQ. IN 00: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1014 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09196387 Patent No. 6277613 GENERAL INFORMATION:
                                                                                                                                          STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEI
TITLE OF INVENTION: OF USE T
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                        TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1009 FKTSLW 1014
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                                                                                                            89 VGKAHVYCEGNDVYDVMLNQTNLQFNNNKYYLIQLLEDDAQRNFSVWMRWGRVGKMGQHS 148
                                                                                                                                        539 EHSAHVLEKGGKVFSATLGLVDIVKGTNSYYKLOLLEDDKENRYWIFRSWGRVGTVIGSN 598
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                                                 APEDSSPAKKTRRCQRQESKKMPVAGGKANKDRTEDKQDESVKALLLKGKAPVDPECTAK 88
                                                                                                                                                                                                                                                                                                                                                                            LVACSGNLNKAKEIFQKKFLDKTKNNWEDREKFEKVPGKYDMLQMDYATNTQDEEETKKE
                                                                                                                                                                                                                                   ESLKSPLKPESQLDLRVQELIKLICNVQAMEEMMMEMKYNTKKAPLGKLTVAQIKAGYOS
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                   29;
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APPLICANT: Weinfeld, Michael
APPLICANT: Waing, James Z.
TITLE OF INVENTION: Methods for Quantitating Low Level
TITLE OF INVENTION: Modifications of Nucleotide Sequences
NUMBER OF SEQUENCES: 3
                   Indels
   Pred. No. 6.6e-89;
; Mismatches 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.30
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220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/078,347A
FILLIO DATE: 13-MAY-1998
CLASSIFCATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE; Patentin Release #1 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09078347A Patent No. 6132968
                 Conservative 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION: NAME: Carroll, Peter G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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US-09-078-347A-3
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COUNTRY:
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                                                                                                                                                                494 APRGKSGAALSKKSKGOV-----KEEGINKSEKRMK-LTLKGGAAVDPD-SGL 539
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Query Match 33.6%; Score 1007.5; DB 4; Length Best Local Similarity 40.5%; Pred. No. 2e-88; Matches 221; Conservative 109; Mismatches 187; Indels
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STREET: 411 Hackensack Avenue, 4th Floor
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83 PECTAKVGKAHVYCEGNDVYDVMLNQTNL---QFNNNKYYLI--QLLEDDAQRNFSVWMR 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 WGRVGKMGQHSLVACSGNLNKAKEIFQKKFLDKTKNNWEDRE----KFEKVPGKYDML-- 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 TLKKOMKYLEQQQDETKQAQEEAGRLRSKMKTMEQIELLLQS-----QLPEVEEMIRDM 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246 KYNTKKAPLGKLTVAQIKAGYQSLKKIEDCIRAGQHGRALMEACNEFYTRIPHDFGLRTP 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        235 KLQTVYSELDQAKLELKSAQKDLQSADK----EIMSLKKKLTMLQETLN--LPPVASET- 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192 ----QMDYATNTQDEEETKKEES--LKSPLKPESQLDLRVQELIKLICNVQAMEEMMMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 -----GVGQSAVEQLAVYCVSLKKEYENLKEAR-----KASGEVADKLRKDLFSSRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            306 PLIRTQKELSE-KIQLLEALGDIEIAIKLVKTELQSPEHPLDQHYRNLHCALRPLDHESY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                     ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza,
                                                                                                                                                                         COMPUTER READABLE FORM:
COMPUTER INDEADABLE FORM:
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              288 ----VDRLVLESPAPV------EVNLKLRRPSFRDDI 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  365 EFKVISQYLQSTHAPTHSDYTMTLLDLFEVEKDGEKEAFREDL 407
                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-198 CIP 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 4.0%; Score 120.5; DB 4; Best Local Similarity 20.7%; Pred. No. 0.0047; Matches 71; Conservative 61; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/052,089A FILING DATE: 31-Mar-1998 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: «Unknown»
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-044-618-6; Sequence 6, Application US/08044618; Patent No. 5449605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 469 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                  STATE: New Jersey
COUNTRY: USA
                                                                                                             CITY: Hackensack
                                                                                          Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-052-089A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          496 LQGKHSTKGLGKMAPSSAHFVTLNGSTVPLGPASDTGILNPDGYTLNYNEYIVYNPNQVR 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HCA-----LRPLDHESYEFKVISQYLQSTHAPTHSD------YTMTLLDLFEVEKD 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GEKEAFRE------DLHNRMLLWHGSRMSNWVGILSHGLRIAPPEAPITGYMFGKGIY 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FADMSSKSANYCFASRLKNTGL------LLLSEVALGQCNELLEANPKAEGL 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               312 KELSEKIQL-LEALGDI-----EIAI-----KLVK----TELQSPEHPLDQHYRNL 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL INFORMATION: Lee, SOO Y.
Choi, Yongwon
Choi, Yongwon
TITLE OF INVENTION: SIGNAL TRANSDUCER FOR THE TNF RECEPTOR SUPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 135; DB 4; Length 1327;
; Pred. No. 0.001;
31; Mismatches 104; Indels 9
                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,387
                                                                                                                                                                                                                                                                                                                                                                                                                         600-1-230 CIP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
4.5%; Score 135;
Best Local Similarity 24.4%; Pred. No. 0.
Matches 75; Conservative 31; Mismatche
                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09052089A Patent No. 6346605 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 133521
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1327 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 201-40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
TOPOLOGY: linear
                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
                       New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1302 PEYLITYQ 1309
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                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE:
; HYPOTHETICAL:
US-09-196-387-2
                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-052-089A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75;
                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----QMDYATNTQDEEETKKEES--LKSPLKPESQLDLRVQELIKLICNVQAMEEMMMEM 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               235 KLQTVYSELDQAKLELKSAQKDLQSADK----EIMSLKKKITMLQETLN--LPPVASET- 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 PECTAKVGKAHVYCEGNDVYDVMLNQTNL---QFNNNKYYLI--QLLEDDAQRNFSVWMR 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188 -----GVGQSAVEQLAVYCVSLKKEYENLKEAR-----KASGEVADKLRKDLFSSRS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246 KYNTKKAPLGKLTVAQIKAGYQSLKKIEDCIRAGQHGRALMEACNEFYTRIPHDFGLRTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306 PLIRTQKELSE-KIQLLEALGDIEIAIKLVKTELQSPEHPLDQHYRNLHCALRPLDHESY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Innerarity, Thomas L.
APPLICANT: Qian, Xiaobing
APPLICANT: Qian, Xiaobing
APPLICANT: Qian, Xiaobing
APPLICANT: Yamanaka, Shinya
TITLE OF INVENTION: Screening Methods to Detect mRNA Targets
TITLE OF INVENTION: of Editing Enzymes
TITLE OF INVENTION: of Editing Enzymes
AUMBER OF SEQUENCES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREEF: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            365 EFKVISQYLQSTHAPTHSDYTMTLLDLFEVEKDGEKEAFREDL 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       288 ----VDRLVLESPAPV-----EVNLKLRRPSFRDDI 314
                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.9%; Score 116.5; DB 2;
20.7%; Pred. No. 0.011;
Live 60; Mismatches 119;
                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Giotta, Gregory
REGISTRATION NUMBER: 32,028
REFERENCE/DOCKET NUMBER: ONYX1024 GG
TELECOMMUNICATION INFORMATION:
                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/08609230A Patent No. 5866333 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (510) 262-8710
TELEFAX: (510) 222-9758
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 3.9%
Best Local Similarity 20.7%
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 469 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-968-751-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                           FILING DATE:
                        94806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-609-230A-9
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                     METHOD OR DETECTING A PREDISPOSITION TO CANCER BY THE USED OF RESTRICTION FRAGMENT LENGTH POLYMORPHISM OF THE GENE FOR THE HUMAN POLY (ADP-RIBOSE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89 VGKAHVYCEGNDVYDVMLNQTNLQFNNNKYYLIQLLEDDAQRNFSVWMRWGRVGK-MGQH 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 APRGKSGAVLSKKSKGQV------KEEGINKSEKRMK-LTLKGGAAVDPD-SGL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57; Indels 20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 APEDSSPAKKTRRCQRQESKKMPVAGGKANKDRTEDKQDESVKALLLKGKAPVDPECTAK 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 4.0%; Score 119; DB 1; Length 163; Best Local Similarity 28.3%; Pred. No. 0.0012; Matches 41; Conservative 27; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Rubinfeld, Bonnee
APPLICANT: Rolakis, Paul G.
APPLICANT: Dolakis, Paul G.
APPLICANT: Ligenfelter, Carol
APPLICANT: Unong, Terllyn T.
TITLE OF INVENTION: MODULATORS OF BRCAL ACTIVITY
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: ONYX PHARMACCEUTICALS, Inc.
                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
ADPLICATION NUMBER: US/08/044,618
FILING DATE: 19930406
                                                                                                                                                                  E: Sterne, Kessler, Goldstein & Fox 1225 Connecticut Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFCATION: 435
PRIOR APPLICATION 1973
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/257,696
FILING DATE: 14-OCT-1988
ATTORNEY/AGENT INFORMATION:
NAME: FOX. SAMUEL L
REGISTRATION NUMBER: 0654.0490001
TELEPHONE: (202)466-0800
TELEPHONE: (202)466-0800
TELEPHONE: (202)833-8716
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 163 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148 SLVACSGNLNKAKEI -- FQKKFLDK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-968-751-2; Sequence 2, Application US/08968751; Patent No. 5948643
                                                                                            POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3031 Research Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, K
APPLICANT: SMULSON, M
TITLE OF INVENTION: O
TITLE OF INVENTION: O
TITLE OF INVENTION: P
TITLE OF SEQUENCES:
                                                                                                                                                                                        STREET: 1225 Conr
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Richmond
                                                                                                                                                                                                             STATE: D.C. 20036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-044-618-6
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446 -LSQLQGQSKDMPPRFSKKGQLNADEISLRPAQSFLMNKNQV 486

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APPLICANT: Peattie, Debra A.
APPLICANT: Harding, Matthew W.
APPLICANT: Livingston, David J.
TITLE OF INVENTION: ISOLATION OF AN Mr 52,000 FK506 BINDING
TITLE OF INVENTION: PROTEIN AND MOLECULAR CLONING OF A CORRESPONDING HUMAN
TITLE OF INVENTION: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : |: | : | : | | : | | STAELRYEVRIKSERKYKESSARSWSRATYVKERGTAYFKEGKYKQALLQYKKIVS 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 -MDYATNTQDEEETKKEESLKSPLKPESQLDLRVQELIKLICNVQAME--EMMMEMKYNT 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 KDRTEDKQDESVKALLLKGKAPVDPECTAKVGKAHVYCEGNDVYDVMLNQTNLQFNNNKY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 YLIQLLEDDA-----QRNFSVWMRWGRVGKMGQHSLVACSGNL------N 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 KAKEI---FQKKFLDKTKNNWE-----DREKFEKVPG------KYDMLQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 560;
                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 32
CORRESPONDENCE HADDRESS: ADDRESSEE: Hamilton, Brook, Smith and Reynolds, P.C. STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,618
FILING DATE: 09-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.8%; Score 112.5; DB 1; 20.7%; Pred. No. 0.037; iive 59; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/777,752
FILING DATE: 11-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 09-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: 92,227
TELECHONE: 617-661-6240
TELECHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/963,325
FILING DATE: 16-0CT-1992
                                                                                                                  ; Sequence 22, Application US/08336618
; Patent No. 5763590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 560 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 3.8°
Best Local Similarity 20.7°
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-618-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U.S.A.
                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 ANNSANEKERHDAIFRKVRGILNK----LTPEKFDKLCLQLLNVGVESKLILKG-----V 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105 MLNQTNLQFNNNKY----YLIQLLEDDAQRNFSVWMRWGRVGKMGQHSLVACSGNLNKA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 KEIFQKKFLDKTKNNWEDREKFEKVPGKYDMLQMDYATNTQDEEETKKEESLKSPLKPES 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QLDLRVQELIKLICNVQAMEEMAMEMKYNTKKAPLGKLTVAQIKAGYQSLKKIEDCIRAG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197 E-EQRAIAKIKMLGNIKFIGE-----LGKL------DLIH-- 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   280 QHGRALMEACNEFYTRIPHDFGLRTPPLIRTQKELSEKIQLLEALGDIEIAIKLVKTELQ 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 ---ESILHKC------IKTLLEKKKRVQLQDMGEDLECLCQIMRTVGP 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           340 SPEHP-----LDQHY------KVI 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               264 RLDHERAKSLMDQYFARMCSLMLSKELPARIRFLLQDTVELREHHWVPRKAFLDNGPKTI 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQ-----YLQSTHAPTHSDYTMT---LLDLFEVEKD---GEKEAFREDLHNRML 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |::|| | |::||
-----KSQGLSQLYHNQSQGL----- 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           413 LWHGSRMSNWVGIL-------SHGLRIAPPEAPITGYMFGKGIYFADMS 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SKSANYCFASRLKNTGLLLLSEVALGQCNELLEANPKAEGLLQGKHS-TKGLGKMAPSSA 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 AGGKANKDRTEDKQDESVKALLLKGKAPVDPECTAK -----VG-KAHVYCEGNDVYDV 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 AARRRRSTGGGRARALNE--SKRVNN----GNTAPEDSS---PAKKTRRCQRQESKKMPV 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             324 NOIRQDAVKDLGVFIPAPMAQGRSDFFLEGPFMPPRMKMDRDPLGGLRDMFGQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 115; DB 2; Length 906;
; Pred. No. 0.047;
87; Mismatches 178; Indels 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -MPGSGIGTGPGVIQDTFSPTMGRHRSNQLFNGHGGHIMPPTQSQFGEMGGKFM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     514 HFVTLNGSTVPLGPA-SDTGILNPDGYTLNYNEYIVYNPNQV 554
                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,230A
FILING DATE: 01-MAR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                        02307U-068100US
                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 0230
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-326-2400
TELEFAX: 650-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 906 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
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Best Local Similarity
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666 YSQFITQLTDENOSCCPVCQRVFQTEAELQEVISDLQSK-----LRLAPDKLKSTESEL 719
                                                                                                                                                                                                                                                 206 KKEESLKSPLKPESQLDLRVQELIKLICNVQAMEEMMMEMKYNTKKAPLGKLTVAQIKAG 265
                                                                                                                                                                                                                                                                             315 SEKIQLL-EALGDIEIAIKLVKTELQSPEHP-LDQHYRNLHCALRPLDHESYEFKVISQY 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                          :| : | | | : : : : | | | : : : | 373
493 KNSNVETLKMEVISLONEKADLDRTLRKLDOEMEQLNHHTTTRTQMEMLIKDKADKD-EQ 551
                                                               86 TAKVGKAHVYCEGNDVYDVMLNQTNLQFNNNKYYLIQLLEDDAQRNFSVWMRWGRVGKMG 145
                                                                                                                                                     146 QHSLVACSGNLNKAKEIFQKKFLDKTKNNWEDREKFEKVPGKYDMLQMDYATNTQDEEET 205
                                                                                                                                                                                                                                                                                                                                       266 Y-QSLKKIED------CIRAGQHGRALMEACNEFYTRIPHDFGLRTPP--LIRTQKEL 314
                                                                                                                                                                                                    581 -HS------KSKEINQ-----TRDRLAKL--NKELASSEQNKNHINNELK
                                                                                                           552 IRKIKSRH----SDELTSLLG---YFPNKKQ-----LED------WL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or Relating to Organic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   373 LOSTHAPTHSD-----YTMTLLDLFEVE-KDGEKE 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: van Grinsven J., Martinus Q.
APPLICANT: De Haan, Petrus T.
APPLICANT: Gielen L., Johannes J.
APPLICANT: Goldbach, Robert W.
TITLE OF INVENTION: Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/214,064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/032,235
FILING DATE: 17-MAR-1993
PPLICATION NUMBER: GB 9206016.9
FILING DATE: 19-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: No. 5773700ris, Allen E. REGISTRATION NUMBER: 34,490 REFERENCE/DOCKET NUMBER: 137-1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/764,100
FILING DATE: 06-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 27, Application US/08764100 Patent No. 5773700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: Sandoz Agro, Inc
975 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 354-3592
TELEFAX: (415) 857-1125
GEOFFENATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 975 Cali
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-764-100-27
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                                                                                                                                                          293 WLEYESSFSGEEMQKVH----ALRLASHLNLAMCHL-KLQAFSAAIESCNKALELDSNN 346
                                          250 KKAPLGK----LTVAQIKAGYQSLKKIEDCIRAGQHGRALMEACNEFYTRIPHDFGLRTP 305
                                                                                                                                   306 PLIRTQKELSEKIQL----LEALGDIEIAIKLVKTELQSPEHPLDQHYRNLHCALRPLDH 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   433 RDKKTGLGRIIELKSEILSKKONELKNVKYELQQLEGSSDRILELDQELIKAERELSKAE 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---APEDSSPAK 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 KTRRCQRQESKKMPVAGGKANKDRTEDKQDESVKAL------LLKGKAPVDPEC 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Human RAD50 Gene and Methods of Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54), NT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                      347 EKGLFRRGEAHLAVNDFDLARADFQKVLQLYPSNKAAKTQLAVCQQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANS. OF RAD50 cDNA (SEQ. 389 TO 4324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.8%; Score 112.5; DB 2; 11.3%; Pred. No. 0.15;
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tive 71; Mismatches 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---ARALNESKRVN-----NGNT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: Dehlinger & Associates
350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/687,080 FILING DATE: 17-JUL-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,126
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 51, Application US/08687080 Patent No. 5965427 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                   447 K-----MOSLPTTHPHPHS 460
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                                                                                                                                                                                                                         362 ESYEFKVISQYLQSTHAPTHS 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 324-0960 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 21.3%
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
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INDIVIDUAL ISOLATE:
US-08-687-080-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
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RESULT 12
US-08-785-190-2
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                                                                                                                                                                                            250 KKAPLGKLIVAQIKAGYQSLKKIEDCIRAGQHGRALMEACNEFYT----RIPHDFGLRTP 305
                                                                                                                                                                       196 ATNTQDEEETKKEES--LKSPLKPESQLDLRVQELIKL----ICNVQAMEEMMMEMKYNT 249
                                                                                                                                                                                                                                                                                     306 PLIRTQKELSEKIQLLEALGDIEIAIKLV-----KTELQSPEHPLDQHY---RNLH 353
                                                                                                                                                                                                                                                                                                                                                                                                        ------YIMTLLDLFEVEKDGEKEAFREDLHNRM 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   468 NTGLLLLSEVALGQCNE-----LLEANPK--AEGLLQGKHSTKGL--GKMAPSSAH 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                              412 LLWHGS-RMSNWVGILSHGLRIAPPEA---PITGYMFGKGIYFADMSSKSANYCFASRLK
                                                                                                                                            Indels 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: LeFebvre, Rance B.
APPLICANT: Perng, Guey-Chen
TITLE OF INVENTION: Methods and Compositions for Diagnosing
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                              3.7%; Score 111; DB 1; Length 3218; 21.2%; Pred. No. 0.93; Live 46; Mismatches 148; Indels 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/720,589
FILING DATE: 19910628
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                               CALRPL ---- DHESYEFKVISQYLQSTHAPTHSD------
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Patent No. 5324630
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: James M. Heslin
STREET: 379 Lytton Avenue
LENGIH: 3218 amino acids
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NAME: Heslin, James M.
                         ESS: unknown
unknown
                                                                                                                                            Conservative
                                                     ; MOLECULE TYPE: protein US-08-764-100-27
                                                                                                                                                                                                                                                         2593 -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 379 Lyttor
CITY: Palo Alto
STATE: California
             TYPE: amino acid
STRANDEDNESS: unk
TOPOLOGY: unknowr
                                                                                                               Query Match
Best Local Similarity
Matches 90; Conserv
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MINQTNLQFNNNKYYLIQLLEDDAQRNFSVWMRWGRVGKMGQHSLVACSGNLNKAKEIFQ 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 ESLKSP---LKPESQLDLRVQELIKLICNVQAMEEMMMEMKYNTKKAPLGKLTVAQIKAG 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          338 KNLPKPGDVSSPKVDKQLQIKE----SLEDLQEQLKETGDENQKREIEK--QIEIKKS 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 YQSLKKIEDCIRAGQHGRALMEACNEFYTRIPHDFGLRTPPLIRTQKELSEKIQLLEALG 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               364
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 KMPVAGGKANKDRTEDK - - QDESVKALLLKGKAPVD - - PECTAKVGKAHVYCEGNDVYDV 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             278 KKEIESQVDAKKKOKEELDKKAINLDKAQOKLDSAEDNLDVORNTVREKIQEDINEINKE 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLHNRMLLWHGSRMSNWVGILSHGLRIAPPEAPITGYMFGKGIYFADMSSKSANYCFASR 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DLNTGVSL----KESTQQGIQRYGI-----YEREKDLVVIKMDSGKAKLQILDK 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       466 LKNTGLLLLSEVALGQCNELLEANPKAEGLLQGKHSTKG--LGKMAPSSAHFVTLNGSTV 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.7%; Score 110.5; DB 1; Length 700;
20.0%; Pred. No. 0.084;
tive 90; Mismatches 227; Indels 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Compositions for Diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENLKVVSESNFEINKNSSLYVDSKMILVAVRDKDSSNDWRLAKFSPK--
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  29,541
R: 2307U-330/UC 90-017-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: LeFebvre, Rance B. APPLICANT: Perng, Guey-Chen TILLE OF INVENTION: Methods and TITLE OF INVENTION: Lyme Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 2, Application US/08785190; Patent No. 5977339; GENERAL INFORMATION:
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 2307
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTER STICS:
LENGTH: 700 amino acids
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CORRESPONDENCE ADDRESS:
ADDRESSEE: James M. Heslin
STREET: 379 Lytton Avenue
CITY: Palo Alto
                                                                                                                                                                                            LENGTH: 700 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.7
Best Local Similarity 20.0
Matches 117; Conservative
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338 KNLPKPGDVSSPKVDKQLQIKE-----SLEDLQEQLKETGDENQKREIEK--QIEIKKS 389
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                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 700;
---NLDEFILSENKIMPFTSFSVRKNFIYLQDEFKSL 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The Floppy disk IBM PC compatible SYSTEM: PC-DOS/MS-DOS PATENTIN Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Brookhaven National Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Bogosian, Margaret C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNL93-28A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/235,836C
FILING DATE: 29-APR-1994
CLASSIFICATION: 435
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APPLICATION NUMBER: US 08/148,191
FILING DATE: 01-11-93
                                                                                                                      ; Sequence 66, Application US/08235836C; Patent No. 6248562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                326 DIEIAIKLVKTELQS-PE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (516) 282-7338
TELEFAX: (516) 282-3729
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | : : : : | | | | 247 ELDNIH-ESDSNITETIENLRD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Bogosian, Margaret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              700 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 117; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-235-836C-66
                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                          RESULT 13
US-08-235-836C-66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               266 YQSLKKIEDCIRAGQHGRALMEACNEFYTRIPHDFGLRTPPLIRTQKELSEKIQLLEALG 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLHNRMLLWHGSRMSNWVGILSHGLRIAPPEAPITGYMFGKGIYFADMSSKSANYCFASR 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 KKDILSGNIESDIDIDSLVTDKVVAALLSENEAGVNFARDITDIOGETHK--ADQDKIDI 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKFL----DKTKNNWEDREK----FEKVPGKYDMLQ--MDYATNT-----QDEEETKKE 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKNTGLLLLSEVALGQCNELLEANPKAEGLLQGKHSTKG--LGKMAPSSAHFVTLNGSTV 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 151; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 KMPVAGGKANKDRTEDK -- QDESVKALLLKGKAPVD--PECTAKVGKAHVYCEGNDVYDV 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105 MLNQTNLQFNNNKYYLIQLLEDDAQRNFSVWMRWGRVGKMGQHSLVACSGNLNKAKEIFQ 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 ELDNIH-ESDSNITETIENLRD-----------QLEKATDEEH 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KKEIESQVDAKKKQKEELDKKAINLDKAQQKLDSAEDNLDVQRNTVREKIQEDINEINKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIEIAIKLVKTELQS-PE--------HPLDQHYR--NLHCALRPLDHESY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          502 IDSKEETVNKDVNLQKTKPQVKDQVTSLNEDLTTMSIDSSSPVFLEVIDPITNLGTLQLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLNTGVSL----KESTQQGIQRYGI-----YEREKDLVVIKMDSGKAKLQILDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |:| :: | :: | :: | :- | :- | TENLKYVSESNFEINKNSSLYVDSKMILVAVRDKDSSNDWRLAKFSPK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---EFKVISQ--YLQSTHAPTHSDYTMTLLDLFEVEKDGEKEAFRE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           524 PLGPASDTGILNPDGYTLNYNEYIVYNPNQVRMRYL-LKVQFNFL 567
                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 3.7%; Score 110.5; DB 2; Best Local Similarity 20.0%; Pred. No. 0.084; Matches 117; Conservative 90; Mismatches 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2307U-330/UC 90-017-1
                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,190
FILING DATE:
                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/720,589
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 2307
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 700 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-08-785-190-2
                                                                             COMPUTER READABLE FORM:
     California
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                                                                                                                                                                                                                                                                                CLASSIFICATION:
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APPLICANT: Olsen, Henrik S.
APPLICANT: Olsen, Henrik S.
APPLICANT: Ruben, Steven M.
APPLICANT: Ruben, Steven M.
APPLICANT: Ruben, Nathalie
APPLICANT: Rom, Eran
TITLE OF INVENTION: Human Prt1-like Subunit Protein (hPrt1) and Human
TITLE OF INVENTION: Human Prt1-like Protein (p97) Genes
FILE REFERENCE: 1488.0700001
CURRENT PAPLICATION NUMBER: US 60/033,151
EARLIER APPLICATION NUMBER: US 60/033,151
EARLIER APPLICATION NUMBER: US 60/033,151
SOFTWARE: PatentIn Ver. 2.1
                                                                                                  DLHNRMLLWHGSRMSNWVGILSHGLRIAPPEAPITGYMFGKGIYFADMSSKSANYCFASR 465
                                                                                                                                                                                                                                                                                                                                                                                                                       562 DLNTGVSL----KESTQQGIQRYGI-----YEREKDLVVIKMDSGKAKLQILDK 606
                                     278 KKEIESQVDAKKQKEELDKKAINLDKAQQKLDSAEDNLDVQRNTVREKIQEDINEINKE 337
                                                                                                                                                                                                                                                                   DLINDENLAMPEDOKLPEVKKLDSKKEFKPVSEVEKLDKIFKSNNNVGELSPLDKSSYKD 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 AARRRESTGGGRARALNE--SKRVNN----GNTAPEDSS---PAKKTRRCQRQESKKMPV 52
                                                                            ESLKSP----LKPESQLDLRVQELIKLICNVQAMEEMMMEMKYNTKKAPLGKLTVAQIKAG
                                                                                                                                                                                 DEKLLKSKD-DKASKDGKAL-DLDRELNSK-----ASSKEKSKAKEEEITKGKSQKSLG
                                                                                                                                                                                                                                    502 IDSKEETVNKDVNLQKTKPQVKDQVTSLNEDLTTMSIDSSSPVFLEVIDPITNLGTLQLI
                                                                                                                                                        266 YQSLKKIEDCIRAGQHGRALMEACNEFYTRIPHDFGLRTPPLIRTQKELSEKIQLLEALG
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20.5%; Pred. No. 0.13;
ive 87; Mismatches 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-990-140-4; Sequence 4, Application US/08990140A; Patent No. 6093795
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 127; Conserv
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                                                                                    502 IDSKEETVNKDVNLQKTKPQVKDQVTSLNEDLTTMSIDSSSPVFLEVIDPITNLGTLQLI 561
                                                                                                                                 DLHNRMLLWHGSRMSNWVGILSHGLRIAPPEAPITGYMFGKGIYFADMSSKSANYCFASR 465
                                                                                                                                                                        DLNTGVRL----KESTQQGIQRYGI-----YEREKDLVVIKMDSGKAKLQILDK 606
                                                                                                                                                                                                                LKNTGLLLLSEVALGQCNELLEANPKAEGLLQGKHSTKG--LGKMAPSSAHFVTLNGSTV 523
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105 MINQINIQFNNNKYYLIQLIEDDAQRNFSVWMRWGRVGKMGQHSLVACSGNLNKAKEIFQ 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----QLEKATDEEH 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 KMPVAGGKANKDRTEDK--QDESVKALLLKGKAPVD--PECTAKVGKAHVYCEGNDVYDV 104
                                                                                                                                                                                                                                      Sequence 2, Application PC/TUS9205539
GENERAL INFORMATION:
APPLICANT: Lefebvre, Rance B.
APPLICANT: Perng, Guey-Chen
TITLE OF INVENTION: Methods and Compositions for Diagnosing
TITLE OF INVENTION: Lyme Disease
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: James M. Heslin
                                                                                                                                                                                                                                                                                          524 PLGPASDTGILNPDGYTLNYNEYIVYNPNQVRMRYL-LKVQFNFL 567
                                                                                                                                                                                                                                                                                                                  ---EFKVISQ--YLQSTHAPTHSDYTMTLLDLFEVEKDGEKEAFRE
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REFERENCE/DOCKET NUMBER: 2307U-330/UC 90-017-1
TELECOMMUNICATION INFORMATION:
TELEFRONE: 415-326-2400
TELEFRAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 700 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05539
FILING DATE: 19920629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn PAILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: James M. Heslin
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 20.09
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein PCT-US92-05539-2
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CLASSIFICATION:
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PCT-US92-05539-2
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466	PPTQSQFGEMGGKFMKSQGLSQLYHNQSQGLLSQLQGQSKDMPPRFSKKGQ	416	qq
533	EVALGQCNELLEANPKAEGLLQGKHS-TKGLGKMAPSSAHFVTLNGSTVPLGPA-SDTGI	476	Qy
415	FMPPRMKMDRDPLG	356	QQ
475	IAPPEAPITGYMFGKGIYFADMSSKSANYCFASRLKNTGLLLLS	432	οy
355	REHHWVPRKAFLDNGPKTINQIRQDAVKDLGVFIPAPMAQGMRSDFFLEGP	305	q
431	EKDG EKEAFREDL	395	οy
304	RIDHERAKSIMDQYFARM-CSLMLSKELPARIRFILQDIVEL	264	Q
394	SPEHP	340	οy
263	ESILHKCIKTLLEKKRVQLKDMGEDLECLCQIMRTVGP	225	g
339	OHGRALMEACNEFYTRIPHDFGLRTPPLIRTQKELSEKIQLLEALGDIEIAIKLVKTELQ	280	Qy
224		197	Q
279	QLDLRVQELIKLICNVQAMEEMMMEMKYNTKKAPLGKLTVAQIKAGYQSLKKIEDCIRAG	220	οy
196	STTFRELISKLODEFENRTRNVDVYDKRENPLLPEE	160	QQ
219	KEIFQKKFLDKTKNNWEDREKFEKVPGKYDMLQMDYATNTQDEETKKEESLK	160	οy
159	ILLIVDKALEEPKYSSLYAQLCLRLAEDAP-NFDGPAAEGQPGQKQ	115	g

Search completed: August 29, 2002, 07:58:08 Job time: 285 sec

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TISSUE-Fibroblast;
MEDLINE-99268466; PubMed-10338144;
MEDLINE-99268466; PubMed-10338144;
MEDLINE-99268466; PubMed-10338144;
Berghammer H., Ebner M., Marksteiner R., Auer B.;
"pADPRT-2: a novel mammalian polymerizing(ADP-ribosyl)transferase gene related to truncated pADPRT homologues in plants and Caenorhabditis elegans.";
FEBS Lett. 449:259-263(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUB-Fetal brain;
MEDLINE-99292755; Pubmed-10364231;
MEDLINE-99292755; Pubmed-10364231;
Ame J.-C., Rolli V., Schreiber V., Niedergang C., Apiou F., Decker P.,
Muller S., Hoeger T., Menissier de Murcia J., de Murcia G.M.;
"PARP-2, a novel mammalian DNA damage-dependent poly(ADF-ribose)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Masuho Y., Kanehori K.;
"NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: HAS DNA-DEPENDENT POLY[ADP-RIBOSE] POLYMERASE ACTIVITY.
SEEMS TO PLAY A ROLE IN THE RESPONSE TO DNA DAWAGE (By similarity).
-I- CATALYTIC ACTIVITY: NAD(+) + {ADP-D-ribosyl}(N)-acceptor = nicotinamide + {ADP-D-ribosyl}(N+1)-acceptor.
                                                                                                                                                                                                                                                                                             PPOZ_HUMAN STANDARD; PRT; 583 AA.
Q9UGN5; Q9Y6C8; Q9NUV2; Q9UMR4;
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
Poly [ADP-ribose] polymerase-2 (EC 2.4.2.30) (PARP-2) (NAD(+) ADP-ribosyltransferase-2) (Poly[ADP-ribose] synthetase-2) (PADPRT-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Placenta;
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,
Anani H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y.,
Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A human poly(ADP-ribose) polymerase gene family (ADPRLL): cDNA cloning of two novel poly(ADP-ribose) polymerase homologues."; Genomics 57:442-445(1999).
                                                                                                                                                                                                                    ALIGNMENTS
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                                                            SMC3_YEAST
KINH_MOUSE
BP28_CAEEL
MYHB_CHICK
                                                                                                                     KLPA_EMENI
MFP1_ARATH
EVPL_MOUSE
PR02_YEAST
              P115_MYCGE
MYH9_CHICK
                                             THU9_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polymerase.";
J. Biol. Chem. 274:17860-17868(1999).
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ADPRTL2 OR PARP2 OR ADPRT2.
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876
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Johansson M.;
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                                                                                                        August 29, 2002, 07:57:23 ; Search time 36.19 Seconds
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             GenCore version
Copyright (c) 1993 - 2000
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PPOL_CRIGR
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1 MAARRRSTGGGRARALNES.
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elegans.";
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PPO2_MOUSE
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                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                 produced by alternative splicing.
TISSUE SPECIFICITY: WIDELY EXPRESSED. THE HIGHEST LEVELS ARE IN
THE BRAIN, HEART, PANCREAS, SKELETAL MUSCLE AND TESTIS; ALSO
DETECTED IN KIDNEY, LIVER, LUNG, PLACENTA, OVARY AND SPLEEN;
LEVELS ARE LOW IN LEUKOCYTES, COLON, SMALL INTESTINE, PROSTATE AND
THYMUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RTEDKOD------ESVKALLLKGKAPVDPECTAKVGKAHVYCEGNDVYDVMLN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QTNLQFNNNKYYLIQLLEDDAQRNFSVWMRWGRVGKMGQHSLVACSGNLNKAKEIFQKKF 167
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                                                                                                                                                                                                                                                                      Pfam; PFUUD44; rans, ...
Pfam; PFUD547; PARP_reg; 1.
Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein;
Transferase; Alternative splicing.
ADP-ribosylation; Alternative splicing.
APP-ribosylation; Alternative POFENTIAL.
-i- SUBCELLULAR LOCATION: NUCLEAR (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEAR LOCALIZATION SIGNAL 2ND PART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 2981.5; DB 1; Length 583; Pred. No. 1.4e-187;
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NUCLEAR LOCALIZATION SIGNAL 1ST
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MISSING (IN ISOFORM 2).
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N -> H (IN REF.
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0; Mismatches
                                                                                      SIMILARITY: BELONGS TO THE PARP FAMILY
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EMBL; AP085734; AAD29857.1; ALT_INIT.
EMBL; AZ336876; CAB41505.2; ALT_INIT.
EMBL; AK001980; BAA92017.1; ALT_TERM.
                                                                                                                                                                                                                                               InterPro, IPR001290; PARP.
InterPro, IPR004102; PARP_reg.
Pfam; PF00644; PARP; 1.
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Best Local Similarity 97.8
Matches 570; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>.</u>
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-!- FUNCTION: HAS DNA-DEPENDENT POLY (ADP-RIBOSE) POLYMERASE ACTIVITY.

SEEMS TO PLAY A ROLE IN THE RESPONSE TO DNA DAMAGE.

-!- CATALYTIC ACTIVITY: NAD(+) + (ADP-D-ribosyl)(N)-acceptor = nicotinamide + (ADP-D-ribosyl)(N+1)-acceptor.
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-i- TISSUB SPECIFICITY: Widely expressed; the highest levels were in testis followed by ovary.
-i- INDUCTION: By high levels of DNA-damaging agents.
-i- SIMILARITY: BELONGS TO THE PARP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ~
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A bidirectional promoter connects the poly(ADP-ribose) polymerase (PARP-2) gene to the gene for RNase P RNA.";
J. Biol. Chem. 276:11092-11099(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-WAR-2002 (Rel. 41, Last annotation update)
Poly [ADP-ribose] polymerase-2 (EC 2.4.2.30) (PARP-2) (NAD(+) ADP-ribosyltransferase-2) (Poly[ADP-ribose] synthetase-2) (PADPRT-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                  HNRMLLWHGSRMSNWVGILSHGLRIAPPEAPITGYMFGKGIYFADMSSKSANYCFASRLK
                                                                                                                                           NTGLLLLSEVALGQCNELLEANPKAEGLLQGKHSTKGLGKMAPSSAHFVTLNGSTVPLGP
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                                                                                                                                                                                                                                                                                              ASDTGILNPDGYTLNYNEYIVYNPNQVRMRYLLKVQFNFLQLW 570
                                                                                                                                                                                                                                                                                                                                            541 ASDTGILNPDGYTLNYNEYIVYNPNQVRMRYLLKVQFNFLQLW 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 559 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polymerase.";
J. Biol. Chem. 274:17860-17868(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Embryo;
MEDLINE=99292755; PubMed=10364231;
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MEDLINE=99268466; PubMed=10338144;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DP02_MOUSE STANDARD,
PP02_MOUSE STANDARD,
088554; 099M29;
16-OCT-2001 (Rel. 40, Last seque
16-OCT-2001 (Rel. 40, Last seque
16-OCT-2001 (Rel. 41, Last annot
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                                                                                                                                                                                                                                                                              180 KFEKVPGKYDMLQMDYATNTQDEEETKKEESLKSPLKPESQLDLRVQELIKLICNVQAME 239
                                                                                                                                                                                                                                                                                                            EMMEMKYNTKKAPLGKLTVAQIKAGYQSLKKIEDCIRAGQHGRALMEACNEFYTRIPHD 299
                                                                                                                                                                                                                                                                                                                                          FGLRTPPLIRTQKELSEKIQLLEALGDIEIAIKLVKTELQSPEHPLDQHYRNLHCALRPL 359
                                                                                                                                                                                                                                                                                                                                                                       DHESYEFKVISQYLQSTHAPTHSDYTMTLLDLFEVEKDGEKEAFREDLHNRMLLWHGSRM 419
                                                                                                                                                                                                                                                                                                                                                                                                    SNWVGILSHGLRIAPPEAPITGYMFGKGIYFADMSSKSANYCFASRLKNTGLLLLSEVAL 479
                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycosyltransferase; NAD; DNA-binding; Nuclear protein;
                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                   GQCNELLEANPKAEGLLQGKHSTKGLGKMAPSSAHFVTLNGSTVPLGPASDTGILNPDGY
                                                                                                                                                                                             13;
                                                                                                                                                                              DB 1; Length 559;
                                                                                           NAD-BINDING (BY SIMILARITY).
NUCLEAR LOCALIZATION SIGNAL
                                                                                                                  SIGNAL
                                                                                                                                                                                             Indels
                                                                                                                                                       E0AEDAEE412C1445 CRC64;
                                                                                                         (POTENTIAL).
NUCLEAR LOCALIZATION
(POTENTIAL).
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                                                                                                                               L -> V (IN REF. 2)
V -> I (IN REF. 2)
R -> Q (IN REF. 2)
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                                                                                                                                                                             85.6%; Score 2565.5;
85.8%; Pred. No. 2e-1
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AJ007780; CAA07679.1; -.
AF191547; AAK13253.1; -.
AF072521; AAC25415.1; ALT_INIT.
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Q11207;
01-OCT-1996 (Rel. 34, Created)
                           MGD; KG:134,
MGD: MGI:1341112; Adprt2.
InterPro; IPR001290; PARP.
InterPro; IPR004102; PARP_reg.
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                                                      Pfam; PF00644; PARP; 1.
Pfam; PF02877; PARP_reg; 1
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                       P26446; 1A26.
                                                                                                                                                                                     Similarity
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DNA_BIND 1
DOMAIN 66
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                                                                     Transferase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-95269779; PubMed-7750552;
MEDLINE-95269779; PubMed-7750552;
MEDLINE-95269779; PubMed-7750552;
MEDLINE-95269779; MEDLINE-DISCOUNTINE E., Kushnir S., van Montagu M., Inze D.;
Lepiniec L., Babiychuk E., Kushnir S., van Montagu M., Inze D.;
Characterization of an Arabidopsis thaliana cDNA homologue to animal poly(ADP-ribose) polymerase.";
FEBS Lett. 364-103-108(1995).
FEBS Lett. 364-103-10
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Poly [App-ribose] polymerase (EC 2.4.2.30) (PARP) (ADPRT) (NAD(+) ADP-
ribosyltransferase) (Poly[ADP-ribose] synthetase).
                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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CATALYTIC ACTIVITY: NAD(+) + {ADP-D-ribosyl}(N)-acceptor = nicotinnamide + {ADP-D-ribosyl}(N+1)-acceptor.

SUBCELLULAR LOCATION: Nuclear.

SIMILARITY: BELONGS TO THE PARP FAMILY.
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NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
527A8F464605D127 CRC64;
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Pfam; PF02877; PARP_reg; 1..
Pfam; PF02037; SAP; 2.
SMART; SM00513; SAP; 2.
Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear
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InterPro; IPR004102;
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Ruf A., de Wurcia G.M., Schulz G.E.;
"Inhibitor and NAD+ binding to poly(ADP-ribose) polymerase as derived
from crystal structures and homology modeling.";
                                                            411
                                                                                                                                                                   542
                                                                                                                                                                                                                                                                                                                                                             15-UUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Poly (ADD-ribose) polymerase-1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+)
ADP-ribosyltransferase-1) (Poly[ADP-ribose] synthetase-1).
236 QAMEEMMMEMKYNTKKAPLGKLTVAQIKAGYQSLKKIEDCIRAGQHGRALMEACNEFYTR 295
                                                                                                                                           LLWHGSRMSNWVGILSHGLRIAPPEAPITGYMFGKGIYFADMSSKSANYCFASRLKNTGL 471
                                                                                                                                                                                          LLLSEVALGQCNELLEANPKAEGLLQGKHSTKGLGKMAPSSAHFVTL-NGSTVPLGPASD 530
                                                                                                                                                                                                                LLLCEVALGDMNELLYSDYNADNLPPGKLSTKGVGKTAPNPSEAQTLEDGVVVPLGKPVE 602
                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEINS BY POLY(ADP-RIBOSYL)ATION. THE MODIFICATION IS DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-98239716; PubMed-9571033; Ruf A., Rolli V., Allil V., Rolli V., de Murcia G.M., Schulz G.E.; "The mechanism of the elongation and branching reaction of poly(ADP-ribose) polymerase as derived from crystal structures and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-96353841; PubMed-8755499;
Ruf A., Mennissier de Murcia J., de Murcia G.M., Schulz G.E.;
"Structure of the catalytic fragment of poly(AD-ribose) polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agenesis.";
Mol. Biol. 278:57-65(1998).
FUNCTION: POLY(ADP-RIBOSE) POLYMERASE MODIFIES VARIOUS NUCLEAR
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                                              IPHDFGLR--TPPLIRTQKELSEKIQLLEALGDIEIAIKLVKTELQSPEHPLDQHYRNLH
                                                                                                          Ittel M.-E., Garnier J.-M., Jeltsch J.-M., Niedergang C.; "Chicken poly(ADP-ribose) synthetase: complete deduced amino acid sequence and comparison with mammalian enzyme sequences.";
                       304 SMMAQHMMEIGYNANKLPLGKISKSTISKGYEVLKRISEVIDRYDRTR-LEELSGEFYTV
                                                                                             CALRPLDHESYEFKVISQYLQSTHAPTHSDYTMTLLDLFEVEKDGEKEAFRE--DLHNRM
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                                                                                                                                                                                                                                        531 TGILNPDGYTLNYNEYIVYNPNQVRMRYLLKVQFNF 566
                                                                                                                                                                                                                                                    603 RSCSKG---MLLYNEYIVYNVEQIKMRYVIQVKFNY 635
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15-JUL-1998
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                MISCELLANEOUS: THE ADP-D-RIBOSYL GROUP OF NAD(+) IS TRANSFERRED TO AN ACCEPTOR CARBOXYL GROUP ON A HISTONE OR THE ENZYME ITSELF, AND FURTHER ADP-RIBOSYL GROUPS ARE TRANSFERRED TO THE 2'-POSITION OF THE TERMINAL ADENOSINE MOIETY, BULLDING UP A POLYMER WITH AN AVERAGE CHAIN LENGTH OF 20-30 UNITS.
SIMILARITY: BELONGS TO THE PARP FAMILY.
SIMILARITY: CONTAINS I BRCT DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00292; BRCT; 1.
PROSITE; PS50172; BRCT; 1.
PROSITE; PS00347; PARP_ZN_FINGER_1; 2.
PROSITE; PS50064; PARP_ZN_FINGER_2; 2.
Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein;
                         CELLULAR PROCESSES SUCH AS DIFFERENTIATION, PROLIFERATION, AND TUMOR TRANSFORMATION AND ALSO IN THE REGULATION OF THE MOLECULAR
                                                                                                                                      nicotinamide + (ADP-D-ribosyl)(N+1)-acceptor.
COFACTOR: ZINC, CONTAINS TWO MOLES OF ZINC PER MOLE OF PROTEIN.
SUBUNIT: HOMODIMER (Potential).
SUBCELLULAR LOCATION: Nuclear.
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DNA AND IS INVOLVED IN THE REGULATION OF VARIOUS IMPORTANT
                                                                                 EVENTS INVOLVED IN THE RECOVERY OF CELL FROM DNA DAMAGE. CATALYTIC ACTIVITY: NAD(+) + {ADP-D-ribosyl}(N)-acceptor =
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NUCLEAR LOCALIZATION SIGNAL 2ND
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PDB; 2PAW; 27-MAY -98.

PDB; 1PAX; 15-MAY -98.

PDB; 2PAX; 27-MAY -98.

PDB; 3PAX; 27-MAY -98.

PDB; 3PAX; 27-MAY -98.

PDB; 1AX6; 27-MAY -98.

PDB; 1AX6; 27-MAY -98.

PDB; PAX; 27-MAY -98.

PEROPOSITION PARP.

PEROPOSITION PA
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-!- FUNCTION: POLY[ADP-RIBOSE] POLYMERASE MODIFIES VARIOUS NUCLEAR PROTEINS BY POLY(ADP-RIBOSYL)ATION. THE MODIFICATION IS DEPENDENT ON DNA AND IS INVOLVED IN THE REGULATION OF VARIOUS IMPORTANT CELLULAR PROCESSES SUCH AS DIFFERENTIATION, PROLIFERATION, AND TUMOR TRANSFORMATION AND ALSO IN THE REGULATION OF THE MOLECULAR EVENTS INVOLVED IN THE RECOVERY OF CELL FROM DNA DAMAGE (BY
                                                                                           RCQRQESKKMPVAGGKANKDRTEDKQDESVKALLLKGKAPVDPECTAKVGKAHVYCEGND 100
                                                                                                                                       VYDVMLNQTNLQFNNNKYYLIQLLEDDAQRNFSVWMRWGRVGKMGQHSLVACSGNLNKAK 160
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                                                                                                                                                                                                                                                                                                                                                                            457
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01-MR-2002 (Rel. 41, Last annotation update)
Poly [App-ribose] polymerase-1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+)
ADP-ribosyltransferase-1) (Poly[ADP-ribose] synthetase-1).
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                                                                                                                                                       SESQILDLSNRFYTLIPHDFGMKKPPLLSNLEYIQAKVQMLDNLLDIEVAYSLLRGGNED
                                                                                                                                                                                                                                                                                                                                            SQRYKPFKQLHNRQLLWHGSRTTNFAGILSQGLRIAPPEAPVTGYMFGKGIYFADMVSKS
                                                                                                                                                                                                           EHFLNLYEEKTGNSWHSK-NFTKYPKKFYPLEIDYG---QDEEAVRK---LIVSAGIKSK
                                                                                                                                                                                                                                  LDLRVQELIKLICNVQAMEEMMMEMKYNTKKAPLGKLTVAQIKAGYQSLKKIEDCIRAGQ
                                                                                                                                                                                                                                                                               HGRALMEACNEFYTRIPHDFGLRTPPLIRTQKELSEKIQLLEALGDIEIAIKLVK-TELQ
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Cricetulus griseus (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  570
                                                                     20;
                                             Length 1011;
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                                                                     Indels
 261AED9383139144 CRC64;
                                                                    Mismatches 186;
                                              DB 1;
                                     Score 1027; DB 1;
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113520 MW;
                                                                    Conservative 110;
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          1011 AA;
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NCBI_TaxID=10029;
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Q9R152;
                                                         Best Local Sim
Matches 218;
CONFLICT
                                              Query Match
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: HOMODIMER (POTENTIAL).
SUBCELLULAR LOCATION: Nuclear.
MISCELLULAR LOCATION: Nuclear.
MISCELLULAR LOCATION: Nuclear.
MISCELLANEOUS: THE ADP-D-RIBOSYL GROUP OF NAD(+) IS TRANSFERRED TO
FURTHER ADP-RIBOSYL GROUP ON A HISTONE OR THE ENZYME ITSELF, AND
FURTHER ADP-RIBOSYL GROUPS ARE TRANSFERRED TO THE 2'-POSITION OF
THE TERMINAL ADENOSYLE MOIETY, BUILDING UP A POLYMER WITH AN
AVERAGE CHAIN LENGTH OF 20-30 UNITS.
SIMILARITY: BELONGS TO THE PARP FAMILY.
SIMILARITY: CONTAINS 1 BRCT DOMAIN.
similarity).
crafilarity).
crafilarity).
crafilarity).
crafilarite AcTIVITY: NAD(+) + {ADP-D-ribosyl}(N+1)-acceptor.
cocrafilarite + {ADP-D-ribosyl}(N+1)-acceptor.
cofactor: zinc, contains TWO WOLES OF ZINC PER MOLE OF PROTEIN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Kofler B.,
 PPOL_MOUSE STANDARD; PRT; 1012 AA.
P1103; Q9JLX4; Q9QVQ3;
01-JUL-1989 (Rel. 11, Created)
01-GT-1989 (Rel. 2, Last sequence update)
16-OCT-2091 (Rel. 40, Last annotation update)
Poly [ADP-ribose] polymerase-1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+)
ADP-ribosyltransferase-1) (Poly[ADP-ribose] synthetase-1) (msPARP).
                                                 206
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"Sequence and organization of the mouse poly (ADP-ribose) polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96007847; PubMed=7578427;
Auer B., Flick K., Wang Z.Q., Haidacher D., Jaeger S., Berghammer H.,
                                                                     651
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STRAIN=129/SV X C57BL/6; TISSUE-Fibroblast;
MEDLINE=20270268; PubMed=10809783;
Sallmann F.R., Vodenicharov M.D., Wang Z.-Q., Poirier G.G.;
"Characterization of spaRP-1. An alternative product of PARP-1 gene with poly(ADP-ribose) polymerase activity independent of DNA strand
         87 AKVGKAHVYCEGNDVYDVMLNQINLQFNNNKYYLIQLLEDDAQRNFSVWMRWGRVGKMGQ
                     SNKLEQMPSKEDAVEHFMKLYEEKTGNAWHSK-NFTKYPKKFYPLEIDYG---QDEEAVK
                                                                                         207 KEESLKSPLKP--ESQLDLRVQELIKLICNVQAMEEMMMEMKYNTKKAPLGKLTVAQIKA
                                                                                                   YTMTLLDLFEVEKDGEKEAFR - - EDLHNRMLLWHGSRMSNWVGILSHGLRIAPPEAPITG
                                                                                                                                                                                                                           YMFGKGIYFADMSSKSANYCFASRLKNTGLLLLSEVALGOCNELLEANPKAEGLLOGKHS
                                                                                                                                                                                                                                                                  502 TKGLGKMAPSSAHFVTLNGSTVPLGPASDTGILNPDGYT---LNYNEYIVYNPNQVRMRY
                                                                                                                                                                                                                                                                                                          946 VKGLGKTTPDPSASITLEGVEVPLG---TGI--PSGVNDTCLLYNEYIVYDIAQVNLKY
                                                 HSLVACSGNLNKAKEIFQKKFLDKTKNNWEDREKFEKVPGKYDMLQMDYATNTQDEEETK
                                                                                                                                 GYOSLKKIEDCIRAGOHGRALMEACNEFYTRIPHDFGLRTPPLIRTQKELSEKIQLLEAL
                                                                                                                                                                         GDIEIAIKLVK-TELQSPEHPLDQHYRNLHCALRPLDHESYEFKVISQYLQSTHAPTHSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 17:3387-3401(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol. Chem. 275:15504-15511(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=89263780; PubMed=2498841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADPRT OR ADPRT1 OR ADPRP. Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                  LLKVQFNF-LQLW 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheri
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein;
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INIT_MET 0 0 BY SIMILARITY.
CHAIN 1 1012 POLY [ADP-RIBOSE] POLYMERASE-1,
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NUCLEAR LOCALIZATION SIGNAL 2N
ADP-RIBOSYLINI (POTENTIAL).
ADP-RIBOSYLINI (POTENTIAL).
ADP-RIBOSYLINI (POTENTIAL).
ADP-RIBOSYLINI (POTENTIAL).
ADP-RIBOSYLINI (POTENTIAL).
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PTR, S04200; S04200.
PTR, S04206; 1A26.
MCD: MGT:1340806; Adprt.
InterPro; IPR001357; BRCT.
InterPro; IPR001290; PARP.
InterPro; IPR004102; PARP.
InterPro; IPR004102; PARP.
InterPro; IPR004102; PARP.
PF00533; BRCT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02877; PARP_reg; 1.
Pfam; PF00645; Zf-PARP; 2.
ProDom; P0004675; Znf-PARP; 2.
SMART; SM00292; BRCT; 1.
PROSITE; PS50172; BRCT; 1.
PROSITE; PS500347; PARP_ZN_FINGER_1; 2.
PROSITE; PS50064; PARP_ZN_FINGER_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PARP-TYPE
Schweiger M., Wagner E.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISOFORM
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16-OCT-2001 (Rel. 40, Last annotation update)
Poly [ADP-ribose] polymerase-1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+)
ADP-ribosyltransferase-1) (Poly[ADP-ribose] synthetase-1).
                                                              Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                 Beneke S., Meyer R., Buerkle A.;
"Isolation of cDNA encoding full-length rat (Rattus norvegicus) poly
                                                                                                                                                                                                                                                                                                   Potvin F., Thibodeau J., Kirkland J.B., Dandenault B., Duchaine C., Poirier G.G.; Structural analysis of the putative regulatory region of the rat gene encoding poly(ADP-ribose) polymerase."; FEBS Lett. 302:269-273(1992).
                                                                                                                                                                                                                          Beneke S., Meyer R., Buerkle A.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                          (ADP-ribose) polymerase.";
Biochem. Mol. Biol. Int. 43:755-761(1997)
                                                                                                             SEQUENCE FROM N.A.
STRAIN=SPRAGUE-DAWLEY; TISSUE=Monocytes;
                                                                                                                                                                                                                                                                            STRAIN-SPRAGUE-DAWLEY; TISSUE-Prostate;
MEDLINE-92290013; PubMed-1601134;
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EMBL; X65497; CAA46478.1; ALT_INIT.
                                                                                                                                       MEDLINE=98046546; Pubmed=9385436;
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Znf-PARP.
                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U94340; AAC53544.1; -.
                                                                                                                                                                                                                                                                SEQUENCE OF 1-11 FROM N.A.
                                                  Rattus norvegicus (Rat).
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KSAAPSKKSKGCFKEEG-------VNKSEKRMK-LTLKGGAAVDPD-SGLEH 539
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                                                                                                                                                                                                                                                                          Length 1012;
                                                             (POTENTIAL).
(POTENTIAL).
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(POTENTIAL).
                                     POTENTIAL).
                                                 (POTENTIAL).
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                        (POTENTIAL).
(POTENTIAL)
                                                                                                                                                                                                                                                                                                    Mismatches 178;
                                                                                                                                                                                                                                                                          33.9%; Score 1017; DB 1; 40.1%; Pred. No. 6.9e-59;
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                                             ADP-RIBOSYL[N]
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                                                                                                                                                                                                      SEQUENCE OF 514-1013 FROM N.A.
STRAIN=SPRAGUE-DAWLEY; TISSUE=Prostate;
MEDLINE=90027702; PubMed=2508713.
Thibodeau J., Gradwohl G., Dumas C., Clairoux-Moreau S., Brunet G.;
"Cloning of rodent cDNA coding the poly(ADP-ribose) polymerase
catalytic domain and analysis of mRNA levels during the cell cycle.";
Biochem. Cell Biol. 67:653-660(1989).
-- FUNCTION: POLY[ADP-RIBOSE] POLYMERASE MODIFIES VARIOUS NUCLEAR
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PF00644; PARP;
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                                                                                SMART; SM00292; BRCT; 1.
PROSITE; PS0347; PARP_ZN_FINGER_1; 2.
PROSITE; PS50064; PARP_ZN_FINGER_2; 2.
TROSITE; PS50064; PARP_ZN_FINGER_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 EDSSPAKKTRRCQRQESKKMPVAGGKANKDRTEDKQDESVKALLLKGKAPVDPECTAKVG 90
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NUCLEAR LOCALIZATION SIGNAL 2ND
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N -> D (IN REF. 4).
WW; AA566F2B29BE97CO CRC64;
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/ A (IN REF. 4)
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01-MAR-1989 (Rel. 10, Created)
01-DBC-1992 (Rel. 24, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Poly [ADP-ribose] polymerase-1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+)
ADP-ribosyltransferase-1) (Poly[ADP-ribose] synthetase-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular cloning of cDNA for human poly(ADP-ribose) polymerase and expression of its gene during HL-60 cell differentiation."; Biochem. Biophys. Res. Commun. 146:403-409(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Fibroblast;
MEDLINE:B8076933. PubMed=3120710;
Uchida K., Morita T., Sato T., Ogura T., Yamashita R., Noguchi S., Suzuki H., Nyunoya H., Miwa M., Sugimura T.;
Nuclechida sequence of a full-length cDNA for human fibroblast poly(ADP-ribose) polymerase.";
Hiochem. Biophys. Res. Commun. 148:617-622(1987).
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506 GKMAPSSAHFVTLNGSTVPLGPASDTGILNPDGYT---LNYNEYIVYNPNQVRMRYLLKV
                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-87298455; PubMed-3113420;
Suzuki H., Uchida K., Shima H., Sato T., Okamoto T., Kimura T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "CDNA sequence, profein structure, and chromosomal location of human gene for poly(ADP-ribose) polymerase."; Proc. Natl. Acad. Sci. U.S.A. 84:8370-8374(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Suzuki H., Uchida K., Shima H., Sato T., Okamoto T., Kimura T.,
Miwa M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cherney B.W., McBride O.W., Chen D., Alkhatib H., Bhatia K.,
Hensley P., Smulson M.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Fibroblast;
MEDLINE-88058958; PubMed=2824474;
Kurosaki T., Ushiro H., Mitsuuchi Y., Suzuki S., Matsuda M.
Matsuda Y., Katunuma N., Kangawa K., Matsuo H., Hirose T.,
Inayama S., Shizuta Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-90091744; Pubmed-2513174; Medr B., Ragl U., Herzog H., Schneider R., Schweiger M.; "Human nuclear NAD+ App-ribosyltransferase(polymerizing): organization of the gene.";
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MEDLINE-88068596; PubMed-2891139;
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P09874;
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SUBUNIT: HOMODIMER (Potential).

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CATALYTIC ACTIVITY: NAD(+) + {ADP-D-ribosyl}{(N)-acceptor = nicotinamide + {ADP-D-ribosyl}{(N+1)-acceptor.}

COFACTOR: ZINC, CONTAINS TWO MOLES OF ZINC PER MOLE OF PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Simonin F., Menissier de Murcia J., Poch O., Muller S., Gradwohl G., Mollnete M., Penning C., Kelth G., de Murcia G.M.;
Expression and site-directed mutagenesis of the catalytic domain of human poly(ADP-ribose)polymerase in Escherichia coli. Lysine 893 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The zinc fingers of human poly(ADP-ribose) polymerase are "The zinc fingers of human poly(ADP-ribose) polymerase are differentially required for the recognition of DNA breaks and nicks and the consequent enzyme activation. Other structures recognize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-9746532; PubMed-9315851;
Rolli V., O'Farrell M., Menissier-de Murcia J., de Murcia G.M.;
Rolli V., O'Farrell M., Menissier-de Murcia J., de Murcia G.M.;
Rolli V., O'Farrell M., Menissier-de Murcia J., de Murcia G.M.;
Rolli V., O'Farrell M., Menissier-de Murcia J., de Murcia G.M.;
Biochemistry 36:12147-12154(1997).
I EUNCTION: POLY (ADP-RIBOSE) POLYMERASE MODIFIES VARIOUS INCLEAR PROTEINS BY POLY (ADP-RIBOSE) ATTON. THE MODIFICATION IS DEPENDE ON DNA AND IS INVOLVED IN THE REGULATION OF VARIOUS IMPORTANT
CELLULAR PROCESSES SUCH AS DIFFERENTIATION, PORLIFERATON, AND
          Yokoyama Y., Kawamoto T., Mitsuuchi Y., Kurosaki T., Toda K.,
Ushiro H., Terashima M., Sumimoto H., Kuribayashi I., Yamamoto Y.,
Maeda T., Ikeda H., Sagara Y., Shizuta Y.;
Human poly(ADP-ribose) polymerase gene. Cloning of the promoter
                                                                                                                                                                           "Characterization of a putative promoter region of the human boly AADP-ribose) polymerase gene: structural similarity to that of the DNA polymerase beta gene."; the DNA polymerase beta gene."; Biochem. Blophys. Res. Commun. 167:701-710(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANALYSIS OF ZINC FINCERS.
MEDLINE-91072398; pubMed-2123876;
Ikelima M., Noguchi S., Yamashita R., Ogura T., Sugimura T.,
                                                                                                                                                                                                                                                                      H., Schneider R., Hirsch-Kauffmann M., Schnitzer D.,
                                                                                                                                                                                                                                                                                    Schweiger M.;
Submitted (JUL-1991) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-92371433; PubMed-1505517;
Schreiber V., Molinete M., Boeuf H., de Murcia G.M.,
Menissier de Murcia J.;
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                                                                                     Eur. J. Biochem. 194:521-526(1990)
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MEDLINE=91035460; PubMed=2121735;
                                                                                                                 SEQUENCE OF 1-39 FROM N.A. MEDLINE-90211250; Pubmed-2108670;
MEDLINE-91099327; PubMed-2125269;
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EMBO J. 11:3263-3269(1992).
                                                                                                                                                                                                                                                    SEQUENCE OF 1-39 FROM N.A.
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                                                                                                                                                                  Esumi H.;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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-i- SUBCELLULAR LOCATION: NUCLEAT.

-i- SUBCELLULAR LOCATION: NUCLEAT.

-i- MISCELLANEOUS: THE ADP-D-RIBOSYL GROUP OF NAD(+) IS TRANSFERRED TO AN ACCEPTOR CARBOXYL GROUP ON A HISTONE OR THE ENZYME ITSELF, AND FURTHER ADP-RIBOSYL GROUPS ARE TRANSFERRED TO THE 2'-POSITION OF THE TERMINAL ADENOSINE MOLETY, BUILDING UP A POLYMER WITH AN AVERAGE CHAIN LENGTH OF 20-30 UNITS.

-i- SIMILARITY: BELONGS TO THE PARP FAMILY.

-i- SIMILARITY: CONTAINS 1 BRCT DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tch 33.8%; Score 1012.5; DB 1; Length 1013; al Similarity 40.5%; Pred. No. 1.4e-58; 221; Conservative 111; Mismatches 185; Indels 29;
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AAA51599.1;
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EMBL, M60436; AA6000
PIR; A26901; A26901.
PIR; A28725; A26498.
PIR; A35635, A35635.
PIR; A3321; A33321.
PIR; B33321; B33321.
PIR; B3321; B3321.
PIR; S14010; S14010.
HSSP; P26446; 1A26.
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InterPro; IPR001510;
Pfam; PF00533; BRCT;
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InterPro; IPR001290;
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Pfam; PF00644; PARP;
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16-CCT-2001 (Rel. 40, Last annotation update)
Poly [ADP-ribose] polymerase-1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+)
ADP-ribosyltransferase-1) (Poly[ADP-ribose] synthetase-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-88151954; PubMed-2450019; Taniguchi T., Yamauchi K., Yamamoto T., Toyoshima K., Harada N., Tanaka H., Takahashi S., Yamamoto H., Fujimoto S.; Paranaka H., Takahashi S., Yamamoto H., Fujimoto S.; Popression in gene expression for poly(ADP-ribose) synthetase during the interferon-gamma-induced activation process of murine macrophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . J. Biochem. 171:571-575(1988).
FUNCTION: POLY[ADP-RIBOSE] POLYMERASE MODIFIES VARIOUS NUCLEAR
PROTEINS BY POLY(ADP-RIBOSYL)ATION. THE MODIFICATION IS DEPENDENT
                                                                                                                                                                                                    387
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                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
---KEEGINKSEKRMK-LTLKGGAAVDPD-SGL
                                LSEVQQAVSQGSSDSQ1LDLSNRFYTL1PHDFGMKKPPLLNNADSVQAKVEMLDNLLD1E
                                                                                                                                                                                                    IAIKLVK-TELQSPEHPLDQHYRNLHCALRPLDHESYEFKVISQYLQSTHAPTHSDYTMT
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                      VGKAHVYCEGNDVYDVMLNQTNLQFNNNKYYLIQLLEDDAQRNFSVWMRWGRVGKMGQHS
                                                                 LVACSGNLNKAKEIFOKKFLDKTKNNWEDREKFEKVPGKYDMLOMDYATNTODEEETKKE
                                                                                                             ESLKSPLKPESQLDLRVQELIKLICNVQAMEEMMMEMKYNTKKAPLGKLTVAQIKAGYQS
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SEQUENCE OF 647-714 AND 838-903 FROM N.A.
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P18493; Q9TSO0;
O1-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequ
16-OCT-2001 (Rel. 40, Last anno
493 APRGKSGAALSKKSKGQV-
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration
                   CELLULAR PROCESSES SUCH AS DIFFERENTIATION, PROLIFERATION, AND TUMOR TRANSFORMATION AND ALSO IN THE REGULATION OF THE MOLECULAR EVENTS INVOLVED IN THE RECOVERY OF CELL FROM DNA DAMAGE.

-!- CATALYTIC ACTIVITY: NAD(+) + {ADP-D-TIDOSY1}(N)-acceptor -
nicotinamide + {ADP-D-TIDOSY1}(N+1)-acceptor -
-- COFACTOR: ZITC, CONTAINS TWO MOLES OF ZINC PER MOLE OF PROTEIN.
-!- SUBGNIT: HOMODIMER (POTENTIAL).
-!- SUBGNIT: HOMODIMER (POTENTIAL).
-!- SUBGNIT: ADP-D-RIBOSYL GROUP OF NAD(+) IS TRANSFERED TO AN ACCEPTOR CARBOXYL GROUP OR A HISTONE OR THE ENZYME ITSELF, AND FURTHER ADP-RIBOSYL GROUPS RE TRANSFERRED TO THE 2'-POSITION OF THE TERMINAL ADENOSINE MOLETY, BUILDING UP A POLYMER WITH AN AVERAGE CHARIN DEVOIT OF 20-30 UNITS.
-!- SIMILARITY: BELONGS TO THE PARP FAMILY.
-!- SIMILARITY: CONTAINS 1 BRCT DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein; ADP-ribosylation; Zinc-finger; Zinc.
DNA AND IS INVOLVED IN THE REGULATION OF VARIOUS IMPORTANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEAR LOCALIZATION SIGNAL 1ST PA NUCLEAR LOCALIZATION SIGNAL 2ND PA ADP-RIBOSYL[N] (POTENTIAL).

ADP-RIBOSYL[N] (POTENTIAL).

ADP-RIBOSYL[N] (POTENTIAL).

ADP-RIBOSYL[N] (POTENTIAL).

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PROSITE; PS00347; PARP_ZN_FINGER_1; 2.
PROSITE; PS50064; PARP_ZN_FINGER_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D90073; BAA14114.1; -.
EMBL; X06986; CAA30046.1; -.
EMBL; X06987; CAA30047.1; -.
PIR, J50428; J50428.
PIR; S00328; S00328.
INSPP, PZ6446; LAZ6.
InterPro; IPR001357; BRCT.
InterPro; IPR001390; PARP.
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Pfam; PF02877; PARP, reg; I.
Pfam; PF00645; zf-PARP; 2.
ProDom; PD004675; Znf-PARP; 2.
SMART; SM00292; BRCT; I.
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Znf-PARP.
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InterPro; IPR001510; Znf
Pfam; PF00533; BRCT; 1.
Pfam; PF00644; PARP; 1.
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Length 1015;

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Score 1009;

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01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Poly [ADP-ribose] polymerase (EC 2.4.2.30) (PARP) (ADPRT) (NAD(+) ADP-ribose)
ribosyltransferase) (Poly[ADP-ribose] synthetase) (Fragment).
Xenopus laevis (African clawed frog).
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                                                                                                                                                                                     384
                                                                                                                                                                                                                                                             KGLGKMAPSSAHFVTLNGSTVPLGPASDTGILNPDGYTLNYNEYIVYNPNQVRMRYLLKV 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        poly(ADP-ribose)
                                    Gaps
                          82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSNKLEQMPSKEDAIEHFWKLYEEKTGNAWHSK-NFTKHPKKFYPLEIDYG---QDEEAV
                                                                                                                                                                                                                              GNTAPEDSSPAKKTRRCQRQESKKMPVAGGKANKDRTEDKQDESVKALLLKGKAPVDPEC
                                                                                       146 QHSLVACSGNLNKAKEIFQKKFLDKTKNNWEDREKFEKVPGKYDMLQMDYATNTQDEEET
                                                                                                                       KKEESLKSPLKPESQLDLRVQELIKLICNVQAMEEMMMEMKYNTKKAPLGKLTVAQIKAG
                                                                                                                                                     YQSLKKIEDCIRAGQHGRALMEACNEFYTRIPHDFGLRTPPLIRTQKELSEKIQLLEALG
                                                                                                                                                               DIEIAIKLVK-TELQSPEHPLDQHYRNLHCALRPLDHESYEFKVISQYLQSTHAPTHSDY
                                                                                                                                                                                               MFGKGIYFADMSSKSANYCFASRLKNTGLLLLSEVALGQCNELLEANPKAEGLLQGKHST
                                                                                                                                                                                                                     TWTLLDLFEVEKDGEKEAFR - - EDLHNRMLLWHGSRMSNWVGILSHGLRIAPPEAPITGY
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
          32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (2)
SEQUENCE OF 742-876 FROM N.A.
SEQUENCE 93277538; PubMed-8503897;
Ozawa Y., Uchida K., Uchida M., Ami Y., Kushida S., Okada N.,
          Indels
2.3e-58;
ches 187;
          Mismatches
                                                                                                                                                                                                                                                                                                                                                                          998 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thesis (1992), University of Rennes, France,
 Š.
                                                                                                                                                                                                                                                                                                                                                                         PRT;
 Pred.
         222; Conservative 108;
                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saulier-Le Drean B.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                1007 KFNFKTSLW 1015
Best Local Similarity
                                                                                                                                                                                                                                                                                                                  QFNF-LQLW 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Ovary;
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P31669;
         Matches
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PROTEINS BY POLY(ADP-RIBOSYL)ATION. THE MODIFICATION IS DEPENDENT
CON DNA AND IS INVOLVED IN THE REGULATION OF VARIOUS IMPORTANT
CELLULAR PROCESSES SUCH AS DIFFERENTIATION, PROLIFERATION, AND
TUMOR TRANSFORMATION AND ALSO IN THE REGULATION OF THE MOLECULAR
CONTINUED IN THE RECOVERY OF CELL FROM DNA DAMAGE.

COTANTITIC ACTIVITY: NAD(+) + {ADP-D-TIDOSY]/(N)-ecceptor -
ILCOTIONAING + {ADP-D-TIDOSY]/(N)-ecceptor -
COFACTOR: ZINC, CONTAINS TWO MOLES OF ZINC PER MOLE OF PROTEIN.
COTACTOR: MICHORY.
COFACTOR: THE ADP-D-TIDOSY]/(N)-acceptor -
COFACTOR: THE CATAINS TWO MOLES OF ZINC PER MOLE OF PROTEIN.
COTACLIANCE OF THE DEPLOY OF NAD(+) IS TRANSFERRED TO
AN ACCEPTOR CARBOXYL GROUP ON A HISTONE OF THE ENZYME ITSELF, AND
FURTHER ADP-RIBOSYL GROUP ON A HISTONE OF THE ENZYME ITSELF, AND
FURTHER ADP-RIBOSYL GROUP ON A HISTONE OF THE 2'-POSITION OF
COTACL OF THE TERMINAL ADENOSINE MOLETY, BULLDING UP A POLYMER WITH AN
AVERAGE CHAIN LENGTH OF 20-30 UNITS.
COTACL OF THE TRANSFERRED TO THE 2'-DOSITION OF
COTACL OF THE TRANSFERRED TO THE 2'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50172; BRCT; 1.
PROSITE; PS00347; PARP_ZN_FINGER_1; 2.
PROSITE: PS50064; PARP_ZN_FINGER_2; 2.
Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PART
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zinc-finger; Zinc.
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InterPro; IPR001510; Znf-PARP.
Pfam; PF00533; BRCT; 1.
Pfam; PF00644; PARP; 1.
Pfam; PF00847; PARP_reg; 1.
Pfam; PF00645; Zf-PARP; 2.
ProDom; PD004675; Znf-PARP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MΨ.
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148
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212
391
397
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428
429
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454
467
471
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InterPro; IPR001357;
InterPro; IPR001290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S31735; S31735.
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DNA_BIND
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CONFLICT
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1D PPOL, DROME STANDARD; PKT; 2.2.....
1C P35875; 09W505; 09W5
                                                           14;
                                                                                                                                                                                                                                                                                                                                128 AQRNFSVWMRWGRVGK-MGQHSLVACSGNLNKAKEIFQKKFLDKTKNNWEDREKFEKVPG 186
                                                                                                                                                                                                                                                                                                                                                                                   RDSRYWVFRSWGRVGTVIGSKKLEEMSSK-EDAIEHFLNLYQDKTGNAWHS-PNFTKYPK 619
                                                                                                                                                                                                                                                                                                                                                                                                                                           KYDMLQMDYATNTQDEEETKKEESLKSPLKPESQLDLRVQELIKLICNVQAMEEMMMEMK 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKIICDYVKNTHADTHNAYDLEVLEIFKIDREGEYQRYKPFKQLHNRQLLMHGSRTTNFA 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GILSHGLRIAPPEAPITGYMFGKGIYFADMSSKSANYCFASRLKNTGLLLLSEVALGQCN 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESVKALLLKGKAPVDPECTAKVGKAHVYCEGNDVYDVMLNQTNLQFNNNKYYLIQLLEDD 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELLEANPKAEGLLQGKHSTKGLGKMAPSSAHFVTLNGSTVPLGPA----SDTGILNPDG 538
                                                             Gaps
                                                                                                          KRVNNGNTAPE-----DSSPAKKTRRCQRQESKKMPVAG-----GKANKDRTEDKQD 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., ALTERNATIVE SPLICING, DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY.
STRAIN-CANTON-S;
                                                                                                                                                                                                                                                          LIRTQKELSEKIQLLEALGDIEIAIKLVKTELQSPE-HPLDQHYRNLHCALRPLDHESYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FKVISQYLQSTHAPTHSDYTMTLLDLFEVEKDGEKEAFR--EDLHNRMLLWHGSRMSNWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | |:| : |:||| ||||:|| : | |:| ||||
E-LKAASQITKLPKGKHSVKGLGRTAPDPSATVQLDGVDVPLGKGTSANISDTSLL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YNTKKAPLGKLIVAQIKAGYQSLKKIEDCIRAGQHGRALMEACNEFYTRIPHDFGLRTPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polymerase:
                                                             41;
  Length 998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=93234521; PubMed=8475096;
Uchida K., Hanai S., Ishikawa K.-I., Ozawa Y.-I., Uchida M., Sugimura T., Mwa M.;
"Cloning of cDNA encoding Drosophila poly(ADP-ribose) polyme: leucine zipper in the auto-modification domain.";
Proc. Natl. Acad. Sci. U.S.A. 90:3481-3485(1993).
                                                           Indels
DB 1;
                                                        196;
     Score 984.5; DB Pred. No. 9e-57;
                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               539 YTLNYNEYIVYNPNQVRMRYLLKVQFNF 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---YNEYIVYDIAQVNLKYLLKKFNY 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98234380; PubMed=9565614;
                                                        Conservative 109;
32.8%;
39.1%;
                            Similarity
     Query Match
                              Local
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B. Genomic cognalization of Drosophila poly(ADD-Libose) polymerase and distribution of ris mank and during deecdopment.*;

B. STRAIN-BERKEREY.

Addams M.D., Celnider S.E., Hölt R.A., Evans C.A., Gocayne J.D., And Mannitides P.G., Scheers E.E., 16 P.M. Hoskins R.A., Galle R.F., And Mannitides P.G., Scheers E.E., 16 P.M. Hoskins R.A., Galle R.F., And Mannitides P.G., Roberts B.C., And Mannitides P.G., Chent G.M.

B. STRAIN-BERKEREY.

Addams M.D., Celnider S.E., Hölt R.A., Evans C.A., Gocayne J.D., And Mannitides P.G., Roberts B.C., Mannitides P.G., Chent G.M.

B. Stricton G.G., Worthan J.R., Yandell M.D., Zhang O., Chen L.M., Barnothan R., Polymer R.G., Mannitides P.G., Chent G.M., Mannitides P.G., Bernardon R.G., Mannitides P.G., Chent G.M., Barnothan R., Bouck J., Brockstein P., Brottler P., Brittler P.G., Barnothan R., Bouck J., Brockstein P., Brottler P., Cang F., Delcher A., Bouck J., Brockstein P., Brottler P., Cang F., Delcher A., Bouck J., Brockstein P., Brottler P., Cang F., Delcher A., Bouck J., Brockstein P., Brottler P., Cang F., Delcher A., Bouck J., Brockstein P., Brottler P., Cang F., Delcher A., Bough J., Wall M., Caller B., Contrel J., Mannitis R., Mannitis R., Mannitis R., Mannitis P., Margon G.H., Re. Z., Kennison J.A., Kerching R., Mannitis R., Mannitis P., Margon G.H., Re. Z., Kennison J.A., Kerching R., Mannitis R., Mannitis P., Margon G.H., Re. Z., Kennison J.A., Kennison B., Mannitis R., Mannitis R., Mannitis P., Margon G.H., Re. Z., Kennison J.A., Mannitis R., M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKAPLGKLTVAQIKAGYQSLKKIEDCIRAGQHGRALMEACNEFYTRIPHDFGLRTPPLIR 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      310 TQKELSEKIQLLEALGDIEIAIKLVKTE-LQSPEHPLDQHYRNLHCALRPLDHESYEFKV 368
                                                                                                                                                                                                                                                                                                                                                                    SMART: SNULZZI, CHORT; 1.
PROSITE; PSSOU347; PARP_ZN_FINGER_1; 1.
PROSITE; PSSO064; PARP_ZN_FINGER_2; 2.
Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein; ADP-ribosylation; Zinc-finger; Zinc; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 VKALLLKGKAPVDPECTAKVGKAHVYCEGNDVYDVMLNQTNLQFNNNKYYLIQLLEDDAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAIKYIN-STCICSWGTDPKSRIPKETTKSLNSNSIYTKSMPVS-------
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NUCLEAR LOCALIZATION SIGNAL 2ND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 979.5; DB 1
Pred. No. 1.9e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAD-BINDING.
                                                                                                                                                        BL; AE002892; AAF45445.2; ALT_SEQ. R; P26446; 1A26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PARP-TYPE.
PARP-TYPE.
                                                                                              EMBL, AF051548; AAC24518.1;
EMBL, AF051544; AAC24518.1;
EMBL, AF051545; AAC24518.1; JOINED.
EMBL, AF051546; AAC24518.1; JOINED.
EMBL, AF051547; AAC24518.1; JOINED.
EMBL, AF002935; AAC24518.1; JOINED.
                                                                                                                                                                                                                                                                                          Pfam: PF00533; BRCT; 1.
Pfam: PF00644; PARP; 1.
Pfam: PF02847; PARP: 1.
Pfam: PF00645; zf-PARP; 2.
ProDom; PD004675; Znf-PARP; 2.
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InterPro; IPR001510; Znf-PARP.
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                                                                                      EMBL; D13806; BAA02964.1; -.
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InterPro; IPR001357; BRCT.
InterPro; IPR001290; PARP.
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994 AA;
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MEDLINE-94170813; PubMed-8125121;

MEDLINE SALCOPAGA EXPRESSION OF POLY(ADP-TIDOSE) POLYMERASE

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MEDLINE AND THE MADP-RIBOSYL GROUPS AND THE MOLECULAR AND THE MADPLE TRANSFERRED TO THE MADPLE THE MADPLE TRANSFERRED TO THE MADPLE THE MADPLE TRANSFERRED TO THE MADPLE THE MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Poly (Appribose) polymerase (EC 2.4.2.30) (PARP) (ADPRT) (NAD(+) ADP-
ribosyltransferase) (Poly[ADP-ribose] synthetase).
Sarcophaga peregrina (Plesh fly) (Boettcherisca peregrina).
Eukaryota: Metazoa; Arthropoda: Tracheatu: Hexapoda: Insecta;
Pteryota: Neoptera: Endopterygota: Diptera; Brachycera: Muscomorpha;
Oestroidea; Sarcophagidae: Sarcophaga.
                                                                                                                                                                                                                                                            SAR-YINKLSNNKHSCFGRGRTMPDPTKSYIRSDGVEIPYGETITDEHLKS---SLLYNE 971
                              ISQYLQSTHAPTHSDYTMTLLDLFEVEKDGEKEAFR--EDLHNRMLLWHGSRMSNWVGIL
                                                                                                            SHGLRIAPPEAPITGYMFGKGIYFADMSSKSANYCFASRLKNTGLLLLSEVALGQCNELL
                                                                                                                                                                                                                           487 EANPKAEGLLQGKHSTKGLGKMAPS-SAHFVTLNGSTVPLGPASDTGILNPDGYTLNYNE
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SIMILARITY: BELONGS TO THE PARP FAMILY.
SIMILARITY: CONTAINS 1 BRCT DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             996 AA
                                                                                                                                                                                                                                                                                                                                          546 YIVYNPNQVRMRYLLKVQFNF 566
                                                                                                                                                                                                                                                                                                                                                                           972 YIVYDVAQVNIQYLFRMEFKY 992
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Znf-PARP.
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InterPro; IPR001357; BRCT
InterPro; IPR001290; PARP.
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InterPro; IPR001510;
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Pfam; PF00644; PARP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 LKSPLKPESQLDLRVQELIKLICNVQAMEEMMMEMKYNTKKAPLGKLTVAQIKAGYQSLK 270
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                                                                            SMART; SM00292; BRCT; 1.
PROSITE; PS50172; BRCT; 1.
PROSITE; PS500347; PARP_ZNLFINGER_1; FALSE_NEG.
PROSITE; PS50064; PARP_ZNLFINGER_2; 2.
Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein; ADP-tibosylation; Zinc-finger; 
                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
NUCLEAR LOCALIZATION SIGNAL 1ST PART.
NUCLEAR LOCALIZATION SIGNAL 2ND PART.
NW; 690DDD36E7487298 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||| | : |:|:| :| :| :| |:| | : | | |:| | : | |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 ACSGNLNKAKEIFQKKFLDKTKNNWEDREKFEKVPGKYDMLQMDYATNTQDEEETKKEES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           642 AEHDIK--SKLPLSVQDIIKLMFDVDSMKRTWMEFDLDMEKMPLGKLSQKQIQSAYKVLT
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                                                                                                                                                                                                                                                                                                                                                     NAD-BINDING
                                                                                                                                                                                                                                                                                                                             BRCT.
                        Pfam; PF00645; zf-PARP; 2.
ProDom; PD004675; Znf-PARP; 2.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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RVQPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSRQQIARGFBALEALEE 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----LDLRVQELIKLICNVQAMEEMMMEMKYNTKKAPLGKLTVAQIKAGYQSLKKIED 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ansorge W., Wirkner U., Mewes H.-W., Gassenhuber J., Wiemann S.;
Ansorge W., Wirkner U., Mewes H.-W., Gassenhuber J., Wiemann S.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: NAD(+) + {ADP-D-ribosyl}(N)-acceptor -
-!- CATALYTIC ACTIVITY: NAD(+) + {ADP-D-ribosyl}(N)-acceptor -
-!- TISSUE SPECIFICITY: Widely expressed; the highest levels are in the kidney, skeletal muscle, liver, heart and spleen; also detected in pancreas, lung, placenta, brain, leukocytes, colon, small intestine, ovary, testis, prostate and thymus.
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                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
:ibosyltransferase-3) (Poly[ADP-ribose] synthetase-3) (pADPRT-3)
                                                                                                                                                                                                                                                                                                                                                                                                      "A human poly(ADP-ribose) polymerase gene family (ADPRTL): cDNA cloning of two novel poly(ADP-ribose) polymerase homologues."; Genomics 57:442-445(1999).
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Matches 193; Conservative 98; Mismatches 188; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pfam; PF00644; PARP; 1.
Pfam; PF02877; PARP_reg; 1.
Transferase; Glycosyltransferase; NAD; Nuclear protein; ADP-ribosylation.
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A -> G (IN REF. 2).
K -> E (IN REF. 2).
7C0AB89E64D1B9FD CRC64;
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                                                                                                                                                                                                                                                                                                       TISSUE-Fetal brain;
MEDLINE-99263509; PubMed-10329013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AF083068; AAD29855.1; --
EMBL, AL050034; CAB43246.1; --
HSSP, SP6446; AA26.
INTEPPC: IPR001290; PARP.
InterPro; IPR004102; PARP_reg.
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SEQUENCE OF 75-533 FROM N.A.
                                                 (HEARF-5).
ADPRTL3 OR PARP3 OR ADPRT3.
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                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                 NCBI_TaxID=9606;
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01-0cT-1994 (Rel. 30, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-0cT-2001 (Rel. 40, Last annotation update)
Poly [ADP-ribose] polymerase (EC 2.4, 2.30) (PARP) (ADPRT) (NAD(+) ADP-ribosyltransferase) (Poly[ADP-ribose] synthetase) (Fragment).
                                                                                                                                                                                                                                                                                                     :|||:::|||||| | :|||||| | 475
                                                                                                                                                                                                                                                                                                                                                                                                                     296 IPHDFGLRTPPLIRTQKELSEKIQLLEAL-GDIEIAIKLVKTELQSPEHPLDQH-YRNLH 353
                                                                                                                                                                                                 246 IPHSFGFCVPPKIDSHAKIQAERELLDALKGSIEASLELKDLKKTASSKDIYQRLYERLP 305
                                                                                                                                                                                                                                                        CHLEPVSEE-----IAGKIGDCLAMRGPTHC-YKLSLIDAFELKDPNEIPTEAPVEVQE 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       poly(ADP-ribose)
                   | ::||: ||: ||:|| || || || || || DCLSLAQLTTGYEILSKIEESIGGKSARRSTRGRPRVADRVLAVKSDGPSLHDINKYYSL
                                                                                                                                                                                                                                                                                                                                                                                                     GKMAPSSAHFVTLNGSTVPLGPASDTGILNPDGYT-LNYNEYIVYNPNQVRMRYLLKVQF
                                                        ---SLKSPLKPESQLDLRVQELIKLICNVQAMEEMMMEMKYNTK-KAPL
                                                                                                                 --ALMEACNEFYTR
                                                                          TRGRKKRGIVKEKKEIKKEEEPVEEVNEKLKELMKCICDEDVHLGLLKQLKFNEAFGRPI
                                                                                                                                                                                                                                                                                      --KEAFREDLH-----NRMLLWHGSRMSNWVGILSHGLRIAPPEAPITGYMFGKG
                                                                                                                                                                                                                                                                                                                                              IYFADMSSKSANYCFASRLKNTGLLLLSEVALGQCNELLEANPKAEGLLQ--GKHSTKGL
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ozawa Y., Uchida K., Uchida M., Ami Y., Kushida S., Okada N.,
  162 IFQKKFLDKTKNNWEDREKFEKVPGKYDMLQMDYATNT-QDEEETKKEE---
                                                                                                                                                                                                                               CALRPLDHESYEFKVISQYL - - QSTHAPTHSDYTMTLLDLFEVEKDGE - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Isolation of cDNAs encoding the catalytic domain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 AA
                                                                                                                GKLTVAQIKAGYQSLKKIEDCI-----RAGQHGR-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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Q08824;
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PPOL_ONCMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                      KLVKTELQSPE---HPLDQHYRNLHCALRPLDHESYEFKVISQYLQSTHAPTHSDYTMTL 388
                                                                                                             LDLFEVEKDGEKEAFR--EDLHNRMLLWHGSRMSNWVGILSHGLRIAPPEAPITGYMFGK 446
                                                                                                                                           411
                                                                                                                                                                                                                            LGKMAPSSAHFVTLNGSTVPLGPASDT-----GILNPDGY-----TLNYNEYI 547
                                                                                                                                                                                                                                               --KSPPPGFDSVIARGHTEP-DPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYL 516
                                                                                                                                                                       GIYFADMSSKSANYCFASR--LKNTGLLLLSEVALGQCNELLEANPKAEGLLQGKHSTKG 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YDVMLNQTNLQFNNNKYYLIQLLEDDAQRNFSVWMRWGRVGKMGQHSLVACSGNLNKAKE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
275 CIRA-GQHGRALMEACNEFYTRIPHDFGLRTPPLIRTQKELSEKIQLLEALGDIEI--AI
                QHIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPH----SGGRVGK
                                                                                                                                                                                       100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.5%; Score 526; DB 1; Length 538;
.larity 29.1%; Pred. No. 3.5e-27;
Conservative 103; Mismatches 182; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: SOME, TO THE MIDDLE PART OF NAD(+) ADP-RIBOSYLTRANSFERASE (EC 2.4.2.30).
                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Hypothetical 61.3 kDa protein E02H1.4 in chromosome II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61268 MW; 3144E25465FC7341 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      538 AA
                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WormPep; E02H1.4; CE01539.
InterPro; IPR001290; PARP.
InterPro; IPR004102; PARP_reg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; 247075; CAA87379.1; -. HSSP; P26446; 1A26.
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Pfam; PF02877; PARP_reg; 1.
                                                                                                                                                                                                                                                                                   548 VYNPNQVRMRYLLKV 562
                                                                                                                                                                                                                                                                                                                531
                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans
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517 IYQESQCRLRYLLEV
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538 AA; 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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SEQUENCE 53
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Local Sr
158;
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Matches
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YON4_CAEEL
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CC -1- MISCELLANBOUS: THE ADP-D-RIBOSYL GROUP OR ADD(+) IS TRANSFERED TO CX AN ACCESTOR CARBOXYL GROUP ON A HISTONE OR THE ENZYME ITSELF, AND FURTHER ADP-RIBOSYL GROUPS ARE TRANSFERED TO THE ENZYME ITSELF, AND FURTHER ADP-RIBOSYL GROUPS ARE TRANSFERED TO THE 2'-POSITION OF THE SMISS INSTITUTE OF DELWARD TO THE PARP FAMILY.

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Search completed: August 29, 2002, 08:02:11 Job time: 288 sec

317 KIQLLEALGDIEIAIKLVKTELQ-SPEHPLDQHYRNLHCALRPLDHESYEFKVISQYLQS 375

434 PPEAPITGYMFGK 446 ||||||:||||||| 123 PPEAPVTGYMFGK 135

Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Database

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Q9txql caenorhabdi
O55721 chilo iride
Q95710 macaca fasc
Q9571 homo sapien
Q9x0r4 thermotoga
Q9xxt2 caenorhabdi
Q9ahk9 borrelia bu
Q27421 drosophila
Q9xx37 drosophila
                                                                                               094bp3 drosophila
091ax2 streptococc
091ax5 streptococc
040546 mycoplasma
049524 mycoplasma
049525 mycoplasma
04952 mycoplasma
09ahk6 borrelia bu
09ahk8 borrelia bu
09bk46 plasmodium
09bk46 plasmodium
09bk47 homo sapien
09517 homo sapien
09547 homo sapien
09h2k2 homo sapien
09h2k2 homo sapien
09h2k2 homo sapien
09h2k2 homo sapien
09h2k3 homo sapien
09h2k3 domo sapien
09h2k3 domo sapien
 Q9swb4 qlycine max
                                                                                                                                                                                                                                                                                                                                                                     081294 PRELIMINARY; PRT; 635 AA.
081294:
01.NOV-1998 (TrEMBLrel. 08, Created)
01.NOV-1998 (TrEMBLrel. 08, Last sequence update)
01.DEC-2001 (TrEMBLrel. 19, Last annotation update)
114P8-19 PROTEIN (NDH-ADP-RIBOSYLTRANSFERASE).
114P8-19 OR AT4G02390.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lamar B., Stoneking T., Stumpf J., Mewes H.W., Lemcke K., Mayer K.F.X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
Kalicki J., Elliott G., Cloud J.;
"The sequence of A. thaliana T14P8.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
Waterston R.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The A. thaliana Genome Sequencing Project.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
        Q9TXQ1
O55721
Q95JR0
O95271
Q9X0R4
Q95XK2
                                                                             09X237
09X237
09LAXD
09LAXD
049546
049546
049555
09AHKI
099HK4
099HX7
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SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
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SEQUENCE FROM N.A.
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RESULT
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0921k2 mus musculu
092k06 dictyosteli
095k06 dictyosteli
095p81 xenopus. na
092k05 arabidopsis
095jw4 arabidopsis
024570 zea mays (m
024570 zea mays (m
02444 caenorhabdi
0914yf mus musculu
0914yf mus musculu
091yf mus musculu
092ua5 caenorhabdi
095ua5 caenorhabdi
                                                                August 29, 2002, 07:55:28; Search time 117.38 Seconds (without alignments) 840.067 Million cell updates/sec
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O50017 zea mays (m
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                                                                                                                                 1 MAARRRSTGGGRARALNES......PNQVRMRYLLKVQFNFLQLW
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        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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09PS81
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0921K2
09TX06
09TX06
09TX05
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024574
09SW1
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091YR6
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Gapop 10.0 , Gapext 0.5
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sp_invertebrate:*
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NCBI_TaxID=4577;
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                          EDDNNGFEEEKKEEKIVTATKKGAAVLDQWIPDEIKSQYHVLQRGDDVYDAILNQTNVRD 178
                                                                                                                                                                                                                                                      NNNKYYLIQLLEDDAQRNFSVWMRWGRVGKMGQHSLVACSGNLNKAKEIFQKKFLDKTKN 173
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                                                                                                                                                                                                                                                                                                                               CNVQAMEEMMMEMKYNTKKAPLGKLTVAQIKAGYQSLKKIEDCIRAGQHGRALMEACNEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NWEDREKFEKVPGKYDMLOMDYATNTQDEEETKKEESLKSPLKPE-SQLDLRVQELIKLI
                                                                                                                                         Length 635;
                                                                                                                                                            Indels
(MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                             635 AA; 72017 MW; E3F1CBE4D367A377 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) POLY(ADP-RIBOSE) POLYMERASE.
                                                                                                                                        39.2%; Score 1176; DB 10; 43.9%; Pred. No. 5.7e-74;
                                                                                                                                                          98; Mismatches 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       528 ASDIGILNPDGYTLNYNEYIVYNPNQVRMRYLLKVQFNF 566
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     EMBL, AF06928; AAC19283.1; --
EMBL, AL161494; CAB80732.1; --
EMBL, AL161494; CAB80732.1; --
EMBL, P26446; 1A26.
InterPro; IPR001290; PARP.
InterPro; IPR001304; SAP.
Fam; PF02444; PARP; 1.
Fam; PF02877; PARP_reg; 1.
Fam; PF02877; PARP; 2.
Transferase.
SEQUENCE 635 AA; 72017 MW; E3
                                                                                                                                                 Best_Local Similarity 43.9%
Matches 254; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268 NFKCYAKKYTWLEMDYG-----ETEKEIEKGSITDQIK-ETKLETRIAQFISLICNIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIQLLEDDAQRNFSVWMRWGRVGKMGQHSLVACSGNLNKAKEIFQKKFLDKTKNNWEDRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 KFEKVPGKYDMLQMDYATNTQDEEETKKE---ESLKSPLKPESQLDLRVQELIKLICNVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHDFGLRTPP--LIRTQKELSEKIQLLEALGDIEIAIKLVKTELQSPEHPLDQHYRNLHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              355 ALRPLDHESYEFKVISQYLQSTHAPTHSDYTMTLLDLFEVEKDGEKEAFRE--DLHNRML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LWHGSRMSNWVGILSHGLRIAPPEAPITGYMFGKGIYFADMSSKSANYCFASRLKNTGLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45;
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 653;
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Babylchuk E., Cottrill P., Storozhenko S., Fuangthong M.,
O'Farrell M., Van Montagu M., Inze D., Kushnir S.;
"Higher plants possess two poly(ADP-ribose) polymerases.";
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ222588; CAA10888.1; -.
HSSP; P26446; 1A26.
                                                                                                                                                                                                                                                                                                                                                                                                                 38.3%; Score 1149.5; DB 10; Length 44.0%; Pred. No. 4.2e-72; Live 89; Mismatches 191; Indels
                                                                                                                                                                                                                                                                                                                                            5FD01923C4ABCD1D CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NAD+: PROYETN(ADP-RIBOSYL)-TRANSFERASE, ADPRT.
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                InterPro; IPR001290; PARP.
InterPro; IPR0011290; PARP_reg.
InterPro; IPR003044; SAP.
Pfam; PF008044; PARP, 1.
Pfam; PF02877; PARP_reg; 1.
SMART; SMO0137; SAP; 2.
SMART; SMO0133; SAP; 2.
SEQUENCE 653 AA; 72995 MW; 51
                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 44.0%
Matches 255; Conservative
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m

15;

Length 1014;

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Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                         Query Match 34.0%; Score 1018; DB 11; Length 1
Best Local Similarity 41.0%; Pred. No. 1.2e-62;
Matches 227; Conservative 106; Mismatches 176; Indels
                                                                                                                                                   SDCE68E4CB3F46EB CRC64;
                                                                                              Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012041; AAH12041.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                   1014 AA; 112721 MW;
                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    559 LLKVQFNF-LQLW 570
               musculus (Mouse).
                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=44689;
                                                                                                                                     Transferase.
SEQUENCE 1
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                                                             MEDLINE-96007847; PubMed=7578427;
MEDLINE-96007847; PubMed=7578427;
Medlar B., Filck K., Wang Z.Q., Haidacher D., Jager S., Berghammer H.,
Kofler B., Schweiger M., Wagner E.F.;
"On the biological role of the nuclear polymerizing NAD+: protein(ADP-
ribosyl) transferase (ADPRT): ADPRT from Dictyostellum discoideum and
lnactivation of the ADPRT gene in the mouse.";
Biochimie 77:44449(1995).
HSSP: P26446: 1A26.
InterPro: IPR001299; PARP.
InterPro: IPR001299; PARP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          281 HGRALMEACNEFYTRIPHDFGLRTPPLIRTQKELSEKIQLLEALGDIEIAIKLVK-TELQ 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             340 SPEHPLDOHYRNLHCALRPLDHESYEFKVISQYLQSTHAPTHSDYTMTLLDLFEVEKDGE 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQRYKPFKQLHNRQLLWHGSRTTNFAGILSQGLRIAPPEAPVTGYMFGKGIYFRDMVSKS 497
                                                                                                                                                                                                                                                                                                                                                                               41 RCQRQESKKMPVAGGKANKDRTEDKQDESVKALLLKGKAPVDPECTAKVGKAHVYCEGND 100
                                                                                                                                                                                                                                                                                                                                                                                                                                   101 VYDVMLNQTNLQFNNNKYYLIQLLEDDAQRNFSVWMRWGRVGKMGQHSLVACSGNLNKAK 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                   400 KEAFR--EDLHNRMLLWHGSRMSNWVGILSHGLRIAPPEAPITGYMFGKGIYFADMSSKS 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            458 ANYCFASRLKNTGLILLSEVALGOCNELLEANPKAEGLLOGKHSTKGLGKMAPSSAHFVT 517
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||| |: ||:|| ||||| || || || || ANYCHTSQADPIGLILIGEVALGNNYELKNASHITK-LPKGKHSVKGLGKTAPDPTATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EIFQKKFLDKTKNNWEDREKFEKVPGKYDMLQMDYATNTQDEEETKKEESLKSPLKPESQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO ADP-RIBOSYLTRANSFERASE (NAD+, POLY (ADP-RIBOSE)
                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                             501/2; BKCT; 1.
607 AA; 68033 MW; 75F6EEID30D8F402 CRC64;
                                                                                                                                                                                                                                                                                                                        Score 1022; DB 13;
Pred. No. 3.1e-63;
); Mismatches 187;
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                                                                                                                                                                                                                                                                                                                                                     Matches 217; Conservative 110;
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Pfam; PF0053; BRCT; 1.
Pfam; PF00644; PARP; 1.
Pfam; PF02877; PARP_reg; 1.
PROSITE; PSS0172; BRCT; 1.
SEQUENCE 607 AA: 64072 ...
                                                                                                                                                                                                                                                                                                                          34.1%;
40.6%;
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Q921K2
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                                                                                                                                                                                                                                                                                                                                653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       502 TKGLGKMAPSSAHFVTLNGSTVPLGPASDTGILNPDGYT---LNYNEYIVYNPNQVRMRY 558
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                      207 KEESLKSPLKP--ESQLDLRVQELIKLICNVQAMEEMMMEMKYNTKKAPLGKLTVAQIKA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GYQSLKKIEDCIRAGQHGRALMEACNEFYTRIPHDFGLRTPPLIRTQKELSEKIQLLEAL 324
                                                   29 APEDSS--PAKKTRRCQRQESKKMPVAGGKANKDRTEDKQDESVKALLLKGKAPVDPECT 86
                                                                                                                                                                                                                                                                                                            SNKLEQMPSKEDAVEHFWKLYEEKTGNAWHSK-NFTKYPKKFYPLEIDYG---QDEEAVK
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                                                                                                                                                                                                                                                                            147 HSLVACSGNLNKAKEIFQKKFLDKTKNNWEDREKFEKVPGKYDMLQMDYATNTQDEEETK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YTMTLLDLFEVEKDGEKEAFR - - EDLHNRMLLWHGSRMSNWVGILSHGLRIAPPEAPITG
44;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DE-2001 (TrEMBLrel 19, Last annotation update)
NAD+:PROTEIN(ADP-RIBOSYL)-TRANSFERASE (EC 2.4.2.30).
Dictyostellum discoideum (Slime mold).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
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MEDLINE=96007847; PubMed=7578427;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                       16;
Auer B., Flick K., Wang Z.Q., Haidacher D., Jager S., Berghammer H., Kofler B., Schweiger M., Wagner E.F.;
"On the biological role of the nuclear polymerizing NAD+: protein(ADP-ribosyl) transferase (ADPRT): ADPRT from Dictyostelium discoideum and inactivation of the ADPRT gene in the mouse.";
HSSP: P26446; 1AA5.
InterPro; IPR001290; PARP.
InterPro; IPR004102; PARP.
Pfam; PF00644; PARP. 1.
SEQUENCE 612 AA; 69241 MW; CB340F7A88FF2364 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RTEDKQDE-SVKALLLKGKAPVDPECTAKVGKAHVYCEGNDVYDVMLNQTNLQFNNNKYY 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIQLLEDDAQRNFSVWMRWGRVGKMGQHSLVAC-SGNLNKAKEIFQKKFLDKTKNNWEDR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKFEKVPGKYDMLQMDYATNTQDE---EETKKEESLKSPL--KPESQLDLRVQELIKLIC 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TDIQPLDENSCEYKNILLYVKNTY---QGGKKPTIVNIFKIDRDGEADRYKTKKHLGNRK 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAKPTRRSSKKAPAKSEEKGEDKNKLTT-----RPTKKTKTNTSEAETKTAASDLDDSSS 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                354 CALRPLDHESYEFKVISQYLQSTHAPTHSDYTMTLLDLFEVEKDGEKEAFREDLH--NRM 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLWHGSRMSNWVGILSHGLRIAPPEAPITGYMFGKGIYFADMSSKSANYCFASRLKNTGL 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L----LLSEVALGQCNELLEANPKAEGLLQGKHSTKGLGKMAPS-SAHFVTLNGSTVPL 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAARRRSTGGGRARALNESKRVNNGNTAPEDSSPAKKTRRCQRQESKKMPVAGGKANKD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRIPHDFGLRTPPLIRTQKELSEKIQLLEALGDIEIAIKLVKTELQSPEHPLDQHYRNLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                Query Match 33.0%; Score 988; DB 5; Length 612; Best Local Similarity 39.6%; Pred. No. 7.4e-61; Matches 230; Conservative 100; Mismatches 207; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NAD+:PROTEIN(ADP-RIBOSYL)-TRANSFERASE, ADPRT.
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01-WAY-2000 (TrEMBLrel. 13, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
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MEDLINE-96007847; PubMed=7578427;
Auer B., Flick K., Wang Z.Q., Haidacher D., Jager S., Berghammer H.,
Kofler B., Schweiger M., Wagner E.F.;
"On the biological role of the nuclear polymerizing NAD+: protein(ADP-
ribosyl) transferase (ADPRT): ADPRT from Dictyostelium discoideum and
inactivation of the ADPRT gene in the mouse.";
Biochimie 77:444-449(1995).
HSSP: P26446; 1A26
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Drosophila sp. (Fruit fly).
Eukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bphydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 QTNLQFNNNKYYLIQLLEDDAQRNFSVWMRWGRVGK-MGQHSLVACSGNLNKAKEIFQKK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELIKLICNVQAMEEMMMEMKYNTKKAPLGKLTVAQIKAGYQSLKKIEDCIRAGQHGRALM 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 ELIKLIFDVESMKKAMVEFEIDLQKMPLGKLSKRQIQSAYSILSQVQQAVSESLSEARLL 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     287 EACNEFYTRIPHDFGLRTPPLIRTQKELSEKIQLLEALGDIEIAIKLVKTELQSPE-HPL 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             464 SRLKNTGLLLLSEVALGQCNELLEANPKAEGLLQGKHSTKGLGKMAPSSAHFVTLNGSTV 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 PVAG---GKANKDRTEDKQDESVKALLLKGKAPVDPECTAKVGKAHVYCEGNDVYDVMLN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210 YQDKTGNAWHS-PNFTKYPKKFYPLEIDYG---QEEDVVKK---LSVGAGTKSKLAKPVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 LVDITRGTNSYYKLQLIEHDRDSRYWVFRSWGRVGTVIGSKKLEEMSSK-EDAIEHFLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DQHYRNLHCALRPLDHESYEFKVISQYLQSTHAPTHSDYTMTLLDLFEVEKDGEKEAFR-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 FLDKTKNNWEDREKFEKVPGKYDMLQMDYATNTQDEEETKKEESLKSPLKPESQLDLRVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54CDEBBE22079886 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.7%; Score 981.5; DB 13;
Local Similarity 40.9%; Pred. No. 2.1e-60;
Les 216; Conservative 101; Mismatches 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67496 MW;
                                                                                                                                                                                                                                                           InterPro; IPR001357; BRCT.
InterPro; IPR001290; PARP.
InterPro; IPR004102; PARP_reg.
                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00644; PARP; 1.
Pfam; PF02877; PARP_reg; 1.
PROSITE; PS50172; BRCT; 1.
SEQUENCE 607 AA; 67496 MW
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271
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105 MLNQTNLQFNNNKYYLIQLLEDDAQRNFSVWMRWGRVG--KMGQHSLVACSGNLNKAKEI 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----FQKKFLDKTKNNWEDREK---FEKVPGKYDMLQMDYATNTQDEEETKKEESL 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              442 YMFGKGIYFADMSSKSANYCFASRLKNTGLLLLSEVALGQCNELLEAN-----PKAEGLL 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        497 QGKHSTKGLGKMAPSSAHFVTLNGS-TVPLGPASDTGILNPDGYTLNYNEYIVYNPNQVR 555
                                                                                                                                                                                                                                                                                                                                                                                                               45 QESKKMPVAGGKANKDRTEDKQDESVKALLLKGKAPVDPECTAKVGKAHVYCEGNDVYDV 104
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    212 KSPLKPESQLDLRVQELIKLICNVQAMEEMMMEMKYNTKKAPLGKLTVAQIKAGYQSLKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       385 IMTLLDLFEVEKDGEKEAF---REDLHNRMLLWHGSRMSNWVGILSHGLRIAPPEAPITG
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                                                                                                                                                                                                                                                                                                                                                                         Matches 213; Conservative 115; Mismatches 151; Indels
                                                                                                                                                                                                                                      Transferase; Glycosyltransferase; NAD.
CHAIN 2 983 POLY(ADP-RIBOSE) POLYMERASE.
SEQUENCE 983 AA; 111232 MW; 468E12A8EF1B6F4F CRC64;
                                                                                                                                                                                  databases
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE POLY (ADP-RIBOSE) POLYMERASE.
AT2G31320.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                    32.2%; Score 966; DB 10; 38.8%; Pred. No. 4.8e-59;
                                                                                                                       SEQUENCE FROM N.A.
STRAIN-CV. LANDSBERG ERECTA;
Doucet-chabeaud G., Kazmaier M.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ (BELE, All31705; CAAl0482.1; -.
HSSP; P26446; 1A26.
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             Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     556 MRYLLKVQF 564
                                                                                      NCBI_TaxID=3702
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LQFLLKVRF
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                     MEDLINE-96007847; PubMed=7578427;
A Auer B., Flick K., Wang Z.Q., Haidacher D., Jager S., Berghammer H.,
A Rofler B., Schweiger M., Wagner E.F.;
A not the bloological role of the nuclear polymerizing NaD+: protein(ADP-
Tibosyl) transferase (ADPRT): ADPRT from Dicryostelium discoideum and
Inscrivation of the ADPRT gene in the mouse.";
Blochimie 77:444.449(1995).
R InterPro; IPR001290; PRRP.
R InterPro; IPR001290; PRRP.
R InterPro; IPR004102; PRRP.
R InterPro; IPR004102; PRRP.
R Pfam; PF00533; BRCT; 1.
R Pfam; PF00544; PARP.; 1.
R Pfam; PF00544; PARP.; 1.
R PGNITE; PS50172; BRCT; 1.
R PROSITE; PS50172; BRCT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 VKALLLKGKAPVDPECTAKVGKAHVYCEGNDVYDVMLNQTNLQFNNNKYYLIQLLEDDAQ 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 RNFSVWMRWGRVGKMGQHSLVACSGNLNKAKEIFQKKFLDKTKNNWEDREKFEKVPGKYD 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 MLQMDYATNTQDEEETKKEESLKSPLKPESQLDLRVQELIKLICNVQAMEEMMMEMKYNT 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKAPLGKLTVAQIKAGYQSLKKIEDCIRAGQHGRALMEACNEFYTRIPHDFGLRTPPLIR 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310 TQKELSEKIQLLEALGDIEIAIKLVKTE-LQSPEHPLDQHYRNLHCALRPLDHESYEFKV 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      369 ISQYLQSTHAPTHSDYTMTLLDLFEVEKDGE--KEAFREDLHNRMLLWHGSRMSNWVGIL 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :|||:::||| || | : ::|:|:|| | : LOYVKNTHASTHKSYDLKIVDVFKVSRQGEARREKPFKKLHNRKLLAHGSRLTNFVGIL 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHGLRIAPPEAPITGYMFGKGIYFADMSSKSANYCFASRLKNTGLLLLSEVALGQCNELL 486
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092P54;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-DEC-2001 (TEMBLrel. 19, Last sequence update)
01-DEC-2001 (TEMBLrel. 19, Last annotation update)
POLY(ADP-RIBOSE) POLYMERASE (EC 2.4.2.30).
                                                                                                                                                                                                                                                                                                                                                                   Query Match 32.4%; Score 972.5; DB 5; Best Local Similarity 38.3%; Pred. No. 8.6e-60; Matches 215; Conservative 110; Mismatches 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      546 YIVYNPNQVRMRYLLKVQFNF 566
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Query Match
32.1%; Score 961.5;
Best Local Similarity 39.3%; Pred. No. 9.8e
Matches 223; Conservative 104; Mismatches
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InterPro; IPR001280; PARP.
InterPro; IPR004102; PARP.
InterPro; IPR003034; SAP.
InterPro; IPR001510; Znf-PARP.
Pfam; PF00533; BRCT; 1.
Pfam; PF00644; PARP; 1.
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997 LQFLLKVRF 1005
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                                                                         STRAIN=CV. COLUMBIA;
MEDLINE=20083487; PubMed=10617197;
MEDLINE=20083487; PubMed=10617197;
MEDLINE=20083487; PubMed=10617197;
MEDLINE=20083487; PubMed=10.2., Shean T.B., Shen M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Gronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adms M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
*Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 MLNQTNLQFNNNKYYLIQLLEDDAQRNFSVWMRWGRVG--KMGQHSLVACSGNLNKAKEI 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              441
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 QESKKMPVAGGKANKDRTEDKQDESVKALLLKGKAPVDPECTAKVGKAHVYCEGNDVYDV 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----FQKKFLDKTKNNWEDREK---FEKVPGKYDMLQMDYATNTQDEEETKKEESL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KSPLKPESQLDLRVQELIKLICNVQAMEEMMEMKYNTKKAPLGKLTVAQIKAGYQSLKK 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IEDCI-----RAGQHGRALMEACNEFYTRIP--HDFGLRTPPLIRTQKELSEKIQLLEAL 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   442 YMFGKGIYFADMSSKSANYCFASRLKNTGLLLLSEVALGQCNELLEAN-----PKAEGLL 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |::||:|| || || || || SKSDAVHEFRRLFLEKTGNTWESWEQKTNFQKQPGKFLPLDIDYGVN------KQVAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDIETAIKLVKTELQSPEHPLDQHYRNLHCALRPLDHESYEFKVISQYLQSTHAPTHSDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 32.2%; Score 966; DB 10; Length 1009; Best Local Similarity 38.8%; Pred. No. 5e-59; Matches 213; Conservative 115; Mismatches 151; Indels 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50172; BRCT; 1.
PROSITE; PS50064; PARP_ZN_FINGER_2; 2.
SEQUENCE 1009 AA; 114133 MW; CDE6E41CC2A3A2DB CRC64;
                                                                                                                                                                                                                                                                                              Lin X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC006593; AAD20677.1; -.
HSSP; P26446; 1A26.
                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00533; BRCT; 1.
Pfam; PF00644; PARP; 1.
Pfam; PF02877; PARP_reg; 1.
Pfam; PF00645; zf-PARP; 2.
Probom; PD004675; znf-PARP; 2.
SMART; SM00292; BRCT; 1.
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Interpro; IPR001390; PARP.
InterPro; IPR004102; PARP.reg.
InterPro; IPR001510; Znf-PARP.
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                                                                    SEQUENCE FROM N.A.
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Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
                             76 KGKAPVDPECTAKVGKAHVYCEGNDVYDVMLNQTNLQFNNNKYYLIQLLEDDAQRNFSVW 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 MRWGRVG--KMGQHSLVACSGNLNKAKEIFQKKFLDKTKNNWEDRE---KFEKVPGKYDM 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                251 KAPLGKLTVAQIKAGYQSLKKIEDCIR-AGQHGRALME----ACNEFYTRIP--HDFGL 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ::: :| || : : | | : : 428 ENAEVRKARRL-----KIPIVREGYIGECVKKNKMLPFDLYKLENALESSKGSTVTVKV 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32 DSSPAKKTRRCQRQESKKMPVAGG-----KANK------DRTEDKQDESVKALLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S41 RKWGRVGSEKIGGQKLEEMS--KTEAIKEFKRLFLEKTGNSWEAWECKTNFRKQPGRFYP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61;
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Pfam; PF00645; 2. PARP; 2.
Probom; PR0064575; Znf-PARP; 2.
SMART; SM00292; BRCT; 1.
PROSTIE; PS50172; BRCT; 1.
PROSTIE; PS500172; BRCT; 1.
SROUENCE 969 AA; 109128 MW; EB23AC62EEC14009 CRC64;
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Last annotation update)
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.8e-59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15,
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Q9N4H4;
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Mahajan P.B., Zuo Z.;
Marajan P.B., Zuo Z.;
Marajan Physiol. 118:895-9051989.
EMBL; AF093627; AAC79704.1; -..
HSSP; P56446; 1A26.
InterPro; IPR001357; BRCT.
InterPro; IPR001290; PARP.
InterPro; IPR004102; PARP.
InterPro; IPR004102; PARP.
                 -- PHIIRDEDDLMIKAKMLEALQDIEIASKIVGFDSDSDE-SLDDKYMKLHCDITPLAHD 763
                                                         SYEFKVISQYLQSTHAPTHSDYTMTLLDLFEVEKDGE---KEAFREDLHNRMLLWHGSRM 419
                                                                         SNWVGILSHGLRIAPPEAPITGYMFGKGIYFADMSSKSANYCFASRLKNTGLLLLSEVAL 479
                                                                                                                                                                                                KGKAPVDPECTAKVGKAHVYCEGNDVYDVMLNQTNLQFNNNKYYLIQLLEDDAQRNFSVW 135
RTPPLIRTQKELSEKIQLLEALGDIEIAIKLVKTELQSPEHPLDQHYRNLHCALRPLDHE 362
                                                                                                                                                  TNFVGILSQGLRIAPPEAPVTGYMFGKGLYFADLVSKSAQYCYVDRNNPVGLMLLSEVAL 883
                                                                                                                                                                              GQCNELLEANPKAEGLLQGKHSTKGLGKMAPSSAHFVTLNGS-TVPLGPASDTGILNPDG 538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC cl
Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9D8AED26BC37E5C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
POLY(ADP)-RIBOSE POLYMERASE (EC 2.4.2.30).
                                                                                                                                                                                                                                                                                                                                                       980 AA
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SMART; SM00292; BRCT; 1.
PROSITE; PS50172; BRCT; 1.
PROSITE; PS50064; PARE_ZN_FINGER_2; 2.
Transferase; Glycosyltransferase.
Transferase 480 Aa; 110475 WW; 9D8AED
                                                                                                                                                                                                                                           539 YTLNYNEYIVYNPNQVRMRYLLKVQFN 565
                                                                                                                                                                                                                                                         --LMYNEYIVYNTSQVKMQFLLKVRFH 966
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InterPro; IPR001510; Znf-PARP.
Pfam; PF00533; BRCT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02877; PARP_reg; 1.
Pfam; PF00645; zf-PARP; 2.
ProDom; PD004675; znf-PARP; 2.
                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF00644; PARP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zea mays (Maize)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                  092SV1:
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                                                                                                                                                                                                                                                                                                                     RESULT 11
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MRWGRVG--KMGQHSLVACSGNLNKAKEIFQKKFLDKTKNNWEDRE---KFEKVPGKYDM 190
                                                                                         661
                                                                                                                       251 KAPLGKLTVAQIKAGYQSLKKIEDCIR-AGQHGRALME----ACNEFYTRIP--HDFGL 302
                                                                                                                                                                                  362
                                                                                                                                                                                                                 774
                                                                                                                                                                                                                                               SYEFKVISOYLOSTHAPTHSDYTMTLLDLFEVEKDGE---KEAFREDLHNRMLLWHGSRM 419
                                                                                                                                                                                                                                                                              834
                                                                                                                                                                                                                                                                                                             479
                                                                                                                                                                                                                                                                                                                                                                                                          895 GDMYELKKAT-SMDKPPRGKHSTKGLGKTVPLESEFVKWRDDVVVPCGKPVPSSIRSSE- 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhabditida; Rhabditoidea;
                 : ||||||: |: |: |::| :| :| :
EMPLGKLSKENIEKGFEALTEIQNLLKDTADQALAVRESLIVAASNRFFTLIPSIH----
                                                                                                                                                                                  303 RTPPLIRTQKELSEKIQLLEALGDIEIAIKLVKTELQSPEHPLDQHYRNLHCALRPLDHE
                                                                                                                                                                                                    GQCNELLEANPKAEGLLQGKHSTKGLGKMAPSSAHFVTLNGS-TVPLGPASDTGILNPDG
                                                           191 LQMDYATNTQDEEETKKEESLKSPLKPESQLDLRVQELIKLICNVQAMEEMMMEMKYNTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (SEP-2001), to the EMBL/GenBank/DDBJ databases.
EMBL; AC034200; AAF36011.1; -.
HSSP; P56446; 1A26.
InterPro; IPR001290; PARP.
InterPro; IPR001510; Znf-PARP.
Pfam; PF00644; PARR; 1.
Probom; PF00645; Zf-PARR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bradshaw-Cordum H., Scott K., Graves T.;
"The sequence of C. elegans cosmid Y71F9AL.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   945
                                                                                                                                                                                                                                                                                                                                                                                                                                        539 YTLNYNEYIVYNPNQVRMRYLLKVQFN 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                     953 -- LMYNEYIVYNTSQVKMQFLLKVRFH 977
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35.0%;

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Matches 194; Conservative
            Best Local Similarity
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Best Local Simi
Matches 184;
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0911R6
AC 0917R6
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DT 01-DEC
DT 01-DEC
DC MARMAN
OC BUKATY
OC MARMAN
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ON NOBL T
RN [1]
RN [1]
RN SEDUEN
RA SETAUN
RA SETAUN
RA SUBMIT
NOBL SHELL;
NOBL S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    860 SKNVSRQTLPAGFQSVQGLGRQCPREIGSYNHPDGYTIPLG----LTYMQLQGKQDVDYH 915
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 409 KRKSKGGTRGEQFIYAAEA----FDSTNNVPIKVGDLTSTNTH------IIKKGTV 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VDPECTAKVGKAHVYCEGND -- VYDVMLNQTNLQFNNNKYYLLQLLEDDAQRNFSVWMRW 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139 GRVG-KMGQHSLVACSGNLNKAKEIFQKKFLDKTKNNWEDREKFEKVPGKYDMLQMDYAT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198 NTQ--DEEETKKEESLKSPLKPESQLDLRVQELIKLICNVQAMEEMMMEMKYNTKKAPLG 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          256 KLTVAQIKAGYQSLKKIED-CIRAGQHGRALMEACNEFYTRIPHDFGLRTPPLIRTQKEL 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEKIQLLEALGDIEIAIKLV-----KTELQSPEHPLDQHYRNLHCALRPLDHESYEFK 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VISQYLQSTHAPTHSDYTMTLLDLFEVEKDGEKEAFREDLHNRMLLWHGSRMSNWVGILS 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    428 HGLRIAPPEAPITGYMFGKGIYFADMSSKSANYCFASRLKNTGLLLLSEVALGQCNELLE 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             488 A-NPKAEGLLQGKHSTKGLGKMAPSS-AHFVTLNGSTVPLGPASDTGILNPDG----YT 540
                                                                                                                                                                                                                                                                                                                                                                   21 KRVNNGNTAPEDSSPAKKTRRCQRQESKKMPVAGGKANKDRTEDKQDESVKALLLKGKAP 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                        53;
                                                                                                                                                                                                          Length 945;
                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL, RC014260; AAH14260.1; -. Hypothetical protein. SEQUENCE 533 AA; 60089 MW; 6296A0E439CC7767 CRC64;
                                                                                      1D0A62C954BC6AD9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 60.1 KDA PROTEIN.
                                                                                                                                                                                                      Query Match 25.9%; Score 777.5; DB 5; Best Local Similarity 34.7%; Pred. No. 6.8e-46; Matches 196; Conservative 103; Mismatches 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          533 AA
PROSITE; PS50064; PARP_ZN_FINGER_2; 1. Hypothetical protein. SEQUENCE 945 Aa; 108006 MW; 1D0A62
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DB 4; Length 533;

24.2%; Score 725;

Query Match

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17;
                     20;
                                                                                                                                                                                                                                                                          388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         299 QAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQTGS---NHRCPTL 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    411
                                                                 ESKKMPVAGGKANKDRTED----KQDESVKALLLKGK-APVDPECTAKVGK-AHVYCEGND 100
                                                                                                                                                       101 VYDVMLNQTNLQFNNNKYYLIQLLEDDAQRNFSVWMRWGRVGKMGQHSLVACSGNLNKAK 160
                                                                                                                                                                                 275 CIRA-GQHGRALMEACNEFYTRIPHDFGLRTPPLIRTQKELSEKIQLLEALGDIEI--AI 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 447 GIYFADMSSKSANYCFASR--LKNTGLLLSEVALGQCNELLEANPKAEGLLQGKHSTKG 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGKANKDRTEDKQDESVKALLLKGKAP-----VDPECTAKVGKAHVYCEGNDVYDVML 106
                       Gaps
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                                                                                                                                                                                                                                                                                                                                                              356 QHIWKVNQEGEEDREQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPH----SGGRVGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 EKKKGRQAG-----REEDPFRSTAEALKAIPAEKRIIRVDPTCPLSSNPGTQVY----E
                                                                                                                                                                                                                                                   161 EIFQKKFLDKTKNNWEDREKFEKVPGKYDMLQMDYATNTQDEEETKKEESLKSPLKPESQ
                                                                                                                                                                                                                                                                                                                                       221 -----LDLRVQELIKLICNVQAMEEMMMEMKYNTKKAPLGKLTVAQIKAGYQSLKKIED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    332 KLVKTELQSPE---HPLDQHYRNLHCALRPLDHESYEFKVISQYLQSTHAPTHSDYTMTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         505 LGKMAPSSAHFVTLNGSTVPLGPASDT-----GILNPDGY-----TLNYNEYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            389 LDLFEVEKDGEKEAFR--EDLHNRMLLWHGSRMSNWVGILSHGLRIAPPEAPITGYMFGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45;
                       16;
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                       Indels
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
; Pred. No. 1.5e-42; 97; Mismatches 188;
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Submitted (OCT-2001) to the EMB EMBL; BC014870; AAH14870.1; --
Hypothetical protein.
SEQUENCE 528 AA; 59413 MW;
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 NQTNLQFNNNKYYLIQLLEDDAQRNFSVWMRWGRVGKMGQHSL--VACSGNLNKAKEIFQ 164
                                                                                          225 VQELIKLICHVQAMEEMMMEMKYNTKKAPLGKLTVAQIKAGYQSLKKIEDCIR--AGQHG 282
                                                                                                                                        RALMEACNEFYTRIPHDFGLRTPPLIRTQKELSEKIQLLEALGDIEIAIKL-----VKT 336
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Caenorhabditis elegans.
Eukaryota: Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
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Science 282:2012-2018(1998).
EMBL: 283097; CAB05448.1; -.
HSSP; P26446; 1A26.
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16;

Gaps

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Query Match 22.9%; Score 685.5; DB 5; Best Local Similarity 31.1%; Pred. No. 1.3e-39; Matches 178; Conservative 110; Mismatches 220;

Length 727;

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303
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ESKRVNNGNTAPEDSSPAKKTRRCQRQESKKMPVAGGKANKDRTEDKQDESVKALLLKGK
                     RPLDHESYEFKVISQYLQSTHAPTHSDYTMTLLDLFEVEKDGEKEAFREDLHNRMLLWHG
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Human brain poly-A Human poly(ADP-rib The poly(ADP-ribos Human protein sequ A poly(ADP-ribose) Human poly (ADP-ri Human poly (ADP-ri Human PARP-1 prote

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Human brain PARP3	Human uterus type	Human PARP-3 prote	Murine PARP1 (shor	Murine PARP1 (long	Mouse PARP-2 prote	hPARP2, Homo sapi	Human ORFX ORF2673	Human PARP-2 prote	Human PARP-2 prote	Human brain PARP2
g:		AAY51176	AAU29021	AAY51178	AAY51177	AAU29022	AAB47029	AAB42909	AAU29023	AAU29020	AAY51174
BB :	21	21	22	21	21	22	22	21	22	22	21
% Query Match Length DB	533	540	533	528	533	522	583	534	534	534	570
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Score	2823	2823	2811	2253.5	2241	738	729.5	726.5	726.5	725.5	725
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Human brain poly-A Human poly(ADP-ribos Human protein seep Human protein protei	AALIGNMENTS AA. Se; human; murine; detection; sepsis; poptosis; neurodegenerative illness; Otterbach B, Lubisch W, Lemaire H; odies and binding partners useful in deficiency associated disease
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PARP; poly(ADP-ribose) polymerase; human; murine; detection; sepsis;
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                                           This invention describes novel human and murine poly(ADP-ribose)
polymerase (PARP) homologues, which are characterised by an amino acid
sequence with a functional NAD^+-binding site and no zinc finger
sequence moitf, of general formula CX_2CX_ZMHX_ZC (I). The nucleic acid
sequences, PARP homologues and antibodies are useful for analytic
detection of PARP homologues and for identifying PARP effectors or
binding partners, as well as for determining their effectiveness.
PARP-binding partners are useful for the diagnosis or therapy of a
disease condition, which may comprise tissue damage from cell death
centry deficiency, which may comprise tissue damage from cell death
following necrosis or apoptosis. The disease condition may be chosen
from a neurodegenerative illness, or sepsis or ischemic tissue damage,
in particular neurotoxic disturbances, etc. This sequence represents the
human PARP3 protein used in the method of the invention.
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                      Claim 4; Page 57-59; 96pp; German.
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Matches 533; Conservative
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This invention describes novel human and murine poly(ADP-ribose)
polymerase (PARP) homologues, which are characterised by an amino acid
sequence with a functional NAD^+-binding site and no zinc finger
sequence motif, of general formula Cx.2Cx_2Mx_2Cr.]. The nucleic acid
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detection of PARP homologues and for identifying PARP effectors or
binding partners as well as for determining their effectiveness.
C PARP-binding partners are useful for the diagnosis or therapy of a
disease condition, which is the result of a PARP protein, especially an
energy deficiency, which may comprise tissue damage from cell death
concrosis or apoptosis. The disease condition may be chosen
from a neurodegenerative illness, or sepsis or ischemic tissue damage,
in particular neurotoxic disturbances, etc. This sequence represents the
human PARP3 protein used in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel genes and proteins, antibodies and binding partners useful in diagnosis and therapy of energy deficiency associated disease
diagnosis; therapy; necrosis; apoptosis; neurodegenerative illness; ischemic tissue damage; PARP3.
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100.0%; Pred. No. 1.1e-249;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                             Otterbach B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 62-64; 96pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                               Kroeger B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.0%;
les 533; Conservative (
                                                                                                                                                                                                                                                                               98DE-1025213.
99DE-1008837.
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                                                                                Homo sapiens
                                                                                                                                                                                                                                04-JUN-1999;
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01-MAR-1999;
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Matches
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Human uterus type 2 PARP3 protein.

(first entry)

31-MAR-2000

XEXEX

AAY51176;

AAY51176 standard; Protein; 540

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Best Local Similarity 99.6
Matches 531; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to antisense oligonucleotides targeted to human PARP nucleic acid and inhibiting expression of human PARP. PARP PARP ply (ADP-ribose) polymerase plays an important role in chromatin decondensation, DNA replication, DNA repair, gene expression, malignant transformation, cellular differentiation and apoptosis. The antisense oligonucleotide inhibitors are useful for inhibiting the expression of PARP in human cells or tissues. They are also useful for treating a human with a disease associated with PARP especially hyperproliferative disorders (e.g. cancer), cellular injury resulting from oxidative stress, neurological (e.g parkinsonism, meningitis-associated intracranial complications and ischaemia), inflammatory and autoimmune disorders (e.g arthritis) and diabetes. The present sequence is a PARP protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic; nootropic; neuroprotective; antiinflammatory; antidiabetic; immunosuppressant; hyperproliferative disorder; cancer; cellular injury; oxidative stress; neurological disorder; parkinsonism; apoptosis; meningitis-associated intracranial complication; ischaemia; inflammatory disorder; autoimmune disorder; arthritis; diabetes.
                    420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polymerase; antisense oligonucleotide;
                                  VNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPHSGGRVGKGIYFASENS
                                                                                           KSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSLKSPPPGFDSVIARGHTEPDPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antisense compound useful for treating hyperproliferative, neurological, inflammatory and autoimmune disorders and diabetes inhibits human PARP -
                                                                                                                                                                    Example 13; Page 105-107; 168pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARP; Poly (ADP-ribose)
                                                                                                                                                                                                                                                                                                          AAU29021 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Human PARP-3 protein.
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                361
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NAMES OF COLOR OF COL

99.6%; Score 2811; DB 22; Length 533;

Query Match

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240
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                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel genes and proteins, antibodies and binding partners useful in
                                                             1 mapkpkpwvqtegpekkkgrqagreedpfrstaealkaipaekriirvdptcplssnpgt
                                                                                      QVYEDYNCTLNQTNIENNNNKFYIIQLLQDSNRFFTCWNRWGRVGEVGQSKINHFTRLED
                                                                                                                                    AKKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGPVRTVTKRV
                                                                                                                                                                                  QPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALEEAL
                                                                                                                                                                                               VSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQTGSNHRCPTLQHIWK
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                                        MAPKPKPWVQTEGPEKKKGRQAGREEDPFRSTAEALKAIPAEKRIIRVDPTCPLSSNPGT
                                                                                                                                                                                                                               KGPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIELAQALQA
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No. 1.3e-248;
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                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY51178 standard; Protein;
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99DE-1008837
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PARP;

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                                                                                                   polymerase (PARP) homologues, which are characterised by an amino acid sequence with a functional NAD^+-binding site and no zinc finger sequence mouti, of general formula Cx_2Cx_2MHX_2C (I). The nucleic acid sequences moutif, of general formula Cx_2Cx_2MHX_2C (I). The nucleic acid detection of PARP homologues and antibodies are useful for analytic detection of PARP homologues and for identifying PARP effectors or binding partners, as well as for determining their effectiveness. PARP-binding partners are useful for the diagnosis or therapy of a disease condition, which is the result of a PARP protein, especially an energy deficiency, which may comprise tissue damage from cell death following necrosis or apoptosis. The disease condition may be chosen from a neurodegenerative illness, or sepsis or ischemic tissue damage, in particular neurotoxic disturbances, etc. This sequence represents the murine PARPI protein used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 QPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALEEAL 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qvhedydctlnqtnignnnnkfyiiqlleegsrff-cwnrwgrvgevggskmnhftcled 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AKKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGPVRTVTKRV
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                                                                                        This invention describes novel human and murine poly(ADP-ribose)
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energy deficiency associated disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                         58;
                                                                                                                                                                                                                                                                                                                                                                                                     79.8%; Score 2253.5; DB 80.9%; Pred. No. 1.7e-197.ive 37; Mismatches 58
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                                                  Claim 4; Page 71-73; 96pp; German.
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 and therapy of
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Murine PARP1 (long) homologue protein.

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(first entry)

31-MAR-2000

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polymerase (PARP) homologues, which are characterised by an amino acid sequence with a functional NAD^+-binding site and no zinc finger sequence with a functional NAD^+-binding site and no zinc finger sequences. PARP homologues and antibodies are useful for analytic detection of PARP homologues and for identifying PARP effectors or binding partners as well as for determining their effectiveness. PARP-binding partners are useful for the diagnosis or therapy of a disease condition, which is the result of a PARP protein, especially an energy deficiency, which may comprise tissue damage from cell death following necrosis or apoptosis. The disease condition may be chosen from a neurodegenerative illness, or sepsis or ischemic tissue damage, in particular neurotoxic disturbances, etc. This sequence represents the murine PARPI protein used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QALQAV-SEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQTGSNHRCPT 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 QVYEDYNCTLNQTNIENNNNKFYIIQLLQDSNRFFTCWNRWGRVGEVGQSKINHFTRLED 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lemaire H;
             poly(ADP-ribose) polymerase; human; murine; detection; sepsis;
                         diagnosis; therapy; necrosis; apoptosis; neurodegenerative illness; ischemic tissue damage; PARP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MAPKPKPWVQTEGPEKKKGRQAGREEDPFRSTAEALKAIPAEKRIIRVDPTCPLSSNPGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 AKKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQAEDEAQEAVVK-----VDRGPVRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 VTKRVQPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEEALKGPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIELA
                                                                                                                                                                                                                                                                                                                                                                         Novel genes and proteins, antibodies and binding partners useful diagnosis and therapy of energy deficiency associated disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes novel human and murine poly(ADP-ribose)
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                                                                                                                                                                                                                                                                                            Lubisch W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.4%; Score 2241; DB 21;
80.1%; Pred. No. 2.4e-196;
tive 37; Mismatches 58;
                                                                                                                                                                                                                                                                                          Otterbach B,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 67-69; 96pp; German.
                                                                                                                                                                                                                                                                                            Kroeger B,
                                                                                                                                                                                                            98DE-1025213.
99DE-1008837.
                                                                                                                                                                             99WO-EP03889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 80.18
Matches 432; Conservative
                                                                                                                                                                                                                                                                                                                           WPI; 2000-087218/07
N-PSDB; AAZ44290.
                                                                                                                                                                                                                                                                                            Hoeger T,
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                                                                                                                                                                                                                                                             (BADI ) BASF AG
                                                                                                              W09964572-A2
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01-MAR-1999;
                                                                                                                                                                             04-JUN-1999;
                                                                                                                                               16-DEC-1999
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                                                                                                                                                                                                                                                                                              Kock M,
                                                                              Mus sp
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Length 522;

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to antisense oligonucleotides targeted to human PARP nucleic acid and inhibiting expression of human PARP. PARP (POLY (ADP-ribose) polymerase plays an important role in chromatin decondensation, DNA replication, DNA repair, gene expression, malignant transformation, cellular differentiation and apoptosis. The antisense oligonucleotide inhibitors are useful for inhibiting the expression of PARP in human cells or tissues. They are also useful for treating a human with a disease associated with PARP especially hyperproliferative disorders (e.g. cancer), cellular injury resulting from oxidative stress, meurological (e.g parkinsonism, meningitis-associated intracranial complications and isohaemia), inflammatory and autoimmune disorders (e.g arthritis) and diabetes. The present sequence is a PARP protein,
                                                                                                                                                                                                                                                                                                                                                                            cytostatic; nootropic; neuroprotective; antiinflammatory; antidiabetic; immunosuppressant; hyperproliferative disorder; cancer; cellular injury; oxidative stress; neurological disorder; parkinsonism; apoptosis; menlingitis-associated intracrantal complication; ischaemia; inflammatory disorder; autoimmune disorder; arthritis; diabetes.
                           295 qtlqaapgeeeekveevphpldrdygllrcqlqlldsgeseykaiqtylkqtgnsyrcpn 354
                                                                                     415 FASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSLKSPPPGFDSVIARGH 474
                                                                                                    Human; PARP; Poly (ADP-ribose) polymerase; antisense oligonucleotide;
                                                                                                                                                             475 TEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYLIYQESQCRLRYLLEVHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antisense compound useful for treating hyperproliferative, neurological, inflammatory and autoimmune disorders and diabetes inhibits human PARP -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 13; Page 109-111; 168pp; English.
                                                                                                                                                                                                                                              AAU29022 standard; Protein; 522 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAR-2000; 2000US-0517467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001; 2001WO-US06572.
                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cowsert LM;
                                                                                                                                                                                                                                                                                                                                     protein.
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                                                                                                                                                                                                                                                                                                                                    Mouse PARP-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus.
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522 AA;

Sequence

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Human; poly(ADP-ribose) polymerase; hPARP2; oxidative stress; ARDS;
Inflammation; ischaemic stroke; hemorrhagic shock; myocardial ischemia;
Inflammation; cerebral vasospasm; rhematoid arthritis; osteoarthritis;
W infarction; cerebral vasospasm; rhematoid arthritis; osteoarthritis;
W douty arthritis; spondylitis; Behcet's disease; sepsis; septic shock;
W douty arthritis; spondylitis; danned; gram positive sepsis; trauma;
W coxic shock syndrome; multiple organ injury syndrome; vasoulitis;
W hemorrhage; conjunctivitis; uveitis; thyroid-associated ophthalmopathy;
W cosinophilic granuloma; asthma; chronic bronchitis; allergic rhinitis;
W pulmonary sarcoidosis; pleurisy; alveolitis; pneumonia; myocardium;
W pronchiectasis; pulmonary oxygen toxicity; keloid formation; brain;
Scar tissue formation; atherosclerosis; systemic lupus erythematosus;
W graft versue host disease; allograft rejection; cystic fibrosis;
Crohn's disease; ulcerative colitis; necrotizing enterocolitis;
W priammatory dermatosis; contact dermatitis; atopic dermatitis;
W psoriasis; urticaria; fever; myalgia; meningliis; encephalitis;
                                                    19;
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123 fldktknnwedrenfekvpgkydmlqmdyaastqdesktkeeetlkpe------- 170
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                                                                                                                                                                                                                              71 NQTNIENNNNKFYIIQLLQ-DSNRFFTCWNRWGRVGEVGQ-SKINHFTRLEDAKKDFEKK 128
                                                                                                                                                                                                                                                                                                     FREKTKNNWAERDHFVSHPGKYTLIEV----QAEDEA---QEAVVKVDRGPVRTVTKRVQ 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 -sqidirvqellklicnvqtmeemmiemkydtkraplgkltvaqikagyqslkkiedcir 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 414
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                                                       Gaps
                                                                                                                                                  62
                                                                                                   16 KKKGRQA-GREEDPFRSTAEALKAIPAEKRIIRVDPTCPLSSNPGTQVY----EDYNCTL 70
                                                                                                                                   344 fevekegekeafr--edlpnrmllwhgsrlsnwygilshglrvappeapitgymfgkgiy
                                                                                                                                                                                                                                                                                                                                                                                                         182 PCSLDPATOKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALEEALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIELAQALQAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPH----SGGRVGKGIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSLKSPPPGFDSVIARGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      475 TEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSS-----TFSQSEYLIYQESQCRLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | | | : : | : | | | 460 mapspa------hfitlngstvplgpasdtgilnpegytlnyneflvyspngvrmr
                                                    64;
                                                    Indels
                                                 Matches 187; Conservative 103; Mismatches 191;
26.1%; Score 738; DB 22; 34.3%; Pred. No. 1.5e-58;
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                          Similarity
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Mon Sep

59 G-TQVY----EDYNCTLNQTNIENNNNKFYIIQLLQ-DSNRFFTCWNRWGRVGEVGQ-SK 111

112 INHFTRLEDAKKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEV----QAEDEAQEAVVK 167

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227

287

346

403 447

336 algdieiaikl-----vktelqspehpldqhyrnlhcalrpldhesyefkvisqylqst 389

288 VLADIELAQALQAVSEQEKTVEEVP-HPLDRDYQLLKCOLQLLDSGAPEYKVIQTYLEQT

Goldman PS, McElligott DL;

GS---NHRCPTLQHIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMP 404 H----SGGRVGKGIYFASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSL 459

------KSPPPGFDSVIARGHTEP-DPTQDTELELDGQQVVVPQGQPVPCPE

460

505

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New human poly(ADP-ribose) polymerase for treating inflammatory, neurological, cardiovascular, or neoplastic tissue growth disorders, such as, arthritis, encephalitis, myocardial ischemia, and leukocyte
Sjogren's syndrome; alcoholic hepatitis; bacterial pneumonia; hypovolemic shock; Type 1 diabetes mellitus; hypersensitivity; leukocyte dyscrasia; thermal injury; cytokine-induced toxicity.
                                                                                                                                                                                                   Claim 3; Page 94-95; 129pp; English.
                                                                                                                         Christenson E, Demaggio AJ,
                                                                           16-JUN-2000; 2000WO-US16629
                                                                                           99US-0139543
                                                                                                                                        WPI; 2001-025335/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           583 AA;
                                                                                                          (ICOS-) ICOS CORP
                                                                                                                                                 N-PSDB; AAC85303
                                              WO200077179-A2.
                               Homo sapiens
                                                                                           16-JUN-1999;
                                                             21-DEC-2000
                                                                                                                                                                                      metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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This sequence represents human poly(ADP-ribose) polymerase (hPARP2).
This protein causes the covalent addition of polymers of ADP-ribose
to protein targets. hPARP2 activity is induced in many instances of
coxidative stress or during inflammation where there is direct damage
to the DNA. hPARP2 may be used to identify antagonists which
may be used to treat a human having a disorder mediated by PARP2
may be used to treat a human having a disorder mediated by PARP2
may be used to treat a human having a disorder mediated by PARP2
cornectivity, such as, inflammatory, neurological, cardiovascular,
cornectivity, such as, inflammatory, neurological, cardiovascular,
cornectivities, shock, myocardial ischemia or infarction,
transplantation, cerebral vasospasm; rheumatoid, osteo- or gouty
arthritis, spondylitis; Behcet's disease; sepsis, septic or endotoxic
shock, gram negative or positive sepsis, toxic shock syndrome; multiple
organ injury syndrome secondary to septicemia, trauma, or hemorrhage;
allergic or vernal conjunctivitis, uveitis, thyroid-associated
ophthalmopathy; eosinophilic granuloma; asthma, chronic bronchitis,
allergic rhinitis, ARBS, chronic obstructive pulmonary disease,
slicosis, pulmonary sarcoidosis, pleurisy, alveolitis, vasculitis,
allergic rhinitis, hand, pulmonary oxygen toxicity; reperfusion
injury of the myocardium, brain or extremities; cystic fibrosis; keloid
formation, scar tissue formation; atherosclerosis; systemic lupus
cerythematosus, autoimmune thyroiditis, multiple sclerosis; Reynaud's
syndrome; graft versus host disease, allograft rejection; chronic
collis, multiple sclerosis; dermatices
collis, multiple sclerosis; desase,
contact or atonic dermatitis entercollising entercollisis; inflammatory dermatesses,
contact or atonic dermatitis entercollising entercollisis; inflammatory dermatesses,
contact or atonic dermatitis; inflammatory dermatesses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        due to leukocyte dyscrasia and metastasis; thermal injury; granulocyte transfusion associated syndromes; and cytokine-induced toxicity. hPARP2 and antibodies to it, can also be used to diagnose these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contact or atopic dermatitis, psoriasis, urticaria, fever and myalgias due to infection; meningitis, encephalitis, and brain and spinal cord
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antigen-antibody complex mediated diseases; hypovolemic shock; Type 1 diabetes mellitus; acute and delayed hypersensitivity; disease states
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             injury due to minor trauma; Sjogren's syndrome; diseases involving
leukocyte diapedesis; alcoholic hepatitis; bacterial pneumonia;
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Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosupressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardlovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
Human ORFX ORF2673 polypeptide sequence SEQ ID NO:5346.
                                                                      | : :||::| :| |:|||:|
553 ----tlnyneyivynpnqvrmryllkv 575
                                                  505 FSSSTFSQSEYLIYQESQCRLRYLLEV 531
                                                                                                                                                                                   AAB42909 standard; Protein; 534 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0127607
99US-0127636
                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thrombosis; contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200058473-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-2000;
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02-APR-1999;
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22;

; Score 729.5; DB 22; Length 583; ; Pred. No. 1.1e-57; 95; Mismatches 184; Indels 87; Gaps

25.8%; 35.4%;

Matches 201; Conservative

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Query Match Best Local S

15 EKKKGRQAG-----REED-----PFRSTA-----EALKAIPAEKRIIRVDPTCPLSSNP 58

us-09-701-586b-4.rag

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                                                                                                                                                                                                                                                                                                                                         AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; sequences have activities such as: cytostatic; hepatotropic; vulnerary; osteopathic; antiparkinsonian; nootropic; neuroprotective; catalant; thrombolytic; cagulant; vasotropic; neuroprotective; catalant; thrombolytic; cagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; or predisposition to, or preventing or treating the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy coliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, cycliferative disorders, neurodegenerative disorders, asthma, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antilifiammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 --EDYNCTLNQTNIENNNNKFYIIQLLQ-DSNRFFTCWNRWGRVGEVGQ-SKINHFTRLE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 DAKKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEV----QAEDEAQEAVVKVDRGPVRT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176 VTKRVQPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 esg-----ldlrvgeliklicnvgameemmmemkyntkkaplgkltvagikagygslkk 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236 LEEALKGPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIELA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         296 QALQAVSEQEKTVEEVP-HPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQTGS---NHR 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     295 ikl-----vktelgspehpldghyrnlhcalrpldhesyefkvisgylgsthapthsdy 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 GPEKKKGRQAGREED-PFRSTA----EALKAIPAEKRIIRVDPTCPLSSNPG-TQVY-- 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 ggkankdrtedkqdgmpgrswaskrvsesvkalllkgk-apvdpec--takvgkahvyce 61
                                                                                                                                                                                                                      Novel nucleic acids and peptides derived from open reading frame X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     352 CPTLQHIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPH----SGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 534;
                                                                                                                                                                                                                                           useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.7%; Score 726.5; DB 21; Length 35.1%; Pred. No. 1.7e-57; ive 99; Mismatches 187; Indels
                                                                                                                                                                                                                                                                                                           Claim 11; Page 4522-4524; 5507pp; English.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 196; Conservative
                                                                                                           Leach M;
                                                                (CURA-) CURAGEN CORP.
                                                                                                                                                    2000-602362/57.
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                                                                                                                                                                           N-PSDB; AAC77118
                                                                                                         Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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The invention relates to antisense oligonucleotides targeted to human PARP nucleic acid and inhibiting expression of human PARP. PARP (POL) (ADP-ribose) polymerase plays an important role in chromatin decondensation, DNA replication, DNA repair, gene expression, malignant transformation, cellular differentiation and apoptosis. The antisense oligonucleotide inhibitors are useful for inhibiting the expression of PARP in human cells or tissues. They are also useful for treating a human with a disease associated with PARP especially hyperproliferative disorders (e.g. cancer), cellular injury resulting from oxidative stress, neurological (e.g parkinsonism, meningitis-associated intracranial complications and ischaemia), inflammatory and autoimmune disorders (e.g arthritis) and diabetes. The present sequence is a PARP protein, the cdNA encoding which was used to design the antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; PARP; Poly (ADP-ribose) polymerase; antisense oligonucleotide; cytostatic; nootropic; neuroprotective; antiinflammatory; antidiabetic; immunosuppressant; hyperproliferative disorder; cancer; cellular injury; oxidative stress; neurological disorder; parkinsonism; apoptosis; meningitis-associated intracranial complication; ischaemia; inflammatory disorder; autoimmune disorder; arthritis; diabetes.
                                                 |||||||| :||||| | : | : | |||||| : : ||
407 mfgkgiyfadmssksanycfasr–-lkntgllllsevalggcnelleanpkaegllggkh
                                                                                                                                                                                                                                                465 stkglgkmapssahfvtlngstvplgpasdt-----gilnpdgy-----tlny
                                                                                                                                                                         ----KSPPPGFDSVIARGHTEP-DPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 726.5; DB 22; Length 534; Pred. No. 1.7e-57;
408 RVGKGIYFASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 16; Page 125-127; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU29023 standard; Protein; 534 AA.
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508 neyivynpnqvrmryllkv 526
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                                                                                                                                                                                                                                                                                                                                          513 SEYLIYQESQCRLRYLLEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human PARP-2 protein #2
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N-PSDB; AAS45684.
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    Gaps
                                           GPEKKKGRQAGREED-PFRSTA----EALKAIPAEKRIIRVDPTCPLSSNPG-TQVY-- 63
                                                                    176 VTKRVQPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEA
                                                                                                                                                                                                                                                                                                                                                     esg-----ldlrvgeliklicnvgameemmmemkyntkkaplgkltvagikagygslkk
                                                                                                                                                                                                                       DAKKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEV----QAEDEAQEAVVKVDRGPVRT
                                                                                                                                                                                                                                                                                                                                                                                                     LEEALKGPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIELA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RVGKGIYFASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSL----
77;
  Indels
187;
  Mismatches
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66
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neyivynpnqvrmryllkv 526
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  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEYLIYQESQCRLRYLLEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Popoff I, Cowsert LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human PARP-2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200164955-A1
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196;
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  Matches
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The invention relates to antisense oligonucleotides targeted to human PARP nucleic acid and inhibiting expression of human PARP. PARP (PDI) (ADP-Tibose) polymerase plays an important role in chromatin decondensation, DNA replication, DNA repair, gene expression, malignant transformation, cellular differentiation and apoptosis. The antisense oligonucleotide inhibitors are useful for inhibiting the expression of PARP in human with a disease associated with PARP especially hyperproliferative disorders (e.g. cancer), cellular injury resulting from oxidative stress, neurological (e.g parkinsonism, meningitis-associated intracranial arthritis) and diabetes. The present sequence is a PARP protein, the cdNA encoding which was used to design the antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 VTKRVQPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEA 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --EDYNCTLNQTNIENNNNKFYIIQLLQ-DSNRFFTCWNRWGRVGEVGQ-SKINHFTRLE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :|: :: | |::| | : ||| |||:|| || | : : | | :| | |||:| iedcira-gqhgralmeacnefytriphdfglrtpplirtqkelsekiqllealgdieia 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 GPEKKKGRQAGREED-PFRSTA----EALKAIPAEKRIIRVDPTCPLSSNPG-TQVY-- 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----KSPPPGFDSVIARGHTEP-DPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295 ikl-----vktelgspehpldghyrnlhcalrpldhesyefkvisgylgsthapthsdy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mfgkgiyfadmssksanycfasr--lkntgllllsevalgqcnelleanpkaegllqgkh
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                                                                                      Antisense compound useful for treating hyperproliferative, neurological, inflammatory and autoimmune disorders and diabetes inhibits human PARP -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.7%; Score 725.5;
                                                                                                                                                                                                                    Example 13; Page 102-104; 168pp; English.
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WPI; 2001-602570/68.
N-PSDB; AAS45586.
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Matches 196;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes novel human and murine poly(ADP-ribose)
polymerase (PARP) homologues, which are characterised by an amino acid
sequence with a functional NAD<sup>+</sup>-binding site and no zinc finger
sequence motif, of general formula CX_2CX_ZMHX_2C (I). The nucleic acid
sequences, PARP homologues and antibodies are useful for analytic
detection of PARP homologues and for identifying PARP effectors or
binding partners, as well as for determining their effectiveness.
PARP-binding partners are useful for the diagnosis or therapy of a
disease condition, which is the result of a PARP protein, especially an
energy deficiency, which may comprise tissue damage from cell death
following necrosis or apoptosis. The disease condition may be chosen
from a neurodegenerative illness, or sepsis or ischemic tissue damage,
in particular neurotoxic disturbances, etc. This sequence represents the
human PARP2 protein used in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDYNCTLNQTNIENNNNKFYIIQLLQ-DSNRFFTCWNRWGRVGEVGQ-SKINHFTRLEDA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 KKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEV----QAEDEAQEAVVKVDRGPVRTVT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 KRVQPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALE 237
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                                                                                                                                                                                                                                                                                                                                                                                                                      Lemaire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel genes and proteins, antibodies and binding partners useful diagnosis and therapy of energy deficiency associated disease conditions -
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                                                                                                                                                                                                                                                                                                                                                                                                                  Lubisch W,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 725; DB 21;
Pred. No. 2.6e-57;
5; Mismatches 185;
                                                                                                                                                                                                                                                                                                                                                                                                                  Otterbach B,
                              AAY51174 standard; Protein; 570 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Hoeger T, Kroeger B,
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35.4%;
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99DE-1008837.
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                                                                                         (first entry)
                                                                                                                    Human brain PARP2 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-087218/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAZ44287
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                                                                                                                                                                                                                Homo sapiens
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RESULT 11
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Human; poly ADP-ribose polymerase; PARP; neuroprotective; nootropic; cerebroprotective; antiparkinsonian; nephrotropic; cardiant; vasotropic; anticonvulsant; cytostatic; antibacterial; immunosuppressive; treatment; antinflammatory; antirheumatic; antiarthritic; antidiabetic; epilepsy; anti-phrhalazin-lone darivative; neurodegenerative disease; tumor; neuronal damage; Alzheimer's disease; Huntington's disease; tumor; parkinson's disease; ischemic damage; microinfarction; sepsis;
459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          503 kglgkmapssahfvtlngstvplgpasdt-----gilnpdgy------tlnyne 545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes novel 4-substituted 2H-phthalazin-1-one derivatives (I) which are used for the treatment or prophylaxis of diseases associated with elevated poly-(ADP-ribose)-polymerase (PARP;
                                                                                                                                                        EALKGPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIELAQA
                                                                                                                                                                                                                                                              LQAVSEQEKTVEEVP-HPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQTGS---NHRCP
                                                                                                                                                                                                                                                                                                                                                                                                               354 TLQHIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPH----SGGRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||||||| :||||| : : | : | |||||||: : ||
445 gkgiyfadmssksanycfasr--lkntgllllsevalgqcnelleanpkaegllggkhst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----KSPPPGFDSVIARGHTEP-DPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKGIYFASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human brain poly-ADP-ribose-polymerase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hoeger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB11480 standard; Protein; 570
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antidiabetic. (I) are especially used for treating or preventing antidiabetic. (I) are especially used for treating or preventing to neurodegenerative disease or neuronal damage (specifically associated with ischemia, trauma or massive bleading, especially apoplexy or spinal-cranial trauma; or Alzheimer's disease, Huntington's disease or Parkinson's disease), treating or preventing ischemic damage (specifically renal damage after renal ischemia or during and after kidney transplantation or heart damage after cardiac ischemia), treating epilepsy, specifically generalized epileptic attacks (e.g. petit mal and tonic-clonic attacks) or partial epileptic attacks (e.g. temporal lope and complex partial attacks), treating microlifarction (e.g. during and after heart valve replacement, aneurym resectioning and heart transplantation), revascularization of critically constricted coronary arteries (e.g. after PCTA or by-pass operations) or peripheral arteries (e.g. leg arteries), treating acute mycoardial ischemia and damage during or after its mechanical or drug-induced lysis and treating tumors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
                                                                                                                                                                                                                                                                                                                                                                                                                                   their metastasis, sepsis and septic shock, inflammatory and rheumatic disease (e.g. rheumatoid arthritis), and diabetes mellitus. Although (I) inhibit PARP (i.e. the known form designated PARPI), they especially selectively and strongly inhibit PARP homologs, specifically the homolog PARP2. In particular (I) have very strong PARP2 inhibitory activity (e.g. with K.i values of 1-20 nM) and high selectivity for PARP2 relative to PARPI (generally by a factor of more than 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |||||||| :|||| | : : | : | |||||| : : || gkgiyfadmssksanycfasr--lkntgllllsevalgqcnelleanpkaegllggkhst 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298 LQAVSEQEKTVEEVP-HPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQTGS---NHRCP 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    354 TLQHIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPH----SGGRV 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GKGIYFASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSL------ 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 503 kglgkmapssahfvtlngstvplgpasdt-----gilnpdgy-----tlnyne 545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 KKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEV----QAEDEAQEAVVKVDRGPVRTVT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238 EALKGPIDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIELAQA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EC 2.4.2.30) activity. The products of the invention have nootropic, neuroprotective, cerebroprotective, antiparkinsonian, nephrotropic, cardiant, vasotropic, anticonvulsant, cytostatic, antibacterial, immunosuppressive, antinflammatory, antirheumatic, antiarthritic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 KRVQPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----KSPPPGFDSVIARGHTEP-DPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 EKKKGRQAG-----REEDPFRSTAEALKAIPAEKRIIRVDPTCPLSSNPG-TQVY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 570;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.7%; Score 725; DB 22; 35.4%; Pred. No. 2.6e-57; iive 95; Mismatches 185;
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Matches 197; Conserv
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This sequence represents a mover numen porty car. This sequences with at least 95% identity to the shipARRS2 variants and sequences with at least 95% identity to the shipARRS2 variants and sequences with at least 95% identity to the shipARRS2 protein an shipARRS2 nucleic acid sequence; the recombinant expression of shipARRS2; and an antibody specific for shipARRS2 shipARRS2 proteins of nucleotides are useful as vaccines for inducing an immunological response in a mammal. The shipARRS2 protein is useful for identifying compounds which inhibit or stimulate its activity or expression level. Such agonists and antagonists of shipARRS2 are useful for treating human diseases including ischaemia and ischaemic tissue injury (e.g., cerebral and cardiac ischaemia, myocardial infarction, stroke), inflammation, and cardiac ischaemia, myocardial infarction, stroke), inflammation, neurodegenerative diseases (e.g., farkinson's disease and Alzheimer's disease). shipARS2 nucleic acids are useful as diagnostic reagents for detecting mutations in the associated gene; as hybridisation probes to isolate full-length shipARS2 colks and sbhPARS2 genomic clones; and for chromosome localisation studies. The sbhPARS2 genomic clones; and for chromosome localisation studies are also useful in screening methods for detecting the effect of added compounds on the production of mRNA and cheecting the effect of added compounds on the production of mRNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human polypeptide of the polyADPribose synthetase family for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 GPEKKKGRQAGREEDPFRSTAEALKAIPAEKRIIRVDPTCPLSSNPG-TQVY----EDYN 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnostic assays and for screening modulators used for preventing treating inflammation, autoimmune disease and Alzheimers disease
                                                                                                                                                                                 Human; poly(ADP-ribose) synthetase; sbhPARS2; vaccine; drug screen ischaemic disorder; cerebral ischaemia; marcardial infarction; stroke; inflammation; autoimmune disease; diabetes; multiple sclerosis; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; chromosome localisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       zhu Y;
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ive 99; Mismatches 184; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence represents a novel human poly(ADP-ribose)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McQueney MS,
                                                                                                                                              Human poly(ADP-ribose) synthetase sbhPARS2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kabnick KS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SMIK ) SMITHKLINE BEECHAM CORP.
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                   AAB60693 standard; Protein; 521
                                                                                                                                                                                                                                                                                                                                                                                                                                              10-AUG-2000; 2000WO-US21775.
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                                                                                                     (first entry)
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Best Local Similarity 34.79
Matches 192; Conservative
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                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                     11-MAY-2001
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                                                             AAB60693;
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AAB60693
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NAP; poly(ADP-ribose) polymerase; PARP; poly(ADP-ribose) transferase; programmed cell death; apoptosis; growth rate; stress; cold; pathogen; pest; drought; heat; fungi; nematode; seed-shatter.
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                                                                                                                               172 ---idlrvqeliklicnvqameemmmemkyntkkaplgkltvaqikagyqslkkiedcir 228
                                                                                                                                                                                                                       413
                                                                                                                                                                                                                                                                    459
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                        68 CTLNQTNIENNNNKFYIIQLLQ-DSNRFFTCWNRWGRVGEVGQ-SKINHFTRLEDAKKDF 125
                                                                                 182 PCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALEEALK 241
                                                                                                                                                              242 GPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIELAQALQAV 301
                                                                                                                                                                             302 SEQEKTVEEVP-HPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQTGS---NHRCPTLQH 357
                                                                   126 EKKFREKTKNNWAERDHFVSHPGKYTLIEV----QAEDEAQEAVVKVDRGPVRTVTKRVQ 181
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5 ggkankdrtedkgd-----esvkalllkgk-apvdpec--takvgkahvycegndvyd
                                    460 KSPPPGFDSVIARGHTEP-DPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYLIY
                                                                                                                                                                                                                                                                                                                                                                 358 IWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPH----SGGRVGKGI
                                                                                                                                                                                                                                                                                                     414 YFASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "these residues are specifically claimed claim 18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The poly(ADP-ribose) polymerase NAP protein of Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               637 AA.
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501 npnqvrmryllkv 513
                                                                                                                                                                                                                                                                                                                                                                                               519 QESQCRLRYLLEV 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana.
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16;
                                                                                                                                                                 poly(ADP-ribose) polymerase (PARP) protein (also known as poly(ADP-ribose) propresse). The PARP enzyme is involved in programmed cell death or apoptosis, and is a nuclear enzyme. The NAP polyvucleotide sequences can be used for modulation of programmed cell death in eukaryotic cells. The method is used, specifically in plants, to induce, or protect against, programmed cell death, depending on the extent to which PARP activity is reduced. Reducing expression of endogenous NAP class PARP only is also used to modulate programmed cell death, to increase growth rate and to produce plant cells that are more tolerant of stress (cold, chemical treatments, pathogens, pests, drought, heat, etc., or during transformation). Particular applications are generation of plants that are resistant to fungi or nematodes; are male or female sterile; or have better seed shatter properties. The methods are also used to improve growth of transformed plant cells (and derived calli or
                                     Modulating cell death, growth and stress resistance in eukaryotes, specifically plants, used, e.g. to impart fungus or nematode resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 YNCTLNQTNIENNNNKFYIIQLLQ-DSNRFFTCWNRWGRVGEVGQSKIN-HFTRLEDAKK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 DFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGPVRTVTKRVQP- 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300 AVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT-GSNHRCPTLQ-- 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | || :|||| |::| |: || || :|:
229 iftnkfndktknywsdrkefiphpksytwlemdygkeendspvnnd---ipssssevkpe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 -CSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALEEALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 GPTDGGQSLEELSSHFYTVIPHNFGHSQPPP--INSPELLQAKKDMLLVLADIELAQALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IYFASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSLKSPPPGFDSVIAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -drydrtrleelsgefytviphdfgfkkmsqfvidtpgklkqkiemvealgeielatkll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           357 HIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPH----SGGRVGKG
                                                                                                                                                 present sequence represents a NAP protein. This protein is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 21; Length 637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Pred. No. 7e-54;
89; Mismatches 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.4%; Score 688.5;
36.2%; Pred. No. 7e-
                                                                                                              Claim 18; Page 99-101; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB93513 standard; Protein; 531 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 36.28
Matches 174; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           637 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     complete plants).
N-PSDB; AAZ60617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            531 V 531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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227

223 slksplkpesq-----ldlrvqeliklicnvqameemmmemkyntkkaplgkltvaq1k 276

VDRGPVRTVTKRVQPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIA

112 INHFTRLEDAKKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEV----QAEDEAQEAVVK 167

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g δ QQ δ q

228 RGFEALEEALEEALEEATDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLL

q

δ

Db

δ

288 VLADIELAQALQAVSEQEKTVEEVP-HPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT

460 KSPPPGFDSVIARGHTEP 477 egllggkhstkglgkmap 523

404 H----SGGRVGKGIYFASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSL 459

346

AAB93513;

```
Human; primer; detection; diagnosis; antisense therapy; gene therapy
             Human protein sequence SEQ ID NO:12844
                                              28-JUL-2000; 2000EP-0116126
      26-JUN-2001 (first entry)
                                                                                                                                                                                                    531 AA;
                                 EP1074617-A2.
                          Homo sapiens
                                                     29-JUL-1999;
                                       07-FEB-2001
                                                                                   Ishii S,
                                                                                                                                                                                                     Sequence
```

The present invention describes primer sets for synthesising 5602

[10] Inagth cDNAs defined in the specification. Where a primer set
comprises: (a) an oligo-dT primer and an oligounclectide complementary
to the complementary strand of a polynuclectide which comprises one of
the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination
oligonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
polynucleotide which comprises at 3'-end sequence. Where the
oligonucleotide which comprises at 3'-end sequence, sequence of an oligonucleotide which comprises at least 15 nucleotides and the combination of
the 5'-end sequence 3'-end sequence; selected from those defined in
the specification. The primer sets can be used in antisense therapy and
in gene therapy. The primers are useful for synthesising polynucleotides,
particularly full-length cDNAs. The primers are also useful for the
connection and/or diagnosis of the abnormality of the full-length
cDNAs easily without any specialised methods. AAH13628 and
AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
AAH13633 to AAH18742 represent human cDNA sequences; and AAH13632
represent cliquourledectides, all of which are used in the exemplification Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. Saito K, Yamamoto, Otsuki T; Claim 8; SEQ ID 12844; 2537pp + CD ROM; English Hayashi K, S A, Nagai K, Isogai T, Nishikawa T, , Sugiyama T, Wakamatsu 27-AUG-1999; 99JP-0300253. 11-JAN-2000; 2000JP-0118776. 02-MAY-2000; 2000JP-0183767. 09-JUN-2000; 2000JP-0241899. of the present invention. (HELI-) HELIX RES INST. WPI; 2001-318749/34

18;

24.2%; Score 682.5; DB 22; Length 531; 36.9%; Pred. No. 1.9e-53; ive 86; Mismatches 173; Indels 55; Gaps

Best Local Similarity 36.9 Matches 184; Conservative

Query Match

g ò qq

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15 EKKKGRQAG-----REED----PFRSTA----EALKAIPAEKRIIRVDPTCPLSSNP 58

59 G-TQVY----EDYNCTLNQTNIENNNNKFYIIQLLQ-DSNRFFTCWNRWGRVGEVGQ-SK 111

Search completed: August 29, 2002, 07:57:14 Job time: 291 sec

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Sequence

Sequence Sequence Sequence Sequence Sequence

Sequence

Sequence 8
Sequence 6
Sequence 6
Sequence 6
Sequence 6
Sequence 6
Sequence 6

Sequence

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PW------VQTEGPEKKKGRQAGR-----EEDPFRSTAEALKAIPAEKRIIRVDPTC 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.7%; Score 668.5; DB 4; Length 1014; 33.4%; Pred. No. 2.4e-59; Live 100; Mismatches 204; Indels 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Le, Xiao-Chun APPLICANT: Weinfeld, Michael APPLICANT: Weinfeld, Michael APPLICANT: Wing, James 2.

TITLE OF INVENTION: Methods for Quantitating Low Level TITLE OF INVENTION: Modifications of Nucleotide Sequences NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS: ADDRESSE: Medlen & Carroll, LLP STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-UDS/MD-LUGS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/078,347A
FILING DATE: 13-MAY-1998
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: CAITOll, Peter 32,837
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 32,837
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 705-8410
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1014 amino acids
                      US-08-973-462-8
US-08-353-700-1
US-09-310-187A-1
US-09-310-187A-1
US-09-150-741-2
US-09-150-741-2
US-08-01-601-8
US-08-021-601-8
US-08-021-601-6
US-08-08-24-01624-8
US-08-08-284-9B-8
US-08-08-284-9B-8
US-08-08-284-9B-8
US-08-08-284-9B-8
US-08-08-284-9B-8
US-08-08-284-9B-8
US-08-08-284-9B-8
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US-09-231-529-6
US-08-977-816-6
US-09-308-375-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09078347A Patent No. 6132968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative 100;
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MOLECULE TYPE: protein
  Query Match
Best Local Similarity
Matches 187; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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                                                                                                                                                                                                                (without alignments)
278.240 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                       Search time 46.79 Seconds
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                                                                                                                                                                                                                                                                                                                                                 1 MAPKPKPWVQTEGPEKKKGR.....EYLIYQESQCRLRYLLEVHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1
Sequence 6
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/cgn2_6/ptodata/2/jaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PcTUS_COMB.pep:*
                                                       Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-860-886-2
US-09-196-387-2
US-08-923-992A-2
US-08-923-992A-6
US-08-923-992A-6
US-08-923-992A-6
US-08-923-992A-1
US-09-349-546-1
US-09-349-546-1
US-08-923-992A-10
US-08-923-992A-10
US-08-923-992A-10
US-08-923-992A-4
US-08-923-992A-4
US-08-933-992A-4
US-08-933-992A-4
US-08-933-992A-4
US-08-933-992A-4
US-08-933-992A-4
US-08-933-992A-4
US-08-933-992A-4
US-08-933-993-7
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US-08-686-599A-16
US-08-795-475-6
US-08-686-599A-17
US-08-185-432-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-078-347A-3
                           GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                                     August 29, 2002, 07:58:08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0 Maximum DB seq length: 20000000000
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2823
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1128
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TELECOMMUNICATION INFORMATION:

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                                                                                                                                                                                                                                                        MLLVLADIELAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLE 344
                                                                                                                                                                                                                                                                                                                                                                      MPH----SGGRVGKGIYFASENSKSAGYVIGMKCGAHH------VGYMFLGEVALGREHH 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKHAS-HISRLPKGKHSVKGLGKTTPDPS--ANISLDG--VDVPLGTGISSGVIDTSLL- 985
                                            PLSSNPGTQVYED----YNCTLNQTNIENNNNKFYIIQLLQD--SNRFFTCWNRWGRVGE
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                                                                                  107 V-GQSKINHFTRLEDAKKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQ-AEDEAQEA
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APPLICANT: Zur Hausen, Harald
APPLICANT: Zur Hausen, Harald
APPLICANT: Jan-Heiner, Kupper
TITLE OF INVENTION: VECTORS AND VIRUSES FOR USE
TITLE OF INVENTION: IN GENE THERAPY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COPEMATING SYSTEM: Windows
SOFTWARE: FastESQ for Windows Version 2.0b
CURRENT APPLICATION NUMBER: US/08/860,886
FILING DATE: 03-0CT-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8484-0028-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       START: NY YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08860886
Patent No. 6335009
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986 YNEYIVYDIAQVNLKYLLKL 1005
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FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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53 PLSSNPGTQVYED----YNCTLNQTNIENNNKFYIIQLLQD--SNRFFTCWNRWGRVGE 106
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                                                                                                                                                                                                                                                                                                                                                          63;
                                                                                                                                                                                                                                                                                                               Length 1013;
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                                                                                                                                                                                                                                                                                                                                                          207;
                                                                                                                                                                                                                                                                                                            Query Match 23.6%; Score 666.5; DB 4 Best Local Similarity 33.4%; Pred. No. 3.9e-59; Matches 186; Conservative 101; Mismatches 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: A PROTEIN THAT TITLE OF INVENTION: OF USE THEREOF CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09196387 Patent No. 6277613 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klauber & Jackson
                                       TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1013 amino acids
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APPLICANT: Smith, Susan
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650-493-4935
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                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
TELEPHONE: 6'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          328 ---LLDSGAP---EYKVIQTYLEQTGSNHRCP-----TLQHIWKVNQEGEEDRF- 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            423 AGYVIGM----KCGAH------HVGYMFLGEVALGREHHINTDNPSLKSPPPGFDSVI 470
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Patent No. 6280738
GENERAL INFORMATION:
APPLICANT: Tal, Joseph Y.
APPLICANT: Blake, Milan S.
TITLE OF INVENTION: No. 6280738-IgA FC Binding Forms of the Group I TILE OF INVENTION: Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 1327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, N.W., Suite 600
                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 138.5; DB 4;
; Pred. No. 0.00011;
41; Mismatches 102;
                                                                                                                                                                                                                                                                                                       REGIGTRATION NUMBER: 26,742
REGIGTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-343-1684
TELEFAX: 201-343-1684
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1327 amino acids
                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 24.4%
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) MOLECULE TYPE: protein
) HYPOTHETICAL: NO
US-09-196-387-2
                                                   ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                 New Jersey
: USA
Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                 07601
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                                  COUNTRY:
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356 QHIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPHSGGRVGKGIYF 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              309 QATQVKNQFLENAQKLKEIQ------PLIKETNVKLYKAMSESLEQVEKELKHN 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 NKFYIIQLLQDSNRFFTCW----NRWGRVGEVGQSKINHFTRLEDAKKDFEKKFREK--- 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----TKNNWAERDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGPV---RTVT 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 KRVQPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALE 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 EALKGPIDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIELAQA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LQAVSEQEKTVEEVP-HPLDRDYQLLKCQLQ-LLDSGAPEYKVIQTYLEQTGSNHRCPTL 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 QAGREEDPFRSTAEALKAIPAEKRIIRVDPTCPLSSNPGTQVYEDYNCTLNQTNIE-NNN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
4.0%; Score 113.5; DB 4; Length 1164;
Best Local Similarity 20.2%; Pred. No. 0.034;
Matches 107; Conservative 72; Mismatches 205; Indels 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----GHTEPD-----PTQDTELELDGQQVVVPQGQPVPCPEFS 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : : : : : : | | : | | 474 TKYNPSVSDRISTNYKTN-----TDNHKIAEITIKNL---KLNESQTV----
                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,992A
FILING DATE: 05-SEP-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1438.0140001/RWE
                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,707
FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1164 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein US-08-923-992A-2
                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
        STATE: D.C.
COUNTRY: USA
20005
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80 NKFYIIQLLQDSNRFFTCW----NRWGRVGEVGQSKINHFTRLEDAKKDFEKKFREK--- 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               272 OATOVKNOFLENAQKLKEIQ------PLIKETNVKLYKAMSESLEQVEKELKHN 319
292 IELAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQTGSNHR 351
                                                                                       352 CPTLQHIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILITSGLRIMPHSGGRVGK 411
                                                                                                                                       ----ASKELEPE---- 428
                                                                                                                                                                                     412 GIYFASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSLKSPPPGFDSVIA 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Tal, JOSEPh Y.
APPLICANT: Blake, Milan S.
TITLE OF INVENTION: No. 6280738-IgA FC Binding Forms of the Group B
TITLE OF INVENTION: Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 QAGREEDPFRSTAEALKAIPAEKRIIRVDPTCPLSSNPGTQVYEDYNCTLNQTNIE-NNN 79
                                              349 AEKEQ-----EEEEGKQEMEVKMEEETEVRESEKQ-QDSQPEEVMDVLEMVE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1098;
                                                                                                                                                                                                                                      429 -MEFEIEPDK-----ECKSLSPGKENVSALDMEKESEEKEEKESPOPEP
                                                                                                                                                                                                                                                                                    472 RGHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYLIYQE 520
                                                                                                                                                                                                                                                                                                                               473 --VAQPQPQSQPQLQLQSQSQPVLQSQPPSQPEDLSLAVLQPTPQVTQE 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, N.W., Suite 600 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 05-SEP-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.0%; Score 112.5; DB 4; 20.0%; Pred. No. 0.039; Live 75; Mismatches 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 1438.0140001/RWE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                           395 --NVKHVIADQEVMETNRVESVEPSENE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,707
FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/08923992A Patent No. 6280738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1098 amino acids
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Best Local Similarity 20.03
Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-08-923-992A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 DFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQAE-DEAQEAVVKVDRGPVRTVTKR--- 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 VQPCSLDPATQKLITNIFSK--EMFKNTMALMDLDVKKMPLG-----KLSKQQIARGFE 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232 ALEALEEALKGPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLAD 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 GPEKKKGRQAGREEDP----FRSTAEALKAIPAEKRIIRVDPTCPLSSNPGTQVYEDYNC 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117;
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                                                                                                                                                                                                                                                                                                                                                                                                                      SUFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,925
FILING DATE:
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE:
ATTORNEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.0%; Score 112.5; DB 4; 19.3%; Pred. No. 0.019;
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81; Mismatches 229;
                                                                                                                                                                                   TITLE OF INVENTION: HUMAN PININ SPLICE VARIANT NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0365 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                         Sequence 1, Application US/08910925
Patent No. 6162601
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 717 amino acids
TYPE: amino acid
STRANDENNESS: single
TODOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 19.3
Matches 102; Conservative
                                                                                                                 APPLICANT: Bandman, Olga
                                                                                                                                       APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY: FIBRNOT01
CLONE: 53219
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                                                                                                                                                                                                                                                                                                                               STATE: CA
COUNTRY: US.
ZIP: 94304
  SULT 5
-08-910-925-1
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                              380 TPKKRLKRDLAANENNQQKIELTVS-PENITVYE--GEDVKFTVTAKSDSKTTLDFSDLL 436
                                                                                                                                                                                                                298 LQAVSEQEKTVEEVP-HPLDRDYQLLKCQLQ-LLDSGAPEYKVIQTYLEQTGSNHRCPTL 355
                                                                                                                                                                                                                                                                                                                                                           ASENSKSAGYVIGMKCGAHHVGYMFLGEV-ALGRE--HHIN--TDNPSLKSPPPGFDSVI 470
-----TKNNWAERDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGPV---RTVT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Tai, Joseph Y.
APPLICANT: Tai, Joseph Y.
APPLICANT: Blake, Milan S.
TILLE OF INVENTION: Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                          603 ------NKYKSHFWNYQLHAQMEMLTRKVVQYMNKYPDNAEIKKI---FESDM
                                                                   178 KRVQPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALE
                                                                                                                                         EALKGPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIELAQA
                                                                                                                                                                                                                                                                                     356 QHIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNWAVVAAILTSGLRIMPHSGGRVGKGIYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                           | | | | | | | | | 647 KRIKEDNYGSLENDALKGYFEKYFLIPFNKIKQIVDDFDKKVEQDQPAPIPENS 700
                                                                                                                                                                                                                                                                                                                                                                                                                                  471 AR-----GHTEPD------PTQDTELELDGQQVVVPQGQPVPCPEFS 506
                                                                                               437 TKYNPSVSDRISTNYKTN-----TDNHKIAEITIKNL---KLNESQTV---
                                                                                                                                                                          477 -TLKAKDDSGNVVEKT----FTITVQKKEEKQVP--KTPE----QKD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: FLOPY disk
COMPUTER: IBM PC compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,992A
FILING DATE: 05-SEP-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,707
FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Esmond, Robert W.
REGIGYRATION NUMBER: 32,893
REFERENCE/DOCKET WUMBER: 1438.0140001/RWE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-923-992A-6; Sequence 6, Application US/08923992A; Patent No. 6280738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1128 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-923-992A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20005
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington
STATE: D.C.
COUNTRY: USA
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                                                                                                                                  273 QATQVKNQFLENAQKLKEMQ-------PLIKETNVKLYKAMSESLEQVEKELKHN 320
                                                                                                                                                                                                                       -----TKNNWAERDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGPV---RTVT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 EALKGPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIELAQA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LQAVSEQEKTVEEVP-HPLDRDYQLLKCQLQ-LLDSGAPEYKVIQTYLEQTGSNHRCPTL 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              356 QHIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPHSGGRVGKGIYF 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           416 ASENSKSAGYVIGMKCGAHHVCYMFLGEVALGREHHIN--TDNPSLKSPPPGFDSVIAR- 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        604 NKYKSDFMNYQL-----HAQMEMLTRKVV----QYMNKYPDNAEIKKI---FESDMKRT 650
                                                                                            21 QAGREEDPFRSTAEALKAIPAEKRIIRVDPTCPLSSNPGTQVYEDYNCTLNQTNIE-NNN 79
                                                                                                                                                                                            NKFYIIQLLQDSNRFFTCW----NRWGRVGEVGQSKINHFTRLEDAKKDFEKKFREK---
                                                                                                                                                                                                                                                                                                                                381 TPKKRVKRDLAANENNQQKIELTVS-PENITVYE--GEDVKFTVTAKSDSKTTLDFSDLL
                                                                                                                                                                                                                                                                                                                                                                                     178 KRVQPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        438 TKYNPSVSDRISTNYKIN-----TDNHKIAEITIKNL---KLNESQTV------
                                               Indels 147;
  Length 1128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  651 KEDNYGSLENDALKGYFEKYFLTPFNKIKQIVDDLDKKVEQDQPAPIPENS 701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             478 -TLKAKDDSGNVVEKT----FTITVQKKEEKQVP--KTPE----QKD----
  DB 4;
3.9%; Score 110.5; DB 4;
20.0%; Pred. No. 0.065;
iive 73; Mismatches 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
IIILE OF INVENTION: HUMAN PININ SPLICE VARIANT
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CUERRATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,925
FILING DATE: Herewith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08910925 Patent No. 6162601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 514
PAROR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                    Best Local Similarity
Matches 106; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Palo Alto
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-910-925-3
  Query Match
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USA
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                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 DFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQAE-DEAQEAVVKVDRGPVRTVTKR--- 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 VQPCSLDPATQKLITNIFSKEMFKNTMALMD------LDVKKMPLG-----KLSKQQI 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 YIPGRMCPATOKLI-----EESQRKMNALFDGRRIEFAEQINKMEARPRRQSMKEKEHQV 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             282 ---KKDMLLVLADIELAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKV 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86 GGERRTRRESRQESDPEDDDVKKPALQSSVVATSKERTRRD-------LIQDQN- 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLNQTNIENNNNKFYII-----QLLQDSNRFFTCWNRWGRVGEVGQSKINHFTRLEDAKK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227 ARGFEALEALEEALKGPTDGGQSLEEL----SSHFYTVIPHNFGHSQPPPINSPELLQA- 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IQTYLEQTGSNHRCPTLQHIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSG 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  459 LKSPPPGFDSVIA------RGHTEPDP-----TQDTELELDGQQVVVPQGQP 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.9%; Score 109; DB 4; Length 743;
20.0%; Pred. No. 0.046;
Live 79; Mismatches 190; Indels 190; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  335 EEEEKEIGIVHSDAEKEQ-----EEEEQKQEMEVKMEEETEVRESEKQ-QDSQPEEVMD 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     399 LRIMPHSGGRVGKGIYFASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPS 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          413 --VEP-----SENEASK------SENEASK-E 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 GPEKKKGRQAGREEDP----FRSTAEALKAIPAEKRIIRVDPTCPLSSNPGTQVYEDYNC 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              388 VLEMVE-----NVKHVIADQEVMETNRVES-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         498 EPAQPQL-----QSQPQLQLQSQCHA--VLQSH 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                500 VPC-PEFSSSTFSQSEYLIYQESQCRLRYLLEVH 532
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERNCE/DOCKET NUMBER: PF-0365 US
TELECOMMUNICATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08694869
Patent No. 5994123
GENERAL INFORMATION:
APPLICANT: Olszewski, N.
APPLICANT: Tzaffrir, I.
APPLICANT: Somers, D. A.
APPLICANT: Lockhart, B.
                                                                                                                                                                             LENGTH: 743 amino acids
TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1684847
                                                                                                                                          INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                   Query Match 3.9%
Best Local Similarity 20.0%
Matches 115; Conservative
                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                   TELEFAX: 650-845-4166
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1133 ENWFRLPITYVGPMYMGEKTQMLIGCNFMQSLA------GGVRLEGRTVTFYKYI--- 1181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                314 PLDRDY------QLLKCQLQLLDSGAPEYKVIQTYLEQTGSNHRCPTLQHIWKVN 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             919 AEAVK--PPEKK-------SOYELLAKQLLIENSKLKMEKEILIEELN 957
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
3.8%; Score 108.5; DB 2; Length 1871;
Best Local Similarity 21.0%; Pred. No. 0.25;
Matches 100; Conservative 64; Mismatches 135; Indels 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 VQPCSLDP----ATQKLITNIFSKEMF------KNTMALMDLDVK---
                                                                                                           ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A. STREET: P.O. Box 2938 CITY: Minneapolis
TITLE OF INVENTION: SUGARCANE BACILLIFORM VIRUS TITLE OF INVENTION: PROMOTER NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 600.369US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-373-6900
TELEFAX: 612-339-3061
TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/694,869
FILING DATE: 09-AUG-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VETSION 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1871 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Woessner, Warren D
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-694-869-1
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                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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us-09-701-586b-4.rai

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US-08-923-992A-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             958 KEIKAHQETKKGKELYIEEASTEVENEIETWKSRAELFEALYNEEVKKNKASTSSVTEGM 1017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  215 ----KMPL---GKL---SKQQIARGFEALEALEEALKGPTDGGQSLEELSSHFYTVIPHN 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              265 FGHSQPPPINSPELLQAKKDMLLVLADIELAQALQAVSEQE------KTVEEVPH 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           314 PLDRDY------QLLKCQLQLLDSGAPEYKVIQTYLEQTGSNHRCPTLQHIWKVN 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93 RFFTCWNRWGR-----VGEVGQSKINHFTRLEDAKKDFEKKFREKTKNNWA----- 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33 AEALKAIPAEKRIIRVDPTCPLSSNPGTQVYEDYNCTLNQTNIENNNNKFYIIQLLQDSN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1267 ----KEAMRKHIDALLERKVIRPSKSPHRTN----AFIVESGTSIDPKTGKEIRGK 1314
                        180 VQPCSLDP-----ATQKLITNIFSKEMF------KNTMALMDLDVK-----
363 QEGEEDRFQAH-SKLGNRKLLW----HGTNMAVVAAILTSGLRIMPHSGGRV-GK 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363 QEGEEDRFQAH-SKLGNRKLLW----HGTNMAVVAAILTSGLRIMPHSGGRV-GK 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.8%; Score 108.5; DB 3; Length 1871; Best Local Similarity 21.0%; Pred. No. 0.25; Matches 100; Conservative 64; Mismatches 135; Indels 177;
                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Olszewski, N.
APPLICANT: Tazafrir, I.
APPLICANT: Somers, D.A.
APPLICANT: Somers, D.A.
APPLICANT: Torbert, K.
TITLE OF INVENTION: Sugarcane bacilliform virus promoter:
FILE REFERENCE: 600.369022
CURRENT FILING DATE: 1996-08-09
EARLIER APPLICATION NUMBER: US/09/349,546
CURRENT FILING DATE: 1996-08-09
EARLIER APPLICATION NUMBER: US/09/349,669
EARLIER PILING DATE: 1996-08-09
EARLIER FILING DATE: 1997-08-13
NUMBER: OF SEQ ID NOS: 10
SUGINGARIANE FILING DATE: 1997-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: sugarcane bacilliform virus US-09-349-546-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09172422A Patent No. 6300485
                                                                                                                                    Sequence 1, Application US/09349546 Patent No. 6093569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1871
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US-09-172-422-1
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APPLICANT: Adams, Arwen E.
APPLICANT: Chiu, Choi Ying
APPLICANT: Chiu, Choi Ying
APPLICANT: Chiu, Choi Ying
APPLICANT: Deng, Song M.
APPLICANT: Leng, Song M.
APPLICANT: Leng, Song M.
APPLICANT: Leng, Song M.
APPLICANT: Sheffield, val
APPLICANT: Welch, Juliat
TITLE OF INVENTION: COMPOSITIONS, METHODS, AND USES THEREOF
TITLE OF INVENTION: COMPOSITIONS, METHODS, AND USES THEREOF
FILE REFERENCE: 200130 442
CURRENT APPLICATION NUMBER: US/09/172,422A
CURRENT FILIG DATE: 1998-10-14
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1003 ---LKEQERQHLQDLLHQEVLRRIILLQRWFRVLLCRQHFL-------HLRQAS- 1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----AWN--GRTG-IRQSRLSSGTSLLDK----DGIFANSTSSKLLERAHGILTRNKNFK 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHPG--KYTLIEVQA------EDEAQEAVVKVDRGPVRTVTKRVQPCSLDPATQ--- 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QSLEELSSHFYTVIPHNFGHSQPPPIN-----SPELLQAKKDMLLVLADIELAQA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 EALKAIPAEK-RIIRVDPTCPLSSNPGTQVYEDYNCTLNQTNIENNNNKFYIIQLLQDSN 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | | | : |:|| : | :|| SKPALPKH-LLEVNSLKHLTRLTLQDRITKSLLHLH------KKKKPPSISAQFQASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 RFFTCWNRWGRVGEVGQSKINHFTRLEDAKKDFEKKFREKTKNNWAERDH-----FV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191 -KLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALE--EALKGPTDGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LQAVSEQEKT-VEEVPHP-----LDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 · 349 NHRCPTLOHIWK--VNQEG-----EEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2548;
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Patent No. 6280738
GENERAL INFORMATION:
APPLICANT: Tai, Joseph Y.
APPLICANT: Blake, Milan S.
TITLE OF INVENTION: No. 6280738-1gA Fc Binding Forms of TITLE OF INVENTION: Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      John Marker Sterne, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, N.W., Suite 600 STATE: D.C. CONWRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.8%; Score 108.5; DB 4; Best Local Similarity 21.0%; Pred. No. 0.42; Matches 88; Conservative 63; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapien
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TITLE OF INVENTION: PLANTS WHICH SYNTHESIZE A MODIFIED STARCH,
TITLE OF INVENTION: PROCESS FOR THE PRODUCTION THEREOF AND MODIFIED STARCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226 QSYLRWERKGKQNYPPEKEKEEYEAARTVL----QEEJARG-ASIQDIRARLTKTNDKSQ 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         295 AQALQAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSG------APEYKVIQTYLEQT 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90 DSNRFFTCWNRWGRVGEVGQSKINHFT-RLEDAKKDFEKKFREKTKNNWAERDHFVSHPG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 KYTLIEVQAEDEAQEAV------VKVDRGPVRTVTKRVQPCSLDPATQKLITNI 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249 SLEELSSHFYTVIPHNFGHSQ------PPPINSPELLQAKKDMLLVL-ADIEL 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197 FS------KEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALEEALKGPTDGGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 1464;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPA)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/04109
FILING DATE: 19-SEP-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 19547733.2
FILING DATE: 20-DEC-1995
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haley JI., James F.
REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                         ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 100.co
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPATIBLE IBM PC COMPATIBLE
COMPATIBLE IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION
TELEPHONE: 212-596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1464 amino acids
                                  APPLICANT: Jens Kossmann
APPLICANT: Ruth Lorberth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212-596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-09-045-360-2
                                                                                                                                                                       NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
SOFTWARE: Patentr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                        CITY: New York
STATE: New York
             SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ద
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    || : :: | | : : | | : : | | 309 QATQVKNQFLENAQKLKEIQ------PLIKETNVKLYKAMSESLEQVEKQLKHN 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 TKNNWAERDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGPVRTVTKRVQPCSLDPATQKL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 ITNIFSKEMFKNTMALMDLDVKKMP-----LGKLSKQQIA----RGFEALEALEE 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 NKFYIIQLLQDSNRFFTCW----NRWGRVGEVGQSKINHFTRLEDAKKDFEKKFR---EK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 KFTLTAKSDSKTTLDFSDLLTKYNPSVSDRISTNYKTNTDNHKIAEITIKNLKLNESQTV 513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                358 IWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPHSGGRVGKGIYFAS 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --AIKELMEQPEIPSNPEYGIQKSIWESQKEPIQEAI-TSFKKIIGDSSSKYYTEHYFNK 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     418 ENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHIN--TDNPSLKSPPPGFDSVIAR--- 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 143; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 QAGREEDPFRSTAEALKAIPAEKRIIRVDPTCPLSSNPGTQVYEDYNCTLNQTNIE-NNN 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.8%; Score 107.5; DB 4; Length 1164; 20.4%; Pred. No. 0.14; Ive 68; Mismatches 210; Indels 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----PTQDTELELDGQQVVVPQGQPVPCPEFS 506
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,992A
FILING DATE: 05-SEP-1997
CLASSIFICATION NUMBER: US 60/024,707
FILING DATE: 06-SEP-1996
APPLICATION NUMBER: US 60/024,707
FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1438.0140001/RWE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1164 anino acids
TYPE: maino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09045360 Patent No. 6207880
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Matches 108; Conservative
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US-09-045-360-2
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18;

Gaps

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301 VSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQTGSNHRCPTLQHIWK 360
                                                                                                                                                                                                                                         361 VNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPHSGGRVGKGIYFASENS 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 KSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSLKSPPPGFDSVIARGHTEPDPT 480
   ---ALAKKEVEAKELEIEKLQYEISTLEQEVATAQHQVDNLKKLLAG 215
                                                                    243 --PTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIELAQALQA 300
                                                                                                                           216 ADPODGTEVIEAKLKK-----GEAE---LNAKQAELAKK-----QTELEKLLDS 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: BULLA, LEE A.
APPLICANT: JI TAR
TITLE OF INVENTION: TOXIN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
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ZIP: 20066-1812

COMPUTER READABLE FORM:
MEDIUM TYPE: FIDPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/326,117B
FILING DATE: 19-0CT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 7112-0037.00
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 887-0763
TELEFAX: (202) 887-0763
TELEFAX: 90-4030
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LEMOTH: AND ASSIGNED ASSIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: MORRISON & FOERSTER STREET: 2000 Pennsylvania Ave. N.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481 QDTELELDGQQVVVPQ-GQPVPCPE 504
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Best Local Similarity 20.39
Matches 120; Conservative
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   168 TLKV-----
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                                                                                                      400 -----PALSKIKLYAKEKEE---QIDDPILNKKIFKVDDGELLVLVAKSSG-KTKVHLA 449
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341 DELRKTITKGEIKTKVEKHLKRSSFAVERIQRKKRDFGHLINKYTSSPAVQV-QKVLEEP 399
                                                             347 GSNHRCPTLQHIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPHSG 406
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19.0%; Pred. No. 0.092;
tive 67; Mismatches 168; Indels 174; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 KKKGRQAGR--EEDPFRSTAEALKAIPAEKRIIRVDPTCPLSSNPGTQVYEDYNCTLNQT 73
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 160, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVERTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <del>-</del> . ... ... ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Brookes, A. Anders
RECISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 160: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
                                                                                                                                                                                                                                                             450 TDLNOPITLHWALSKSPG 467
                                                                                                                                                                                         407 GRVGKGIYFASENSKSAG 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 19.0%
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 641 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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VGQSKINHFT		TSLNEVTSPLHIFSVTALDSLPNTHTVTMMVQVANVNSRPPRWL-EIFA		VQQFEEKSYQNFTVRAIDGDTEINMPINYRLITNEEDTFFSIEALPGGKSGAVFLVSPID	GGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVL	RDTLQREVFPLTIVAYKYDEEAFSTSTNVVIIVTDINDQRPEPIHKEYRLAIMEETPLTL	ADIELAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQLQLL	415 NFDKEFGFHDKDĽGÓNAQYTVRĽESVDPPGAAEAFYIAPEVGYOROTFIMGTLNHSML	DSGAPEYKVIQTYLEQTGSNHRCPTLQHIWKVNQEGEEDRFQ	DYEVPEFGSITIRVVATDNNDTRHVGVALVHIDLINWNDEQPIFEHAVQTVTFDETEGEG		: : : : :		- SFNYHRESELFVQVRATDTLGEPFHTATSQLVIRLNDINNTPPTLRLPRGS		POVEENVPDGHVITOE
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Search completed: August 29, 2002, 07:58:13 Job time: 290 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

August 29, 2002, 08:02:11; Search time 36.19 Seconds (Without alignments) 570.255 Million cell updates/sec Run on:

US-09-701-586B-4

1 MAPKPKPWVQTEGPEKKKGR......EYLIYQESQCRLRYLLEVHL 533 2823 Perfect score:

Sequence:

105224 segs, 38719550 residues Searched:

Gapop 10.0 , Gapext 0.5

BLOSUM62

Scoring table:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q9v6fl homo sapien	mus m						~	P09874 homo sapien	P27008 rattus norv	P31669 xenopus lae	P11103 mus musculu	P35875 drosophila	Q09525 caenorhabdi	Q9ukk3 homo sapien	Q08824 oncorhynchu				P27595 bos taurus	P27951 streptococc	Q27171 paramecium	P16900 ovine lenti	_	P51834 bacillus su		Q09897 schizosacch	P53804 homo sapien	P58301 pyrococcus	simian	-	5 ictalum	P41004 schizosacch
SUMMARIES	ID	PPO3_HUMAN	PPO2_MOUSE	PPO2_HUMAN	PPOL_ARATH	PPOL_BOVIN	PPOL_SARPE	PPOL_CHICK	PPOL_CRIGR	PPOL_HUMAN	PPOL_RAT	PPOL_XENLA	PPOL_MOUSE	PPOL_DROME	YON4_CAEEL	PPOV_HUMAN	PPOL_ONCMA	YMP3_CAEEL	MYS_AEQIR	SP41_YEAST	HXK1_BOVIN	BAG_STRAG	DYHC_PARTE	GAG_OMVVS	MYB_AVIMB	SMC_BACSU	HMMR_HUMAN	YAIA_SCHPO	TTC3_HUMAN	RA50_PYRFU	POL_SIVAI	MYB_CHICK	VG22_HSVI1	CUT3_SCHPO
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ф	Query	9.66	26.1	25.8				23.9				23.1				9.1	6.7	4.5	4.3	4.1	4.0	4.0	4.0	3.9	ж Ж	3.8	3.8	3.8	3.7	3.7	3.7	3.7	3.7	3.7
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042184 gallus gall p26123 influenza a p12847 rattus norv p10242 homo sapien p21576 saccharomyc p49454 homo sapien p26122 influenza a p41214 homo sapien p11109 bacteriopha p7933 pasteurella p55391 homo sapien p55391 homo sapien p1109 bacteriopha p55391 homo sapien p55391 homo sapien	
REST_CHICK RRP2_LALEZ MYH3_RAT MYB_HUMAN VPS1_YEAST CENF_HUMAN EXP2_LALE1 LIGA_HUMAN EXOZ_BPT5 SYA_PASMU TAMAI	L100_ADE12
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEAR LOCALIZATION SIGNAL (POTENTIAL). R -> N (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                              09Y6FI; 09UG81;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last anotation update)
16-OCT-2001 (Rel. 40, Last anotation update)
Poly [ADP-ribose] polymerase-3 (EC 2.4.2.30) (PARP-3) (NAD(+) ADP-ribosyltransferase-3) (Poly[ADP-ribose] synthetase-3)
                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                       "A human poly(ADP-ribose) polymerase gene family (ADPRTL): cDNA cloning of two novel poly(ADP-ribose) polymerase homologues."; Genomics 57:442-445(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P26446; 1A26.
InterPro; IPR001290; PARP.
InterPro; IPR004102; PARP_reg.
Pfam; PF00644; PARP; 1.
Pfam; PF02877; PARP_reg; 1.
Transferase; Glycosyltransferase; NAD; Nuclear protein;
ADP_ribosylation.
                           533 AA.
                           PRT;
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE-Fetal brain;
MEDLINE-99263509; PubMed-10329013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF083068; AAD29855.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AL050034; CAB43246.1; -.
                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 75-533 FROM N.A.
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Adpril3 or parp3 or adpri3.
                           STANDARD;
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80
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                                                                                                                                                                                                                                                                Johansson M.
                           PPO3_HUMAN
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RESULT 1
PPO3_HUMAN
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    RARENE REPRESENTATION OF STREET STREE
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                                                                                                                                                                                                                                                                                                                                                                               121 AKKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRAPVRTVTKRV 180
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MEDLINE=99292755; PubMed=10364231;
MEDLINE=99292755; PubMed=10364231;
Ame J.-C., Rolli V., Schreiber V., Niedergang C., Apiou F., Decker Ame J.-C., Rolli V., Schreiber V., Muller S., Hoger T., Amelissier-de Murcia J., de Murcia G.M.;
"PARP-2, A novel mammalian DNA damage-dependent poly(ADP-ribose)
                                                                                                                                                                                                  PPO2_MOUSE STANDARD; PRT; 559 AA.
088554; Q99N29;
116-OCT-2001 (Rel. 40, Last sequence update)
116-OCT-2002 (Rel. 41, Last annotation update)
101-WAR-2002 (Rel. 41, Last annotation update)
101-WAR-2002 (Rel. 41, Last annotation update)
1021y [ADP-ribose] polymerase-2 (EC 2.4.2.30) (PARP-2) (NAD(+) ADP-ribosyltransferase-2) (Poly[ADP-ribose] synthetase-2) (PADPRT-2)
                                                                                                                                                                               1 MAPKPKPWVQTEGPEKKKGRQAGREEDPFRSTAEALKAIPAEKRIIRVDPTCPLSSNPGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQTGSNHRCPTLQHIWK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butherla; Rodentia; Sclurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                        ö
                                                                                                 Length 533;
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  -> G (IN REF. 2).
-> E (IN REF. 2).
7C0AB89E64D1B9FD CRC64;
                                                                                                   Score 2811; DB 1;
Pred. No. 5.1e-189;
0; Mismatches 2;
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J. Biol. Chem. 274:17860-17868(1999)
        Z X
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                                         60117
                                                                                                                                      Matches 531; Conservative
171
411
533 AA;
                                                                                                                   Similarity
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CONFLICT
CONFLICT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                   STRAIN=129/Sv X C57BL/6;
MEDILINE-99268466; PubMed=10338144;
Bergjammer H., Ebner M., Marksteiner R., Auer B.;
"pADPRT-2: a novel mammalian polymerizing(ADP-ribosyl)transferase gene
                                                                                                                                                                                                                                                                                      NQTNIENNNNKFYIIQLLQ-DSNRFFTCWNRWGRVGEVGQ-SKINHFTRLEDAKKDFEKK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FREKTKNNWAERDHFVSHPGKYTLIEV----QAEDEA---QEAVVKVDRGPVRTVTKRVQ 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00644; PARP; 1.
Pfam; PF02877; PARP_reg; 1.
Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 KKKGRQA-GREEDPFRSTAEALKAIPAEKRIIRVDPTCPLSSNPGTQVY----EDYNCTL 70
                                                                                                                                                                                                                                                                        related to truncated pADPRT homologues in plants and Caenorhabditis
MEDLINE=21179160; PubMed=11133988; Ame J.-C., Schreiber V., Fraulob V., Dolle P., de Murcia G.M., Niedergang C.P.; "A bidirectional promoter connects the poly(ADP-ribose) polymerase (PARP-2) gene to the gene for Rhase P RNA."; J. Biol. Chem. 276:11092-11099(2001).
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NUCLEAR LOCALIZATION SIGNAL 2ND PART
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NUCLEAR LOCALIZATION SIGNAL 1ST
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V -> I (IN REF. 2).
R -> Q (IN REF. 2).
V; EOAEDAEE412C1445 CF.
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EMBL; AF191547; AAK13253.1; -.
EMBL; AF072521; AAC25415.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative 103;
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InterPro; IPR001290; PARP.
InterPro; IPR004102; PARP_reg
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                                                                                                                                                          SEQUENCE OF 9-559 FROM N.A.
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Berghammer H., Ebner M., Markstein, and B.; "pADPRT-2: a novel mammalian polymerizing(ADP-ribosyl)transferase gene related to truncated pADPRT homologues in plants and Caenorhabditis elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ρ.,
                                           |::| | : || || || || || || || || A-GQHGRALVEACHEFYTRIPHDFGLSIPPVIRTERELSDKVKLLEALGDIEI--ALKLY 323
                                                                                                                                                                                                                        MAPSPA-----HFITLNGSTVPLGPASDTGILNPEGYTLNYNEFIVYSPNOVRMR 546
                                 301
                                                                         SEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT-GSNHR--CPTLQHI 358
                                                                                                                      414
                                                                                                                                 FASENSKSAGYVICMKCGAHHVGYMFLGEVALGREHHINTDNPSLKSPPPGFDSVIARGH 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 2).
TISSUB-Fetal brain;
MEDLINE-92929255; Pubmed-10364231;
Ame J.-C., Rolli V., Schreiber V., Niedergang C., Apiou F., Decker Muller S., Hoeger T., Menissier-de Murcia J., de Murcia G.M.;
"PARP-2, a novel mammalian DNA damage-dependent poly(ADP-ribose)
324 KSERQGLE---HPLDQHYRNLHCALRPLDHESNEFKVISQYLQSTHAPTHKDYTWTLLDV
                                                                                                                                                                             GPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIELAQALQAV
                                                                                                                     WKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPH----SGGRVGKGIY
                                                                                                                                                                                                          TEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSS-----TFSQSEYLIYQESQCRLR
                                                                                                                                                                                                                                                                                                                              PPO2_HUMAN STANDARD; PRT; 583 AA.
9040NS; Q99CG8; Q910NR4;
16-CCT-2001 (Rel. 40, Last sequence update)
16-OCT-2002 (Rel. 41, Last annotation update)
Poly (ADP-ribose) polymerase-2 (EC 2 4.2.30) (PARP-2) (NADF-ribose) polymerase-2 (EC 2 4.2.30) (PARP-2) (NADF-100SE)
                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cloning of two novel polymerase gene family (ADPRTL): cDNA Genomics 57:442-445(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 22-583 FROM N.A. (ISOFORM 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-99268466; PubMed-10338144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-99263509; PubMed-10329013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEBS Lett. 449:259-263(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                  ADPRIL2 OR PARP2 OR ADPRIZ.
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                                                                                                                                                                                                                                                    527 YLLEV 531
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YLLKI 551
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                             Similarity).

CATALYTIC ACTIVITY: NAD(+) + {ADP-D-ribosyl}(N)-acceptor-
nicotinamide + {ADP-D-ribosyl}(N+1)-acceptor.

SUBCELLULAR LOCATION: NUCLEAR (By similarity).

ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be
produced by alternative splicing.

TISSUE SPECIFICITY: WIDELY EXPRESSED. THE HIGHEST LEVELS ARE IN
THE BRAIN, HEART, PANCRESS, SKELETAL MUSCLE AND TESTIS; ALSO
DETECTED IN KIDNEY, LIVER, LUNG, PLACENTA, OVARY AND SPLEEN;
LEVELS ARE LOW IN LEUKOCYTES, COLON, SMALL INTESTINE, PROSTATE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRAHVYCEGNDVYDVMLNQTNLQFNNNKYYLIQLLEDDAQRNFSVWMRWGRVGKMGQHSL 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167
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Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y., Tanai H., Kimata M., Watanabe M., Nakamura Y., Nagahari K., Masuho Y., Kanahori K., Masuho Y., Kanahori K., "NEDO human cDNA sequencing project."; Submitted (FEB-200) to the EMBL/Genbank/DDBJ databases.

-i- FUNCTION: HAS DNA-DEPENDENT POLY (ADP-RIBOSE) POLYMERASE ACTIVITY. SEEMS TO PLAY A ROLE IN THE RESPONSE TO DNA DAMAGE (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EKKKGRQAG-----REED-----PFRSTA-----EALKAIPAEKRIIRVDPTCPLSSNP
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MISSING (IN ISOFORM 2).
P -> H (IN REF. 2).
N -> H (IN REF. 4).
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NUCLEAR LOCALIZATION SIGNAL 1ST (POTENTIAL).
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35.4%; Pred. No. 1.4e
iive 95; Mismatches
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EMBL, AAJ36876; CAB41505.2; ALT_INIT.
EMBL, AK001980; BAA92017.1; ALT_TERM.
HSSP; P26446; 1A26
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InterPro; IPR001290; PARP.
InterPro; IPR004102; PARP_reg.
Pfam; PF00644; PARP_reg.
Pfam; PF02877; PARP_reg; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                poly(ADP-ribose) polymerase.";
FEBS Lett. 364:103-108(1995).
-!- FUNCTION: POLY(ADP-RIBOSE) POLYMERASE MODIFIES VARIOUS NUCLEAR PROTEINS BY POLY(ADP-RIBOSE).
ON DIA AND IS INVOLVED IN THE REGULATION OF VARIOUS IMPORTANT CELLULAR PROCESSES SUCH AS DIFFERENTIATION, PROLIFERRATION, AND
                                                                                                                                                                         447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-CCT-1996 (Rel. 34, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Poly [ADP-ribose] polymerase (EC 2.4.2.30) (PARP) (ADPRT) (NAD(+) ADP-ribosyltransferase) (Poly[ADP-ribose] synthetase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-95269779; PubMed-7750552;
Lepiniec L., Babiychuk E., Kushnir S., van Montagu M., Inze D.;
"Characterization of an Arabidopsis thaliana cDNA homologue to animal
                                                           346
                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
403
                                                                                                                                                                                                                404 H----SGGRVGKGIYFASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSL 459
                                                                                                                                                                                                                                                                                              ------KSPPPGFDSVIARGHTEP-DPTQDTELELDGQQVVVPQGQPVPCPE 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TUMOR TRANSFORMATION AND ALSO IN THE REGULATION OF THE MOLECULAR EVENTS INVOLVED IN THE RECOVERY OF CELL FROM DNA DAMAGE.

CATALYTIC ACTIVITY: NAD(+) + (ADP-D-ribosyl)(N)-acceptor = nicotinamide + (ADP-D-ribosyl)(N+1)-acceptor.
                                                                                                                                                           390 HAPTHSDYTMTLIDLFEVEKBGEKEAFR--EDLHNRMLLWHGSRMSNWVGILSHGLRIAP
                                                                                              336 ALGDIEIAIKL-----VKTELQSPEHPLDQHYRNLHCALRPLDHESYEFKVISQYLQST
                                                                                                                                    GS---NHRCPTLOHIWKVNOEGEEDRFOAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMP
                                                                                                                                                                                                                                                                                                                                     EGLLQGKHSTKGLGKMAPSSAHFVTLNGSTVPLGPASDT-----GILNPDGY----
                                                         288 VLADIELAQALQAVSEQEKTVEEVP-HPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Nuclear SIMILARITY: BELONGS TO THE PARP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              637 AA
                                                                                                                                                                                                                                                                                                                                                                                                ----TLNYNEYIVYNPNQVRMRYLLKV 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                         505 FSSSTFSQSEYLIYQESQCRLRYLLEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR001290; PARP.
InterPro; IPR004102; PARP_reg.
InterPro; IPR003034; SAP.
Pfam; PF00644; PARP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF02877; PARP_reg; 1. PF02037; SAP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z48243; CAA88288.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPOL_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam;
                                                                                                                                                                                                                                                                                                                                     206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPOL_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300 AVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT-GSNHRCPTLQ-- 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        413 IYFASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSLKSPPPGFDSVIAR 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                66 YNCTLNQTNIENNNNKFYIIQLLQ-DSNRFFTCWNRWGRVGEVGQSKIN-HFTRLEDAKK 123
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                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                             POTENTIAL.
NAD-BINDING (BY SIMILARITY).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
527A8F464605D127 CRC64;
Transferase; SM0513; SAP; 2.
Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein; ADP-ribosylation. 1 140 POTENTAL
DOWALN 140 6.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=90382673; PubMed=2119324; MEDLINE=90382673; PubMed=2119324; Saito I., Hatakeyama K., Kido T., Ohkubo H., Nakanishi S., Ueda K.; Saito I., Hatakeyama K., Kido T., Ohkubo H., Nakanishi S., Ueda K.; Cloning of a full-length cDNA encoding bovine thymus poly (ADP-ribose) synthetase: evolutionarily conserved segments and their potential functions."; Gene 90:249-254(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos. NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229 IFTNKFNDKTKNYWSDRKEFIPHPKSYTWLEMDYGKEENDSPVNND---IPSSSSEVKPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 -CSLDPATOKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALEEALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 GPTDGGQSLEELSSHFYTVIPHNFGHSQPPP--INSPELLQAKKDMLLVLADIELAQALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          357 HIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPH----SGGRVGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GHTEPDPTQDTELELDGQQVVVPQGQPV - PCPEFSSSTFSQSEYLIYQESQCRLRYLLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGPVRTVTKRVQP-
                                                                                                                                                                                                                                                                                                                                                                                     33;
                                                                                                                                                                                                                                                                                                                                  Length 637;
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16-OCT-2001 (Rel. 40, Last annotation update)
Poly [ADP-ribose] polymerase-1 (EC 2.4.2.30) (PARP-1) (ADF
ADP-ribosyltransferase-1) (Poly[ADP-ribose] synthetase-1).
                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                               24.4%; Score 688.5; DB 1; 36.2%; Pred. No. 1.2e-40; iive 89; Mismatches 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1015 AA
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PPOL_SARPE
Q11208;
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                                                                       Taniguchi T., Yamauchi K., Yamamoto T., Toyoshima K., Harada N., Tanaka H., Takahashi S., Yamamoto H., Fujimoto S.; "Depression in gene expression for poly(ADP-ribose) synthetase during the interferon-gamma-induced activation process of murine macrophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00644; PARP; 1.
Pfam; PF00645; Z-PARP; 1.
Pfam; PF00645; Z-PARP; 2.
SWART; SW00292; BRCT; 1.
PROSITE; PS0172; BRCT; 1.
PROSITE; PS00347; PARP_ZN_FINGER_1; 2.
PROSITE; PS50064; PARP_ZN_FINGER_2; 2.
Transferase; G1ycosyltransferase; NAD; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEAR LOCALIZATION SIGNAL 1ST PART.
NUCLEAR LOCALIZATION SIGNAL 2ND PART.
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ADP-RIBOSYL (N) (POTENTIAL).
ADP-RIBOSYL (N) (POTENTIAL).
ADP-RIBOSYL (N) (POTENTIAL).
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                           647-714 AND 838-903 FROM N.A.
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                                                                                                                                                                                                               Biochem. 171:571-575(1988)
                                                   MEDLINE-88151954; PubMed-2450019;
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INIT_MET 0 0 BY
DNA_BIND 1 374
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InterPro; IPR001510; Znf-PARP.
Pfam; PF00533; BRCT; 1.
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InterPro; IPR001290; PARP.
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S00328; S00328.
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24;
 01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Poly (ADP-ribose) polymerase (EC 2.4.2.30) (PARP) (ADPRT) (NAD(+) ADP-ribose) polymerase (EC 2.4.2.30) (Park) (ADP-ribose)
Sarcophaga peregrina (Flesh fly) (Boettcherisca peregrina).
Sarcophaga peregrina (Flesh fly) (Boettcherisca peregrina).
Eukaryota; Metazoa; Arthropad: Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 NPGTQVYED----YNCTLNQTNIENNNNKFYIIQLLQDSNRF-FTCWNRWGRVGEV-GQS 110
 N--AHVLEKGGKVFSATLGLVDIVKGTNSYYKLQLLEDDKESRYWIFRSWGRVGTVIGSN 600
 111 KINHFTRLEDAKKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQ-AEDEAQEAVVKVD 169
 657
 288
 347
 458
 LKSPPPGFDSVIARGHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYLIY 518
 824
 404
 884
 Gaps
 1 MAPKPK----PWVQTEGPEKKKGRQAGREEDPFRSTAEALKAIPAEKRIIRVDPTCPLSS 56
 VNP-GTKSKLPKP-----VQNLIKMIFDVESMKKAMVEYEIDLQKMPLGKLSKRQIQAA
 230 FEALEALEEAL-KGPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLV
 SILSEVQQALSQGSSD--SHILDLSNRFYTLIPHDFGMKKPPLLNNANSVQAKVEMLDN
 LADIELAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT-G
 : | |: |: ||: ||| ||: || ||| || THNAYDLEVVDIFKIEREGESQRYKPFKQLHNRRLLWHGSRTTNFAGILSQGLRIAPPE
 ---SGGRVGKGIYFASENSKSAGYVIGMKCGAHH---VGYMFLGEVALGREHHINTDNPS
 885 APVTGYMFGKGIYFADMVSKSANY----CHTSQGDPIGLILLGEAALGNMYELKHAR-H
 170 RGPVRTVTKRVQPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARG
 SNHRCPTLQ - - HIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPH -
 62;
 Length 1015;
 Masutani M., Nozaki T., Hitomi Y., Ikejima M., Nagasaki K.,
 (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
 (POTENTIAL)
 (POTENTIAL)
 OA5FE9D9F04F5B04 CRC64
 ADP-RIBOSYL[N]
ADP-RIBOSYL[N]
ADP-RIBOSYL[N]
ADP-RIBOSYL[N]
ADP-RIBOSYL[N]
ADP-RIBOSYL[N]
 996 AA
 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-94170813; PubMed-8125121;
 Sarcophagidae; Sarcophaga.
 PRT;
 113355
 Conservative
 STANDARD;
 994 DIAQVHLKYLLKL 1006
472
485
489
514
521
521
 519 QESQCRLRYLLEV 531
 AA:
 Best Local Similarity
Matches 187; Conserv
472
485
489
492
514
521
1015
 NCBI_TaxID=7386;
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NCBI_TaxID=9031;
 TISSUE=Oviduct;
 mutagenesis
 PPOL_CHICK
P26446;
 ADPRT.
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 PPOL_CHICK
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 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 22;
 between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa
 PROFEINS BY POLY (ADP-RIBGSYL)ATION. THE MODIFICATION IS DEPENDENT ON DNA AND IS INVOLVED IN THE REGULATION OF VARIOUS IMPORTANT CELLULAR PROCESSES SUCH AS DIFFERENTIATION, PROLIFERATION, AND
 KTKNNWAERDHFVSHPGKYTLIEVQ-AEDEAQEAVVKVDRGPVRTVTKRVQPCSLDPATQ 190
 IENNNNKFYIIQLLQD--SNRFFTCWNRWGRVG-EVGQSKINHFTRLEDAKKDFEKKFRE 131
 PROSITE; PS50172; BRCT; 1.
PROSITE; PS00347; PARP_ZN_FINGER_1; FALSE_NEG.
PROSITE; PS50064; PARP_ZN_FINGER_2; 2.
Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein;
ADP-Tibosylation; Zinc-finger; Zinc-
DNA_BIND

1 369
SYSMILARITY.
 EEDPFRSTAEALKAIPAEKRI-----IRVDPTCPLSSNPGTQVY-----EDYNCTLNQTN 74
 cDNA from Sarcophaga peregrina.";

Eur. J. Biochem. 220:607-614(1994).
-!- FUNCTION: POLY[ADP-RIBOSE] POLYMERASE MODIFIES VARIOUS NUCLEAR
 IQKNKNSFYKLQLLESDMKNRFWV-FRSWGRIGTTIGGNKLDNFSNLVDAIVQFKELYLE
de Prati A.C., Kurata S., Natori S., Sugimura T., Esumi H.;
"Cloning and functional expression of poly(ADP-ribose) polymerase
 PART
 PART
 55;
 23.9%; Score 674.5; DB 1; Length 996; 33.6%; Pred. No. 2.1e-39;
 BY SIMILARITY.

BY SIMILARITY.

NUCLER LOCALIZATION SIGNAL 1ST

NUCLER LOCALIZATION SIGNAL 2ND

1, 690DDD36E7467298 CRC64;
 Indels
 AUTOMODIFICATION DOMAIN
 195;
 2.1e-39
 Pred. No. 2.1e
; Mismatches
 NAD-BINDING
 Pfam; PF00533; BRCT; 1.
Pfam; PF00644; PARP; 1.
Pfam; PF02877; PARP_reg; 1.
Pfam; PF00645; zf-PARP; 2.
ProDom; PD004675; znf-PARP; 2.
SMART; SM00292; BRCT; 1.
 Conservative 104;
 InterPro; IPR001357; BRCT.
InterPro; IPR001290; PARP.
InterPro; IPR001402; PARP_reg.
InterPro; IPR001510; Znf-PARP.
 EMBL; D16482; BAA03943.1; -.
 113018
 211
232
996 AA;
 HSSP; P26446; 1A26.
 Similarity
 Local Sim
 DOMAIN
SEQUENCE
 Query Match
 ZN_FING
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 Best Loca
Matches
 548
 25
 190
 75
 132
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01-Aug-1992 (Rel. 23, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Poly [ADP-ribose] polymerase-1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+)
ADP-ribosyltransferase-1) (Poly[ADP-ribose] synthetase-1).
 308
 888
 421
 derived
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 of poly(ADP
 X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 659-1011.
MEDLINE-96353841; PubMed-e755499;
Ruf A., Mennissier de Murcia J., de Murcia G.M., Schulz G.E.;
"Structure of the catalytic fragment of poly(AD-ribose) polymerase from chicken.";
 J. Mol. Biol. 278:57-65(1998).
-1- FUNCTION: POLY[ADP-RIBOSE] POLYMERASE MODIFIES VARIOUS NUCLEAR
 191 KLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALEEALKGPTDGGQSL
 E--ELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIELAQALQAVSEQEKTV
 :|:|: |: ||: ||: || :| ||: || ||: || ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: |
 889 SANYC----CTSHHNSTGLMLLSEVALGDMMECTAAKYVTKLPNDK-HSCFGRGRTMPNP
 309 EEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT-GSNHRCPTLQ--HIWKVNQEG
 SAGYVIGMKCGAHH -- VGYMFLGEVALGREHHINTDNPSLKSPPPGFDSVIARGHTEPDP
 Ittel M.-E., Garnier J.-M., Jeltsch J.-M., Niedergang C.;
"Chicken poly(ADP-ribose) synthetase: complete deduced amino acid
 366 EEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPH----SGGRVGKGIYFASENSK
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 659-1011, AND REVISION
 :: | | | | :: | :| :| :| :| 344 SESIIRE-DG--VEIPLGKPITNDSLKSSLL-YNEFIIYDIAQVNIQYMLRMN 992
 480 TQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYLIYQESQCRLRYLLEVH 532
 MEDLINE-98191351; PubMed-9521710;
Ruf A., de Murcia G.M., Schulz G.E.;
"Inhibitor and NaD+ binding to poly(ADP-ribose) polymerase as
from crystal structures and homology modeling.";
Biochemistry 37:3893-3900(1998).
 sequence and comparison with mammalian enzyme sequences.";
 MEDLINE-98239716; PubMed-9571033;
Ruf A., Rolli V., de Murcia G.M., Schulz G.E.;
"The mechanism of the elongation and branching reaction of
ribose) polymerase as derived from crystal structures and
 X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 659-1011.
 Natl. Acad. Sci. U.S.A. 93:7481-7485(1996).
 Ą
 1011
 MEDLINE=91340148; PubMed=1840535;
 STANDARD;
 Gallus gallus (Chicken)
 Gene 102:157-164(1991).
 SEQUENCE FROM N.A.
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PPOL_CRIGR
Q9R152;
 Cricetulus
MOD_RES
CONFLICT
SEQUENCE
 Query Match
 RESULT 8
PPOL_CRIGR
 ADPRT
 477
 701
 Matches
 52
 106
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 THE MODIFICATION IS DEPENDENT
 DNA-binding; Nuclear protein;
 PART.
 SIGNAL 1ST
SIGNAL 2ND
 (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
 (POTENTIAL).
 (POTENTIAL)
 (POTENTIAL)
 (POTENTIAL)
 (POTENTIAL)
 (POTENTIAL)
 (POTENTIAL)
 (POTENTIAL)
 AUTOMODIFICATION DOMAIN
 Probom: PD004675; Znf-PARP; 2.
SMART; SM0292; BRCT; 1.
PROSITE; PS50172; BRCT; 1.
PROSITE; PS500347; PARP_ZN_FINGER_1; 2.
PROSITE; PS50064; PARP_ZN_FINGER_2; 2.
Transferase; Glycosyltransferase; NAD; DNA-binding AND-ribosylation; Zinc-finger; Zinc; 3D-structure.
DNA_END 1 370
 NUCLEAR LOCALIZATION NUCLEAR LOCALIZATION
 ADP-RIBOSYL[N]
ADP-RIBOSYL[N]
ADP-RIBOSYL[N]
ADP-RIBOSYL[N]
ADP-RIBOSYL[N]
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ADP-RIBOSYL[N]
ADP-RIBOSYL[N]
 ADP-RIBOSYL[N]
ADP-RIBOSYL[N]
 ADP-RIBOSYL[N]
 NAD-BINDING.
PROTEINS BY POLY(ADP-RIBOSYL)ATION.
 PARP-TYPE
 PDB; 1A26; 27-MAY-50.
InterPro; IPR001357; BRCT.
InterPro; IPR001290; PARP.
InterPro; IPR001402; PARP_reg.
InterPro; IPR001510; Znf-PARP.
 Pfam; PF00644; PARP; 1.
Pfam; PF02877; PARP. Eeg; 1.
Pfam; PF00645; zf-PARP; 2.
ProDom; PD0004675; Znf-PARP; 2.
 EMBL; X52690; CAA36917.1; -. PIR; JH0581; JH0581.
 458
1011
56
 162
209
225
225
403
404
410
432
432
 2PAX; 27-MAY-98.
3PAX; 27-MAY-98.
4PAX; 27-MAY-98.
1A26; 27-MAY-98.
 2PAW; 27-MAY-98
1PAX; 15-MAY-97
 523
21
125
207
 154
154
168
181
 DOMAIN
ZN_FING
ZN_FING
DOMAIN
 MOD_RES
MOD_RES
MOD_RES
MOD_RES
MOD_RES
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MOD_RES
 MOD_RES
MOD_RES
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 DOMAIN
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 PDB;
 PDB;
 PDB;
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24;
 SEQUENCE FROM N.A.
MEDLINE=21276334; PubMed=11382339;
Ganesh A., Phillips E., Thacker J., Meuth M.;
Ganesh A., Potillips E., Thacker J., Meuth M.;
Suppression of the radiation-sensitive phenotype of hamster irsl and irs2 strains selected for resistance to 3-aminobenzamide.";
Int. J. Radiat. Biol. 77:609-616(2001).
-:- FUNCTION: POLY[ADP-RIBOSE] POLYMERASE MODIFIES VARIOUS NUCLEAR
 223
 281
 813
 873
 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Poly [ADP-ribose] polymerase-1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+)
ADP-ribosyltransferase-1) (Poly[ADP-ribose] synthetase-1).
 EV-GOSKINHFTRLEDAKKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQ-AEDEAQE 163
 757
 282 KKDMLLVLADIELAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQT 341
 342 YLEQT-GSNHRCPTLQ--HIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSG 398
 511
 PWGAEVKTEHQEVAVDGKCSKPANMKSAGKVKEEQGPSKSEKKMKLTV---KGGAAVDPD 533
 CPLSSNPGTQVYED----YNCTLNQTNIENNNNKFYIIQLLQD--SNRFFTCWNRWGRVG 105
 LRIMPH----SGGRVGKGIYFASENSKSAGYVIGMKC---GAHHVGYMFLGEVALGREHH 451
 Gaps
 -----KKKGRQAGREEDPFRSTAEALKAIPAEKRIIRVDPT 51
 452 INTDNPSLKSPPPGFDSVIARGHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFS
 QQIARGFEALEALEEALKGPTDGGQSLE--ELSSHFYTVIPHNFGHSQPPPINSPELLQA
 AVVKVDRGPVRTVTKRVQPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSK
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 .69
 Length 1011;
 Indels
ADP-RIBOSYL[N] (POTENTIAL).
A -> R (IN REF. 1).
W; 261AED9383139144 CRC64;
 / Match 23.9%; Score 674.5; DB 1; Local Similarity 33.4%; Pred. No. 2.1e-39; les 187; Conservative 100; Mismatches 204;
 PRT; 1012 AA
 Cricetulus griseus (Chinese hamster).
 113520 MW;
 512 QSEYLIYQESQCRLRYLLEV 531
 STANDARD;
 7 PW---VQTEGPE-----
 517
895
517 5
895 8
1011 AA;
 NCBI_TaxID=10029;
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Matches 186;
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 AN ACCEPTOR CARBOXYL GROUP ON A HISTONE OR THE ENZYME ITSELF, AND FURTHER ADP-HEDGSTL GROUPS ARE TRANSFERRED TO THE 2'-POSITION OF THE TERMINEL ADENOSITE MOIETY, BUILDING UP A POLYMER WITH AN AVERAGE CHAIN LENGTH OF 20-30 UNITS.
SIMILARITY: BELONGS TO THE PARP FAMILY.
SIMILARITY: CONTAINS I BRCT DOMAIN.
 -!- SUBUNIT: HOMODIMER (Potential).
-!- SUBCELLULAR LOCATION: Nuclear.
-!- MISCELLANEOUS: THE ADP-D-RIBOSYL GROUP OF NAD(+) IS TRANSFERRED TO
 CATALYTIC ACTIVITY: NAD(+) + {ADP-D-ribosyl}(N)-acceptor = nicotinamide + {ADP-D-ribosyl}(N+1)-acceptor. COFACTOR: ZINC, CONTAINS TWO MOLES OF ZINC PER MOLE OF PROTEIN (BY
PROTEINS BY POLY (ADP-RIBOSYL) ATION. THE MODIFICATION IS DEPENDENT
 ON DNA AND IS INVOLVED IN THE REGULATION OF VARIOUS IMPORTANT CELLULAR PROCESSES SUCH AS DIFFERENTIATION, PROLIFERATION, AND TUMOR TRANSFORMATION AND ALSO IN THE REGULATION OF THE MOLECULAR
 SIMILARITY)
 PROSITE; PS50172; BRCT; 1.
PROSITE; PS00147; PARP_ZN_FINGER_1; 2.
PROSITE; PS50064; PARP_ZN_FINGER_2; 2.
Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein;
 NUCLEAR LOCALIZATION SIGNAL 1ST PART
 NUCLEAR LOCALIZATION SIGNAL 2ND PART
 EVENTS INVOLVED IN THE RECOVERY OF CELL FROM DNA DAMAGE (BY
 AUTOMODIFICATION DOMAIN (BY
 NAD-BINDING (BY SIMILARITY)
 8D617C4DBF0CB0F7 CRC64;
 (POTENTIAL)
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 ADP-RIBOSYL(N)
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 SIMILARITY
 (POTENTIAL)
 or send an email to license@isb-sib.ch).
 (POTENTIAL)
 ADP-ribosylation; Zinc-finger; Zinc
 InterPro: IPR001357; BRCT.
InterPro: IPR001357; BRCT.
InterPro: IPR001102; DARP_reg.
InterPro: IPR001510; Znf-PARP.
Pfam; PF00333; BRCT; 1.
Pfam; PF00645; Zf-PARP; 2.
ProDom; PD004675; Znf-PARP; 2.
SMART; SM00292; BRCT; 1.
 ΒX
 EMBL; AF168781; AAD45817.1; -.
 112400
 475
 225
 511 5
512 5
518 5
1012 AA;
 HSSP; P26446; 1A26
 4443
444
470
470
483
487
 406
 similarity)
 SIMILARITY)
 INIT_MET
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DOMAIN
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MOD_RES
SEQUENCE
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ZN_FING
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 DOMAIN
 DOMAIN
 DOMAIN
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DB 1; Length 1012;

Score 673.5; DB 1 Pred. No. 2.5e-39;

23.9%;

Best Local Similarity

Query Match

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350
 01-DEC-1992 (Rel. 24, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Poly (IADP-ribose] polymerase-1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+)
ADP-ribosyltransferase-1) (Poly[ADP-ribose] synthetase-1).
 231
 824
 521
 59 GTQVYED----YNCTLNQTNIENNNNKFYIIQLLQDSNRF-FTCWNRWGRVGEV-GQSKI 112
 404
 884
 405 SGGRVGKGIYFASENSKSAGYVIGMKCGAHH----VGYMFLGEVALGREHHINTDNPSLKS 461
 Gaps
 2 APKPK---PWVQTEGPEKKKGRQAGREEDPFRSTAEALKAIPAEKRIIRVDFTCPLSSNP 58
 TISSUE=Fibroblast;

MEDLINE-B8076933, PubMed=3120710;
Uchida K., Morita T., Sato T., Ogura T., Yamashita R., Noguchi S., Suzuki H., Nyunoya H., Miwa M., Sugimura T.;

Nuclectide sequence of a full-length cDNA for human fibroblast poly(ADP-ribose) polymerase.";
Biochem. Biophys. Res. Commun. 148:617-622(1987).
 SBS TGYMFGKGIYFADMVSKSANY----CHTSQGDPIGLILLGEVALGHWYELKHAS-HISK
 113 NHFTRLEDAKKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQ-AEDEAQEAVVKVDRG
 172 PVRTVTKRVQPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFE
 232 ALEALEEALKGPTDGGOSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLAD
 292 IELAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT-GSNH
 351 RCPTLQ--HIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPH----
 462 PPPGFDSVIARGHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYLIYQES
 493 APKGKSAAPSKKSKGLYKEEG--VNKSEKRMKLTLKGGAA-----VDPDSGLEHS-
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
 59;
 SEQUENCE FROM N.A.
BEDLINE-20091744; PubMed-2513174;
Auer B., Nagl U., Herzog H., Schneider R., Schweiger M.;
"Human nuclear NAD+ ADP-ribosyltransferase(polymerizing):
Conservative 100; Mismatches 205; Indels
 1013 AA.
 01-MAR 1989 (Rel. 10, Created)
01-DEC-1992 (Rel. 24, Last seq
01-MAR-2002 (Rel. 41, Last anno
 organization of the gene.";
DNA 8:575-580(1989).
 STANDARD;
 994 QVNLKYLLKL 1003
 (Human)
 522 QCRLRYLLEV 531
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 Homo sapiens
 PPOL_HUMAN
P09874:
 PPOL_HUMAN
 ID ACC DD THE SERVICE OF THE SERVICE
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EMBL:
 "Molecular cloning of cDNA for human poly(ADP-ribose) polymerase and expression of its gene during HL-60 cell differentiation."; Blochem. Blophys. Res. Commun. 146:403-409(1987).
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 SEQUENCE OF 440-1013 FROM N.A.
MEDLINE-87298455; PubMed-3113420;
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 Suzuki H., Uchida K., Shima H., Sato T., Okamoto T., Kimura T.,
 Gradwohl G., Menissier de Murcia J., Molinete M., Simonin F., Gradwohl G., Menissier de Murcia J., Molinete M., Simonin F., Koken M.H.M., Hoeljmakers J.H.J., de Murcia G.M.; The second zinc-finger domain of poly(ADP-ribose) polymerase determines specificity for single-stranded breaks in DNA."; Proc. Natl. Acad. Sci. U.S.A. 87:2990-2994(1990).
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Hensley P., Smulson M.E.;
 ANALYSIS OF ZINC FINGERS.
MEDLINE-91072398; PubMed-2123876;
IKelima M., Noguchi S., Yamashita R., Ogura T., Sugimura T.,
 SEQUENCE OF 1-39 FROM N.A. Hirsch-Kauffmann M., Schnitzer D., Schweiger M.; Schweiger M.; Submitted (JUL-1991) to the EMBL/GenBank/DDBJ databases.
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 Biochem. Biophys. Res. Commun. 167:701-710(1990)
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[12]
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 SEQUENCE OF 1-39 FROM N.A.
MEDLINE-90211250; PubMed-2108670;
 SEQUENCE OF 1-94 FROM N.A.
 ANALYSIS OF ZINC FINGERS.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 Miwa M.;
 Miwa M.:
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RA RADILAR OF PETELL M., Menissier de Murcia J., de Murcia G.M.;
RA RADILAR OF PETELL M., Menissier de Murcia J., de Murcia G.M.;
RT andom mutagenesis of the poly(ADP-ribose) polymerase catalytic
domain reveals amino acida involved in polymer branching.";
RL Blochemistry 36:12147-12154(1997).
C. I DOCHEMISTRY 36:12147-12154(1997).
C. PROPEINS BY POLY(ADP-RIBOSE) POLYMERASE MODIFIES VARIOUS NUCLEAR
DE ROPEINS BY POLY(ADP-RIBOSE), PATION. THE MODIFICATION IS DEPENDENT
ON DNA AND IS INVOLVED IN THE REGULATION OF THE MOLECULAR
CELLULAR PROCESSES SUCH AS DIFFERENTIATION, PROLIFERATION, AND
CELLULAR PRANSFORMATION AND ALSO IN THE REGULATION OF THE MOLECULAR
C TUMOR TRANSFORMATION AND ALSO IN THE REGULATION OF THE MOLECULAR
C TOTALITIC ACTIVITY: NAD(+) + {ADP-D-ribosy1}(N)-acceptor =
nicotinamide + {ADP-D-ribosy1}(N+1)-acceptor =
nicotinamide + {ADP-D-ribosy1}(N+1)-
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 "The human poly(ADP-ribose) polymerase nuclear localization signal is a bipartite element functionally separate from DNA binding and
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 Simonin F., Menissier de Murcia J., Poch O., Muller S., Gradwohl G., Molinete M., Penning C., Keith G., de Murcia G.M.; "Expression and site-directed mutagenesis of the catalytic domain of human poly ADP-ribose)polymerase in Escherichia coli. Lysine 893 is
 NUCLEAR LOCALIZATION SIGNAL.
MEDILNE-92371433; PubMed=1505517;
Schreiber V., Molinete M., Boeuf H., de Murcia G.M.,
Menissier de Murcia J.;
 or send an email to license@isb-sib.ch).
 critical for activity."; Biol. Chem. 265:19249-19256(1990).
 MEDLINE=97461532; PubMed=9315851;
 AAA51599.1; ALT_SEQ
MUTAGENESIS OF CATALYTIC DOMAIN, MEDLINE-91035460; PubMed-2121735;
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 MUTAGENESIS OF CATALYTIC DOMAIN.
 EMBL; X16674; CAA34663.1; -.
 catalytic activity.";
EMBO J. 11:3263-3269(1992).
 AAA51663.1;
AAA51663.1;
AAA51663.1;
 AAA51663.1;
AAA51663.1;
AAA51663.1;
 AAA60137.1;
AAB59447.1;
 AAA60155.1;
 AAA51663.1;
 AAA51663.1;
AAA51663.1;
 AAA51663.1
 AAA51663.1
 M29545;
M29766;
 M29767;
M29768;
M29769;
 M29779;
M29780;
 J03473;
 M29770;
M29771;
 M17081;
 M29786;
 M29772;
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AAA51663.1;

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ADPRT
 24;
 53 PLSSNPGTQVYED----YNCTLNQTNIENNNNKFYIIQLLQD--SNRFFTCWNRWGRVGE 106
 V-GOSKINHFTRLEDAKKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQ-AEDEAQEA 164
 VVKVDRGPVRTVTKRVQPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQ 224
 QIARGFEALEALEEALKGPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKD 284
 MLLVLADIELAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLE 344
 401
 AS-HISKLPKGKHSVKGLGKTTPDPS--ANISLDG--VDVPLGTGI-SSGVNDTSLLYNE 987
 Gaps
 PW------VQTEGPEKKKGRQAGR-----EEDPFRSTAEALKAIPAEKRIIRVDPTC 52
 QT-GSNHRCPILQ--HIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRI
 455 DNPSLKSPPPGFDSVIARGHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSE
 402 MPH----SGGRVGKGIYFASENSKSAGYVIGMKCGAHH---VGYMFLGEVALGREHHINT
 63;
 Length 1013;
 Indels
 Score 666.5; DB 1;
Pred. No. 7.7e-39;
; Mismatches 207;
 <u>:</u>
 JOINED.
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JOINED.
 PIR; A39976; A39976.
PIR; S14010; S14010.
HSSP: P26446; 1A26.
Aarhus/Ghent-2DPAGE; 1620; NEPHGE.
 M29782; AAA51663.1; JOINED.
X56140; CAA39606.1; -.
X56141; CAA39606.1; JOINED.
M60436; AAA60000.1; -.
 Best Local Similarity 33.45; ran
Matches 186; Conservative 101;
 PARP_reg.
Znf-PARP.
 23.68;
 |::| :| |:||:|
XIVYDIAQVNLKYLLKL 1004
 PARP.
 M29544; AAA51663.1;
M29544; AAA51663.1;
 515 YLIYQESQCRLRYLLEV 531
 AAA51663.1;
 AAA51663.1;
 A35635.
A33321.
B33321.
 InterPro; IPR001357;
 IPR004102;
 IPR001510;
 Pfam; PF00533; BRCT;
Pfam; PF00644; PARP;
 IPR001290;
 A29725.
 A28498
 M29785;
 M29784;
 M29783;
 A33321;
B33321;
 A28498;
 A35635;
 MIM; 173870;
 InterPro;
 InterPro;
 InterPro;
 Query Match
 EMBL;
EMBL;
EMBL;
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SEQUENCE OF 514-1013 FROM N.A.

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SEQUENCE OF 514-1013 FROM N.A.

MEDINNE-90027702; PubMed-5208731;

Thibodeau J., Gradwohl G., Dumas C., Clairoux-Moreau S., Brunet G.;

Thibodeau J., Gradwohl G., Dumas C., Clairoux-Moreau S., Brunet G.;

Thibodeau J., Gradwohl G., Dumas C., Clairoux-Moreau S., Brunet G.;

Thibodeau J., Gradwohl G., Dumas C., Clairoux-Moreau S., Brunet G.;

Thibodeau J., Gradwohl G., Dumas C., Clairoux-Moreau S., Brunet G.;

Blochem. Cell Biol. 67:653-660(1989).

Thibodeau J., Gradwohl G., Dumas C., Clairoux-Moreau S., Brunet G.;

Blochem. Cell Biol. 67:653-660(1989).

THE RECORTINE SP POLY(ADP-RIBOSTI)ATION. THE MODIFICATION IS DEPENDENT ON DNA AND IS INVOLVED IN THE REGOLATION OF VARIOUS IMPORTANT

CELLULAR PROCESSES SUCH AS DIFFERENTIATION, PROLIFERATION, AND TOWN TRANSFORMATION AND ALSO IN THE REGOLATION OF VARIOUS IMPORTANT

CELLULAR PROCESSES SUCH AS DIFFERENTIATION, PROLIFERATION, AND TOWN TRANSFORMATION AND ALSO IN THE REGOLATION OF PREM MOLECULAR ENGLE ACTIVITY: NAD(+) + {ADP-D-ribosyl}(N-)-acceptor = nicotinamide + {ADP-D-ribosyl}(N+1)-acceptor = nicotinamide + {ADP-D-ribosyl}(N+1)-acceptor = nicotinamide + {ADP-D-ribosyl}(N+1)-acceptor = NASCELLANEONS: THE ADP-D-RIBOSYL GROUP OF NAD(+) IS TRANSFERRED TO MASCELLANEONS: THE ADP-D-RIBOSYL GROUP OF NAD(+) IS TRANSFERRED TO THE TERMINAL ADENOSINE MOLETY, BULLDING UP A POLYMER WITH AN ADENOSINE MOLETY, BULLDING UP A POLYMER WITH AN AVERAGE CHAIN LENGTH PRAPE PARM PRAMILY.

SIMILARITY: BELONGS TO THE PARP PAMILY.
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 oetween the Swiss Institute of Bioinformatics and the EMBL outstation
 the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
 P27008; 035937;
01-M0G-1992 (Rel. 23, Created)
15-JUL-1998 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Poly [ADP-ribose] polymerase-1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+)
ADP-ribosyltransferase-1) (Poly[ADP-ribose] synthetase-1).
 Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
 SEQUENCE FROM N.A. STRANGE DAMLEY, TISSUE-Monocytes; STRAIN-SPREAGUE-DAMLEY, TISSUE-Monocytes; MEDLINE-98046546; Pubmed-9385436; Beneke S., Meyer R., Buerkle A.; "Isolation of cDNA encoding full-length rat (Rattus norvegicus) poly
 the
 Potvin F., Thibodeau J., Kirkland J.B., Dandenault B., Duchaine C., Poirier G.G.; Structural analysis of the putative regulatory region of gene encoding poly(ADP-ribose) polymerase. "FEBS Lett. 302:269-273(1992).
 Beneke S., Meyer R., Buerkle A.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases
 1013 AA
 (ADP-ribose) polymerase.";
Biochem. Mol. Biol. Int. 43:755-761(1997).
 SEQUENCE OF 1-11 FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-Prostate;
MEDLINE-92290013; PubMed-1601134;
PRT;
 EMBL, X65496; CAA46477.; -. EMBL, X65497; CAA46478.1; ALT_INIT. HSSP; P26446; 1A26.
 Chordata; C
Rodentia; S
 EMBL; U94340; AAC53544.1; -.
STANDARD;
 Rattus norvegicus (Rat).
 Eukaryota; Metazoa;
Mammalia; Eutheria;
 NCBI_TaxID=10116;
 REVISION TO 811
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InterPro; IPR001357; BRCT

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990 VYDIAQVNLKYLLKL 1004
 517 IYQESQCRLRYLLEV 531
 STANDARD;
 Xenopodinae; Xenopus.
 SEQUENCE FROM N.A.
 NCBI_TaxID=8355;
 TISSUE-Ovary;
 PPOL_XENLA
P31669;
 Miwa M.
 PPOL_XENLA
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 23;
 538 LEHS--AHVLEKGGKVFSATLGLVDIVKGTNSYYKLQLLESDKESRYWIFRSWGRVGTVI 595
 GOSKINHFTRLEDAKKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQ-AEDEAQEAVV 166
 KVDRGPVRTVTKRVQPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQI 226
 ARGFEALEALEEALKGPIDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDML 286
 -GSNHRCPTLQ--HIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMP 403
 54 LSSNPGTQVYED----YNCTLNQTNIENNNNKFYIIQLLQ-DSNRFFTCWNRWGRVGEV- 107
 LVLADIELAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT 346
 SMART; SM00292; BRCT; 1.
PROSITE; PS50172; BRCT; 1.
PROSITE; PS501747; PARP_IN_FINGER_1; 2.
PROSITE; PS50664; PARP_IN_FINGER_2; 2.
Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein;
 Gaps
 1 MAPKPKPWVQTEGPEKKKGRQAGREEDPFRSTAEALKAIPAEKRI-----IRVDPTCP 53
 PART.
PART.
 67;
 23.6%; Score 665.5; DB 1; Length 1013; 33.5%; Pred. No. 9.1e-39; ive 99; Mismatches 203; Indels 67;
 1ST 1
 NUCLEAR LOCALIZATION SIGNAL NUCLEAR LOCALIZATION SIGNAL
 ADP-RIBGSYL NI POTENTIAL)
ADP-RIBGSYL NI POTENTIAL)
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 AA566F2B29BE97C0 CRC64;
 AUTOMODIFICATION DOMAIN. NAD-BINDING.
 (BY SIMILARITY
 -> H (IN REF. 4
-> A (IN REF. 4
-> D (IN REF. 4
 ADP-ribosylation; Zinc-finger; Zinc.
INIT MET 0 0 BY SIMILARITY
 BLOCKED

 23.5%; F±-
 Pfam; PF02877; PARP_reg; 1.
Pfam; PF00645; zf-PARP; 2.
ProDom; PD004675; znf-PARP; 2.
 IPR004102; PARP_reg. IPR001510; Znf-PARP.
 112529
 Matches 186; Conservative
 Pfam; PF00533; BRCT; 1.
Pfam; PF00644; PARP; 1.
 456
484
488
 641 64
752 75
1013 AA;
 Similarity
 444
445
456
484
488
 491
512
513
519
638
 INIT_MET
DNA_BIND
DOMAIN
DOMAIN
DOMAIN
ZN_FING
 InterPro;
 CONFLICT
 Query Match
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 polymerase from Xenopus laevis and cherry salmon using heterologous polymerase from Xenopus laevis and cherry salmon using heterologous oligonucleotide consensus sequences."; 193:194-125(1993).

11. Blochem. Blophys. Res. Commun. 193:119-125(1993).

12. FUNCTION: POLY(ADP-RIBOSE) POLYMERASE MODIFIES VARIOUS NUCLEAR ON DNA AND IS INVOLYED IN THE REGULATION OF VARIOUS INFORMATION OF USE CELLULAR PROCESSES SUCH AS DIFFERENTIATION, PROLIFERATION, AND TOMOR TRANSFORMATION AND ALSO IN THE REGULATION OF THE MOLECULAR EVENTS INVOLVED IN THE REGULATION OF THE MOLECULAR EVENTS INVOLVED IN THE RECOVERY OF CELL FROM DNA DAMAGE.

11. CATALYTIC ACTIVITY: NAD(+) + {ADP-D-ribosyl}(N)-acceptor = nicotinanide + {ADP-D-ribosyl}(N+1)-acceptor.

12. COFACTOR: ZINC, CONTAINS TWO MOLES OF ZINC PER MOLE OF PROTEIN.
 -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN OVARY, OCCYTES,
AND BRAIN. LOW IN LIVER.
-!- MISCELLANEOUS: THE ADP-D-RIBOSYL GROUP OF NAD(+) IS TRANSFERRED TO
 01-JUL-1993 (Rel. 26, Last sequence update)
16-027-2001 (Rel. 40, Last annotation update)
Poly (ADP-ribose] polymerase (EC 2.4.2.30) (PARP) (ADPRT) (NAD(+) ADP-ribosyltransferase) (Poly[ADP-ribose] synthetase) (Fragment).
Xenopus laevis (African clawed frog).
 AN ACCEPTOR CARBOXYL GROUP ON A HISTONE OR THE ENZYME ITSELF, AND FURTHER ADP-RIBOSYL GROUPS ARE TRANSFERRED TO THE 2'-POSITION OF THE TERMINAL ADENOSINE MOIETY, BUILDING UP A POLYMER WITH AN AVERAGE CHAIN LENGTH OF 2030 UNITS.
SIMILARITY: BELONGS TO THE PARP FAMILY.
SIMILARITY: CONTAINS 1 BRCT DOMAIN.
HATTHNAYDLEVIDIFKIEREGESQRYKPFRQLHNRRLLWHGSRTTNFAGILSQGLRIAP 880
 H----SGGRVGKGIYFASENSKSAGYVIGMKCGAHH----VGYMFLGEVALGREHHINTDN
 PEAPVTGYMFGKGIYFADMVSKSANY----CHTSQGDPIGLILLGEVALGNMYELKHAS
 457 PSLKSPPPGFDSVIARGHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYL
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
 SEQUENCE OF 742-876 FROM N.A.
MEDLINE-93277538; PubMed-8503897;
Ozawa Y., Uchida K., Uchida M., Ami Y., Kushida S., Okada N.,
 Saulier-Le Drean B.M.;
Thesis (1992), University of Rennes, France.
 998 AA
 01-JUL-1993 (Rel. 26, Created)
 EMBL; Z12139; CAA78126.1; -. EMBL; D13810; BAA02966.1; -.
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SUBCELLULAR LOCATION: Nuclear.
ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a short form/SPARP-1; may be produced by alternative initiation.
MISCELLANEOUS: THE ADP-D-RIBOSYL GROUP OF NAD(+) IS TRANSFERRED TO AN ACCEPTOR CARBOXYL GROUP ON A HISTONE OR THE BUZYME ITSELF, AND FURTHER ADP-RIBOSYL GROUPS ARE TRANSFERRED TO THE 2'-POSITION OF THE TERMINAL ADENOSINE MOIETY, BUILDING UP A POLYMER WITH AN
 PPOL_MOUSE STANDARD; PRT; 1012 AA.
PPOL_MOUSE (1990)
PPOL_MOUST, 090V03;
P11103; 091LX4; 090V03;
P1100-1969 (Rel. 11, Created)
P1-100-1969 (Rel. 12, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Poly [ADP-ribose] polymerase-1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+)
ADP-ribosyltransferase-1) (Poly[ADP-ribose] synthetase-1) (mspARP).
 Auer B., Flick K., Wang Z.Q., Haidacher D., Jaeger S., Berghammer H., Kofler B., Schweiger M., Wagner E.F.;
"On the biological role of the nuclear polymerizing NAD+: protein(ADP-ribosyl) transferase (ADPRT): ADPRT from Dictyostellum discoideum and
 PROTEINS BY POLY(ADP-RIBOSYL)ATION. THE MODIFICATION IS DEPENDENT ON DNA AND IS INVOLVED IN THE REGULATION OF VARIOUS IMPORTANT CELLULAR PROCESSES SUCH AS DIFFERENTIATION, PROLIFERATION, AND TUMOR TRANSFORMATION AND ALSO IN THE REGULATION OF THE MOLECULAR EVENTS INVOLVED IN THE RECOVERY OF CELL FROM DNA DAMAGE.
 Huppi K., Bhatia K., Siwarski D., Klinman D., Cherney B., Smulson M.; "Sequence and organization of the mouse poly (ADP-ribose) polymerase
 SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION.
STRAIN=129/SV X C57BL/6; TISSUE=Fibroblast;
MEDLINE=20270268; bubMed=10809783;
Sallmann F.R., Vondenicharow M.D., Wang Z.-Q., Poirier G.G.;
"Characterization of spARP-1. An alternative product of PARP-1 gene with poly(ADP-ribose) polymerase activity independent of DNA strand
 CATALYTIC ACTIVITY: NAD(+) + {ADP-D-ribosyl}(N)-acceptor = nicotinanide + {ADP-D-ribosyl}(N+1)-acceptor.
COFACTOR: ZINC, CONTAINS TWO MOLES OF ZINC PER MOLE OF PROTEIN.
SUBMUNIT: HOMODIMER (Potential).
 inactivation of the ADPRT gene in the mouse.";
Biochimie 77:444-449(1995).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 DSVIARGHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYLIYQESQCRLR
 GRVGKGIYFASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSLKSPPPGF
 Nucleic Acids Res. 17:3387-3401(1989)
 Biol. Chem. 275:15504-15511(2000).
 MEDLINE-89263780; PubMed-2498841;
 MEDLINE=96007847; PubMed=7578427;
 SEQUENCE FROM N.A. (ISOFORM 1).
 ADPRT OR ADPRTI OR ADPRP.
 (Wouse)
 NCBI_TaxID=10090;
 527 YLLEV 531
 YLLKL 988
 Mus musculus
 STRAIN-BXSB;
 KNOCK - OUT
 breaks.
 PPOL_MOUSE
 407
 467
 984
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 20;
 649
 PSSGPVAGKSSGKVKEEKGSIKSEKKMKLTVKGGAAIDPDSEL---EDSCHVLETGG---533
 63 YEDYNCTLNQTNIENNNNKFYIIQLLQ-DSNRFFTCWNRWGRVGEV-GQSKINHFTRLED 120
 AKKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGPVRTVTKRV 180
 181 QPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALEEAL 240
 241 KGPTDGGQSLEE----LSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIELA 295
 PTLQ--HIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPH----SG 406
 Gaps
 PKPKPWVQTEGPEKKKGRQAGREEDPFRSTAEALKAIPAEKRIIRVDPTCPLSSNPGTQV 62
 DNA-binding; Nuclear protein;
 PART.
 -KIFSATLGLVDITRGTNSYYKLQLIEHDRDSRYWVFRSWGRVGTVIGSKKLEEMSSKED
 AIEHFLNLYQDKTGNAW-HSPNFTKYPKKFYPLEIDYGQE-EDVVKKLSVG-AGTKSKLA
 QAL--QAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT-GSNHRC
 52;
 1ST
2ND
 23.1%; Score 653; DB 1; Length 998; 32.5%; Pred. No. 6.6e-38; tive 102; Mismatches 214; Indels
 SIGNAL
 (POTENTIAL). (POTENTIAL). (POTENTIAL).
 (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
 (POTENTIAL)
 (POTENTIAL)
 (POTENTIAL)
 > E (IN REF. 2).
F5A25E4A3366BAE7 CRC64;
 (POTENTIAL)
 (POTENTIAL)
 AUTOMODIFICATION DOMAIN.
 PARP-TYPE.
NUCLEAR LOCALIZATION
NUCLEAR LOCALIZATION
 ADP-RIBOSYL[N]
ADP-RIBOSYL[N]
ADP-RIBOSYL[N]
ADP-RIBOSYL[N]
ADP-RIBOSYL[N]
ADP-RIBOSYL[N]
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ADP-RIBOSYL[N]
ADP-RIBOSYL[N]
ADP-RIBOSYL[N]
ADP-RIBOSYL[N]
ADP-RIBOSYL[N]
 BINDING
 PROSITE: PS50172; BRCT: 1.
PROSITE; PS50172; BRCT: 1.
PROSITE; PS500347; PARP_ZN_FINGER_1; 2.
PROSITE; PS50064; PARP_ZN_FINGER_2; 2.
Transferase; Glycosyltransferase; NAD;
ADP_ribosylation; Zinc-finger; Zinc.
NON_TER.
 ^
 Conservative 102;
 PARP_reg.
Znf-PARP.
 Ψ.
 Pfam; PF02877; PARP_reg; 1.
Pfam; PF00645; zf-PARP; 2.
ProDom; PD004675; znf-PARP; 2.
 111126
 SM00292; BRCT; 1
 Pfam; PF00533; BRCT; 1
Pfam; PF00644; PARP; 1
 InterPro; IPR001357;
 InterPro; IPR004102;
InterPro; IPR001510;
 IPR001290;
 746
998 AA;
 Similarity
 P26446; 1A26
 111
193
207
391
 419
428
429
445
4447
4477
4471
4471
 Query Match
Best Local Simi
Matches 177;
 InterPro;
 CONFLICT
 DNA_BIND
 DOMAIN
DOMAIN
ZN_FING
 MOD_RES
MOD_RES
MOD_RES
MOD_RES
MOD_RES
MOD_RES
 MOD_RES
MOD_RES
MOD_RES
MOD_RES
MOD_RES
 ZN_FING
DOMAIN
 MOD_RES
 SMART;
 DOMAIN
 DOMAIN
 121
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Query Match
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 rransferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein;
ADP-ribosylation; Zinc-finger; Zinc; Alternative initiation.
INIT_MET 0 0 BY SIMILARITY.
 POLY [ADP-RIBOSE] POLYMERASE-1, SHORT
 POLY [ADP-RIBOSE] POLYMERASE-1,
 ADP-RIBOSYL[N] (POTENTIAL).
ADP-RIBOSYL[N] (POTENTIAL).
ADP-RIBOSYL[N] (POTENTIAL).
ADP-RIBOSYL[N] (POTENTIAL).
ADP-RIBOSYL[N] (POTENTIAL).
ADP-RIBOSYL[N] (POTENTIAL).
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ADP-RIBOSYL[N] (POTENTIAL).
ADP-RIBOSYL[N] (POTENTIAL).
ADP-RIBOSYL[N] (POTENTIAL).
ADP-RIBOSYL[N] (POTENTIAL).
 NUCLEAR LOCALIZATION SIGNAL NUCLEAR LOCALIZATION SIGNAL
 4354C3E5F01B9439 CRC64;
 AUTOMODIFICATION DOMAIN.
 FOR SHORT ISOFORM
 REF.
 REF.
 REF.
REF.
REF.
 REF.
 SIMILARITY: BELONGS TO THE PARP FAMILY. SIMILARITY: CONTAINS 1 BRCT DOMAIN.
 REF.
 BINDING.
AVERAGE CHAIN LENGTH OF 20-30 UNITS
 PROSITE; PSS0172; BRCT; 1.
PROSITE; PS00347; PARP_ZN_FINGER_1; 2.
PROSITE; PS50064; PARP_ZN_FINGER_2; 2.
 EMBL; AF126717; AAF61293.1; ALT_INIT.
PIR; S04200; S04200
HSSP; P26446; 1A26.
MGD; MGI:1340806; Adprtl.
InterPro; IPR001357; BRCT.
InterPro; IPR001290; PARP.
 ISOFOR
 ^ ^ ^ ^ ^ ^ ^ ^ ^
 ^ ^
 Pfam; PF02877; PARP_reg; 1.
Pfam; PF00645; zf-PARP; 2.
ProDom; PD004675; znf-PARP; 2.
 InterPro; IPR004102; PARP_reg
InterPro; IPR001510; Znf-PARP
 112968
 EMBL; X14206; CAA32421.1;
 SMART; SM00292; BRCT; 1.
 Pfam; PF00533; BRCT; 1.
Pfam; PF00644; PARP; 1.
 1012
 487
 511
512
518
590
607
 611
628
678
702
716
757
856
 1012
 716 71
757 75
856 85
981 98
 455
483
487
490
 CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
 INIT_MET
DNA_BIND
 CONFLICT
 DOMAIN
ZN_FING
ZN_FING
DOMAIN
DOMAIN
 MOD_RES
MOD_RES
MOD_RES
MOD_RES
MOD_RES
MOD_RES
MOD_RES
MOD_RES
MOD_RES
MOD_RES
MOD_RES
 RES
 DOMAIN
 CHAIN
 CHAIN
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22;
 PPOL_DROME STANDARD; PRT; 994 AA.
PPOL_DROME STANDARD;
P36875; O99465; O994651;
P36875; O99465; O994651;
P36876; O99467; O994 AA.
P96876; O9946; D120N-1994 (Rel. 29, Last sequence update)
O1-MAR-2002 (Rel. 41, Last annotation update)
POLY (ADP-ribose] POlymerase (EC 2.4.2.30) (PARP) (ADP-ribose] (POLYMED-ribose] synthetase).
PARP OR CG17696/CG1718.
 286
 763
 346
 819
 | : | | : | | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
 GOSKINHFTRLEDAKKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQ-AEDEAQEAVV 166
 651
 704
 H----SGGRVGKGIYFASENSKSAGYVIGMKCGAHH----VGYMFLGEVALGREHHINTDN 456
 PSLKSPPPGFDSVIARGHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYL 516
 LSSNPGTQVYED----YNCTLNQTNIENNNNKFYIIQLLQDSNRF-FTCWNRMGRVGEV- 107
 -GSNHRCPTLQ--HIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMP 403
 880 PEAPVTGYMFGKGIYFADMVSKSANY-----CHTSQGDPIGLIMLGEVALGNMYELKHAS 934
 Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:
Pterygota: Neoptera: Endopterygota: Diptera: Brachycera: Muscomorpha;
Ephydroidea: Drosophilidae; Drosophila.
 Gaps
 1 MAPKPKPWVQTEGPEKKKGRQAGREEDPFRSTAEALKAIPAEKRI------IRVDPTCP 53
 SEQUENCE FROM N.A., ALTERNATIVE SPLICING, DEVELOPMENTAL STAGE, AND STASUE SPECIFICITY.
STRAIN-CANTON-S.
MEDLINE-98234380; Pubmed-9565614;
 167 KVDRGPVRTVTKRVQPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQI
 227 ARGFEALEALEEALKGPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDML
 287 LVLADIELAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT
 OAAYSILSEVQQPVSQGSSESQIL-DLSNRFYTLIPHDFGMKKPPLLNNADSVQAKVEML
 MEDLINE-93234521; Pubmed-8475096;
Orbida K., Hanai S., Ishikawa K.-I., Ozawa Y.-I., Uchida M.,
Sugimura T., Miwa M.;
"Cloning of cDNA encoding Drosophila poly(ADP-ribose) polymerase:
 67;
 Length 1012;
 Indels
Query Match 23.0%; Score 649.5; DB 1; Best Local Similarity 32.4%; Pred. No. 1.2e-37; Matches 180; Conservative 103; Mismatches 205;
 Proc. Natl. Acad. Sci. U.S.A. 90:3481-3485(1993)
 zipper in the auto-modification
 :| :| |:| |:|| |:| | 989 VYDIAQVNLKYLLKL 1003
 517 IYQESQCRLRYLLEV 531
 SEQUENCE FROM N.A.
 NCBI_TaxID=7227;
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Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Manatides P.G., Scherer S.E. Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Hichards S., Ashburner M., Henderson S.N.,
RA Gutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Brandon R.C., Rogers Y.H.C., Mazel R.G., Champe M., Pielifer B.D.,
RA Man K.H., Doyle G., Barkendale J., Bayraktaroglu L., Beasley E.M.,
RA Mali J.F., Agbayani A., An H.J., Andrews Pienankoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Meril J.F., Agbayani A., An H.J., Andrews Pienankoch C., Baldwin D.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottlier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottlier B.,
RA Grangelista C., Ferraz C., Ferriera S., Durkov B.C., Dunn P.,
RA Grangelista C.C., Ferraz C., Ferriera S., Durkov B.C., Dunn P.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Houston K.A., Howlend T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Marvey D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Marvey D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Marvey D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Marvey D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Marvey D., Mollard T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Marvey D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Milanna N.V., Mobarry C., Morris J., Monts J., Lia Z.,
RA Mount S.M., Woodsof T., Wolders E., Shen H.,
Spiar E., Spradling A.C., Stapleton M., Strong R., Santh H.O.,
RA Mang Z.-Y., Rassaman D.A., Wainstock G.M., Weissenbach J.,
RA Waing Z.-Y., Rassaman D.A., Wainstock G.M., Weissenbach J.,
RA Waing Z.-Y., Rassaman D.A., Wainstock G.M., Weissenbach J.,
RA Waing S.N., Weodoge T., Woolly K.C., Who D., Staple C., Siden Kianos I.S., Shon M., Vehrer E., Wen W., Phys.
 EMBRYOS, PUPAE AND ADULTS. EXPRESSION IS HIGHEST IN EMBRYOS.

AN ACCEPTOR CARBOXYL GROUP ON A HISTONE OR THE ENZYME ITSELF, AND FURTHER ADP-RIBOSYL GROUP ON A HISTONE OR THE ENZYME ITSELF, AND FURTHER ADP-RIBOSYL GROUPS ARE TRANSFERRED TO THE 2'-POSITION OF THE TERMINAL ADENOSINE MOIETY, BUILDING UP A POLYMER WITH AN STRANGE CHAIN LENGTH OF 20-30 UNITS.

SIMILARITY: BELONGS TO THE PARP FAMILY.
SIMILARITY: CONTAINS I BRCT DOMAIN.
 SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: EXPRESSED IN ADULT FEMALE OCCYTES, ANAL PLATES
OF STAGE 12 EMBRYOS AND IN CELLS AROUND THE CENTRAL NERVOUS SYSTEM
IN LATER EMBRYOS.
DEVELOPMENTAL STAGE: EXPRESSED BOTH MATERNALLY AND ZYGOTICALLY IN
 EVENTS INVOLVED IN THE RECOVERY OF CELL FROM DNA DAWAGE.

CATALYTIC ACTIVITY: NAD(+) + {ADP-D-ribosyl}(N)-acceptor = nicotinamide + {ADP-D-ribosyl}(N+1)-acceptor.

COFACTOR: ZINC, CONTAINS TWO MOLES OF ZINC PER MOLE OF PROTEIN.
SUBCELLULAR LOCATION: Nuclear.

ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
 TUMOR TRANSFORMATION AND ALSO IN THE REGULATION OF THE MOLECULAR
Hanai S., Uchida M., Kobayashi S., Miwa M., Uchida K.; "Genomic organization of Drosophila poly(ADP-ribose) polymerase and distribution of its mRNA during development."; J. Biol. Chem. 273:11881-11886(1998).
 MEDLINE=20196006; PubMed=10731132;
 SEQUENCE FROM N.A. (LONG ISOFORM).
 STRAIN-BERKELEY;
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 19;
 325
 88 LQ-DSNRFFTCWNRWGRVG-EVGQSKINHFTRLEDAKKDFEKKFREKTKNNWAERDHFVS 145
 726
 842
 617
 Gaps
 SMART; SM00292; BRCT; 1.
PROSITE; PS50172; BRCT; 1.
PROSITE; PS50147; PARP_ZN_FINGER_1; 1.
PROSITE; PS50064; PARP_ZN_FINGER_2; 2.
Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein;
ADP_ribosylation; Zinc-finger; Zinc; Alternative splicing.
 37 KAIPAEKRI----IRVDPTCPLSSNPGTQVYED----YNCTLNQTNIENNNNKFYIIQL
 500 KSMPVSRTFKVKDGLAVDPDSGLEDI---AHVYVDSNNKYSVVLGLTDIQRNKNSYYKVQL
 GHSQPPPINSPELLQAKKDMLLVLADIELAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQ
 146 HPGKYTLIEVQAEDEAQEAVVKVDRGPVRTVTKRVQPCSLDPATQKLITNIFSKEMFKNT
 618 RIGRMYPIEIQYDDD--QKLVKHE-----SHFFTSKLEISVQNLIKLIFDIDSMNKT
 206 MALMDLDVKKMPLGKLSKQQIARGFEALEALEEALKGPTDGGQSLEELSSHFYTVIPHNF
 LQLLDSGAPEYKVIQTYLEQT-GSNHRCPTLQ--HIWKVNQEGEEDRFQAHSKLGNRKLL
 58;
 NUCLEAR LOCALIZATION SIGNAL 1ST
NUCLEAR LOCALIZATION SIGNAL 2ND
 Length 994;
 Conservative 100; Mismatches 195; Indels
 MISSING (IN SHORT ISOFORM).
; ACA85A270DD29E08 CRC64;
 AUTOMODIFICATION DOMAIN.
 Score 638; DB 1;
Pred. No. 7.4e-37;
 NAD-BINDING.
 PARP-TYPE.
PARP-TYPE.
 EMBL; AE002892; APF45445.2; ALT_SEQ. PIR; A47474; A47474; A47474; A47474; PISSP. P26446; 1A26.
 EMBL, AF051548; AAC24518.1; -...
EMBL, AF051544; AAC24518.1; JOINED.
EMBL, AF051546; AAC24518.1; JOINED.
EMBL, AF051546; AAC24518.1; JOINED.
EMBL, AF051547; AAC24518.1; JOINED.
EMBL, AE002935; AAF45400.1; -...
 FlyBase; FBgn0010247; Parp.
InterPro; IPR001357; BRCT.
InterPro; IPR001290; PARP.
InterPro; IPR004102; PARP.
InterPro; IPR004102; PARP.
Fam: PF00533; BRCT; 1.
 210 NUC
228 NUC
564 MIS
113791 MW;
 Pfam; PF02877; PARP_reg; 1.
Pfam; PF00645; zf-PARP; 2.
ProDom; PD004675; znf-PARP; 2.
 22.6%;
 D13806; BAA02964.1;
 Pfam; PF00644; PARP; 1.
 454
994
54
161
 376
994 AA;
 Local Similarity
 168;
 VARSPLIC
SEQUENCE
 Query Match
 DNA_BIND
 DOMAIN
ZN_FING
ZN_FING
DOMAIN
 DOMAIN
 DOMAIN
 DOMAIN
 EMBL;
 Matches
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(193-kDa vault (PH5P).
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 295
 397
 507
 У. ў.
 LSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVL----ADIELAQALQAVSEQEKT
 -----IYQRLYERLPCHLEPVSE------EIAGKIGDCLAMRGPTHCYKLSLI
 398 MNGLQFPVGDRCGLMFGNGVYFANVPTKSANYC----CPEASKRVFMLLCEVETANPLVL
 449 - EHHINTDNPSLKSPPPGFDSVIARGHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSS
 ------OEGEEDRFQAHSKLG-----NRKLLWHGTNMAVVAAIL
 396 TSGLR--IMPHSGGRVGKGIYFASENSKSAGYVIGMKC-GAHHVGYMFLGEVALGR----
 MEDLINE-99408776; PubMed-10477748; Kickhoefer V.A., Siva A.C., Kedersha N.L., Inman E.M., Ruland C., Strulli M., Rome L.H.; Trrulli WPARP, is a novel poly(ADP-ribose) polymerase.";
 Nagase T., Seki N., Ishikawa K.-I., Tanaka A., Nomura N.; Prediction of the coding sequences of unidentified human genes. The coding sequences of 40 new genes (KIAA0161-KIAA0200) deduced analysis of cDNA clones from human cell line KG-I.";
 308 VEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQTGSNHRCPTLQ---HIWKVN--
 Euteleostom1;
 still I.H., vince P., Cowell J.K.;
"Identification of a novel gene (ADPRTL1) encoding a potential
poly(ADP-ribosy))transferase protein.";
Genomics 62:533-536(1999).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
 PPOV_HUMAN STANDARD; PRT; 1724 AA. 09UKK3, 075903; 09HIMG; 024682; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Vault poly(ADP-ribose) polymerase (EC 2.4 2.30) (VPARP) protein) (PARP-related/Talphal-related H5/prolline-rich)
 Tromans A.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
 Jean L., Risler J.-L., Nagase T., Coulouarn C., Nomura Salier J.-P.;
 SEQUENCE FROM N.A., AND SEQUENCE OF 306-319
 | : | | :: | | | | | ETIEEETRLLYDEYVMFNKEHFKIKYVVEV 526
 508 STFSQ-----SEYLIYQESQCRLRYLLEV 531
 SEQUENCE FROM N.A.
TISSUE-Thymus;
MEDLINE-20112770; PubMed-10644454;
 DISCUSSION OF SEQUENCE. MEDLINE-99198702; Pubmed=10100603;
 MEDLINE=96281124; PubMed=8724849;
 Cell Biol. 146:917-928(1999).
 ADPKTLL C...
Homo sapiens (Human)
Motazoa; Chordata;
 ADPRTL1 OR PARPL OR KIAA0177.
 SEQUENCE OF 94-1724 FROM N.A.
 DNA Res. 3:17-24(1996)
 TISSUE-Bone marrow;
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 RESULT 15
PPOV_HUMAN
 497
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 27;
 MFLGEVALG-----REHHIN--TDNPSLKSPPPGFDSVIARGHTEPDPTQDTELELDGQ 490
 | || || || :| || || || || || || ::|:
71 ESKFYEKTHLHWEERDD-EPVPNKYAVVELATNARQTEKEVKKEEPEPEPKVDEKNTRGR 129
 170 --RGPV---RTVTKRVQPCSLDPATQKLITNIFSKEMFKNTMALMDLDV----KKM--- 216
 WHGTNMAVVAAILTSGLRI----MPHSGGRVGKGIYFASENSKSAGYVIGMKCGAHHVGY 438
 66 YNCTLNQTNIENNNNKFYIIQLLQDSNRFFTCWNRWGRVGEVGQSKINHFTRLEDAKKDF 125
 -----PLGKLSKQQIARGFEALEEALKGPT---------DGGQSLEE 252
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
 Gaps
 12 YKVHLCKTNIAQNNNKFYDMELLDEGGDFIVKLIN-GRIGYRGVTQLKDFDDLDRAKKFF 70
 EKKFREKTKNNWAERDHFVSHPGKYTLIEV------QAEDEAQEAVVKVD-----
 Indels 159;
 Length 538;
 Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: SOME, TO THE MIDDLE PART OF NAD(+) ADP-RIBOSYLTRANSFERASE (EC 2.4.2.30).
 01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Hypothetical 61.3 kDa protein E02H1.4 in chromosome II.
 11 protein. 5
538 AA; 61268 MW; 3144E25465FC7341 CRC64;
 | :| |: : | |: :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|
 QVVVPQGQPVPCPEFSSSTFSQSEYLIYQESQCRLRYLLEV 531
 DB 1;
 172;
 Score 393.5; DB 1
Pred. No. 3.8e-20;
 Ž
 Mismatches
 JA26.

"UnterPro; E0241.4; CE01539.

R InterPro; IPR001290; PARP.
R Pfam: PF00644; PARP; 1.
R Pfam: PF02877; PARP; 1.
R Hypothetical protein.
SEQUENCE 518
 13.9%; Scor
26.1%; Pred
ative 90; }
 EMBL; Z47075; CAA87379.1; -. HSSP; P26446; 1A26.
 Matches 149; Conservative
 STANDARD;
 Caenorhabditis elegans
 Local Similarity
 SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
 NCBI_TaxID-6239;
 YON4_CAEEL
Q09525;
 Smith A.;
 Query Match
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 INTERACTION WITH THE MAJOR VAULT PROTEIN.
nuclear protein PH5P of the inter-alpha-inhibitor superfamily: a
 PROTEINS OF 193 AND 240-kba.

-!- SUBCELLULAR LOCATION: CYTOPLASMIC, BUT IS ALSO FOUND IN THE NUCLEUS, ASSOCIATED WITH MITOTIC SPINDLES.

-! TISSUE SPECIFICITY: WIDELY EXPRESSED; THE HIGHEST LEVELS ARE IN THE KIDNEY; ALSO DETECTED IN HEART, PLACENTA, LUNG, LIVER, SKELETAL MUSCLE, SPLEEN, LEUKOCYTES AND PANCREAS.

-!- SIMILARITY: CONTAINS 1 BRCT DOMAIN.
-!- SIMILARITY: CONTAINS 1 WAFA DOMAIN.
 inter-alpha-inhibitor family and a novel actor of DNA repair?";
FEBS Lett. 446:6-8(1999).
-!- CATALYTIC ACTIVITY: NADP(+) + {ADP-D-ribosyl}(N)-acceptor = nicotinamide + {ADP-D-ribosyl}(N+1)-acceptor.
-!- SUBUNIT: BINDS TO THE MAJOR VAULT PROTEIN (MPV). THE VAULT, A LARGE RIBONUCLEOPROTEIN COMPLEX, CONTAINS THE 100-KDA MPV AND
 NUCLEAR LOCALIZATION SIGNAL 1ST PART
 NUCLEAR LOCALIZATION SIGNAL 2ND PART (POTENTIAL).
 NAD-BINDING (BY SIMILARITY).
 A009F34934460EDC CRC64;
 ransferase; Glycosyltransferase; NAD; Nuclear protein;
 4 4 . .
 AND 4).
AND 4).
 AND 4).
 between poly(ADP-ribose)polymerase and
 AND
 REF.
 REF.
REF.
REF.
REF.
REF.
REF.
 POTENTIAL
 Ribonucleoprotein.
 EMBL; AF158255; AAD47250.1; -. EMBL; AF057160; AAC62491.1; -. EMBL; AL359763; CAC21562.1; -.
 AA; 192587
 EMBL; D79999; BAA11494.1;
HSSP; P26446; 1A26.
 InterPro; IPR002035; vWFA.
 Pfam, PF00533 BRCT; 1.
Pfam, PF00644; PARP; 1.
Pfam, PF00092; wwa; 1.
SAMRT; SM00292; BRCT; 1.
 PROSITE; PS50172; BRCT; 1.
PROSITE; PS50234; VWFA; 1.
 InterPro; IPR001357; BRCT.
InterPro; IPR001290; PARP.
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1046
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 1249
 ADP-ribosylation;
 1724
 1237
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                                 Gaps
                                                               EKRIIRV----DPTCPLSSNP-----GTQVYEDYNCTLNQTNIEN-----NNNKFYI 84
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                               92; Mismatches 193; Indels 146;
Length 1724;
 Score 258; DB 1;
Pred. No. 5.5e-10;
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                                    Conservative
                   Local Similarity
                                    Matches 127;
    Query Match
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095271 homo sapien
O97271 homo sapien
O87242 homo sapien
O66878 aquifex aeo
O97273 drosophila
O97273 drosophila
O924M2 mus musculu
O97240 homo sapien
O97240 homo sapien
O9722 aequipecten
O97121 mus musculu
O9171 mus musculu
O91747 mus musculu
O91x49 mus musculu
O91x47 chara coral
O91874 homo sapien
O03291 saccharomyc
O03291 saccharomyc
O91875 streptococc
O90463 mus musculu
O91877 streptococc
O90463 mus musculu
O91874 homo sapien
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 60. I KDA PROTEIN.
HOMO sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUB-PRIMARY B-CELLS FROM TONSILS;
Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBa
REBL; BC014260; AAH14260.1; -..
W Hypothetical protein.
SEQUENCE 533 AA; 60089 MW; 6296A0
                                                                                                                                                                                      Q9NJ23
Q9NJ22
Q9NJ21
Q9NJ20
Q17 Q42
Q91V71
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Q91XT8
Q91XT9
Q91XT7
Q95XT7
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O66878
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Q9XZ37
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Q924M2
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                                 Compugen Ltd
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                GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
sp_lung1:*
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Maximum Match 100%
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InterPro; IPR004102; PARP_reg.
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Matches 217; Conservative
                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                          VSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQTGSNHRCPTLQHIWK
                                                                                                                                                                                                                        VNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPHSGGRVGKGIYFASENS
                                                                                                                                                                                                                                             KSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSLKSPPPGFDSVIARGHTEPDPT
                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAPKPKPWVQTEGPEKKKGRQAGREEDPFRSTAEALKAIPAEKRIIRVDPTCPLSSNPGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC014870; AAH14870.1; -.
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80.7%; Pred. No. 2.4e-164;
iive 37; Mismatches 59; In
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 59.4 KDA PROTEIN.
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Hypothetical protein.
SEQUENCE 528 AA; 5
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Best Local Similarity
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Auer B., Filck K., Wang Z.Q., Haidacher D., Jager S., Berghammer H.,
KOfler B., Schweiger M., Magner E.F.;
"On the biological role of the nuclear polymerizing NAD+: protein(ADP-
ribosyl, transferase (ADPRT): ADPRT from Dictyostellum discoideum and
inactivation of the ADPRT gene in the mouse.";
Biochimie 77:444-449(1995).
                                                              479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QAKKDMLLVLADIELAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVI 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421
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PKPKPWVQTEGPEKKKGRQAGREEDPFRSTAEALKAIPAEKRIIRV------DPTCPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 SSRKDFGKGGLNOAISLFCSKFYEKTKNTFTDRANFKKVAGKYDMIELDYSTDS----K
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                                                                                     168 VDRG----PVRTVTKRV----QPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLSKQQIARGFEALEALEEALKGPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELL
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                                                                                                                                                 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74;
                                                                                                                                                 480 TQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYLIYQESQCRLRYLLEVHL
                                                                                                                                                                          Length 612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194; Indels
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                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NAD+:PROTEIN(ADP-RIBOSYL)-TRANSFERASE (EC 2.4.2.30).
Dictyostelium discoideum (Slime mold).
ENRARYOER, Mycetozoa; Dictyostelium.
NIBI_TAXID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 826; DB 5;
Pred. No. 5.8e-55;
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Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
  SNAPVKSSNDEAEDDNNGFEEEKKEEKIVTATKKGAAVLDQWIPDEIKSQYHVLQRGDDV 166
                                                      66 YNCTLNQTNIENNNNKFYIIQLLQ-DSNRFFTCWNRWGRVGEVGQSKIN-HFTRLEDAKK 123
                                                                                                                                                                                                                                                                                                                                                                                                        357 HIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPH----SGGRVGKG 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             413 IYFASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSLKSPPPGFDSVIAR 472
                                                                                     124 DFEKKFREKTKNNWAERDHFVSHPCKYTLIEVQAEDEAQEAVVKVDRGPVRTVTKRVQP-
                                                                                                                                                                                          183 -CSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALEALK
                                                                                                                                                                                                                                                                                                242 GPTDGGQSLEELSSHFYTVIPHNFGHSQPPP--INSPELLQAKKDMLLVLADIELAQALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 AVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT-GSNHRCPTLQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                473 GHTEPDPTQDTELELDGQQVVVPQGQPV--PCPEFSSSTFSQSEYLIYQESQCRLRYLLE
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Babyichuk E., Cottrill P., Storozhenko S., Fuangthong M.,

O'Farrell M., Van Montagu M., Inze D., Kushir S.,

"Higher plants possess two poly(ADP-ribose) polymerases.";

L. Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.

R. HSSP, P26446, 1A26.

R. InterPro; IPR001290; PARP.

R. InterPro; IPR001209; PARP_reg.

R. InterPro; IPR0014102; PARP_reg.

R. Pfen; PF00644, PARP, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 653;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) POLY(ADP-RIBOSE) POLYMERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 670.5; DB 1
Pred. No. 5.5e-43;
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PF02037; SAP; 2.
SM00513; SAP; 2.
VCE 653 AA; 72995 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1998 (TrEMBLrel. 06,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      531 V 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       629 V 629
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                                                                                                                                                                                                                                                                                                                                                                                                                081294;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
11-NOV-1998 (TREMBLrel. 19, Last sequence update)
11-NOST (TREMBLREL.)
11-NOST (NAD-+ ADP-RIBOSYLTRANSFERASE).
11-NOST (19 OR AT4G02390.
11-NOST (19 OR AT4G023
400 RIMPH----SGGRVGKGIYFASENSKSAGYVIGMKCGAHHVGY-----MFLGEVALGREH 450
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 TEGPEKKKGRQAGREEDPFRSTAEALKAIPAEKRIIRV-DPTCPLSSNPGTQVYED---- 65
                                                                                                     451 HINTONPSLKSPPPGFDSVIARGHTEPDPT---QDTELELDGQQVVVPQGQPVPCPEFSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; APG05298; AGC19283.1; -.
EMBL; ALIG1404; CAB80732.1; -.
HSSP; P26446; 1A26.
A InterPro; IPR001209; PARP.
A InterPro; IPR00304; SAP.
A InterPro; IPR003034; SAP.
B Pfam; PF02077; SAP. 2.
B Pfam; PF02077; SAP. 2.
B SARRI; SAMRI; SAP. 2.
B SARRI; SAMRI; SAP. 2.
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34.2%; Pred. No. 8.3e-45;
ative 97; Mismatches 221; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lamar B., Stoneking T., Stumpf J., Mewes H.W., Lemcke K., Mayer K.F.X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing Project.";
the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CV. COLUMBIA;
Kalicki J., Elliott G., Cloud J.;
"The sequence of A. thaliana T1478.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    635 AA; 72017 MW; E3F1CBE4D367A377 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                635 AA
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SCY-EHQYVVYDVAQVHLKYLLQL 610
                                                                                                                                                                                                             STFSQSEYLIYQESQCRLRYLLEV 531
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                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The A. thaliana Genome
Submitted (JUN-1998) to
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Submitted (MAY-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAR-2000)
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SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-CV. COLUMBIA; WASHU;
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342 YLEQT-GSNHRCPTLQ--HIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSG 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       525 LKNASHITKL-PKGKHSVKGLGKTAPDPTATT--TLDG--VEVPLGNGI-STGINDICLL 578
                                                                                                                                                                399 LRIMPH----SGGRVGKGIYFASENSKSAGYVIGMKC---GAHHVGYMFLGEVALGREHH 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 LSSNPGTQVYED----YNCTLNQTNIENNNNKFYIIQLLQDSNRF-FTCWNRWGRVGEV- 107
CPLSSNPGTQVYED----YNCTLNQTNIENNNNKFYIIQLLQD--SNRFFTCWNRWGRVG 105
                                                                                       EV-GQSKINHFTRLEDAKKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQ-AEDEAQE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                     KKDMLLVLADIELAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         452 INTONPSLKSPPPGFDSVIARGHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               494 VAPKGK-----SAAPSKKSKGAVKEEGVNKS-----EKRMKLTLKGGAAVDPDSG
                                                                                                                                                                                                                                                                                                        QQIARGFEALEALEEALKGPTDGGQSLE--ELSSHFYTVIPHNFGHSQPPPINSPELLQA
                                                                                                                                                                                                                           164 AVVKVDRGPVRTVTKRVQPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO ADP-RIBOSYLTRANSFERASE (NAD+, POLY (ADP-RIBOSE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99; Mismatches 203; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012041; AAH12041.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDCE68E4CB3F46EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.7%; Score 669.5; DB 11; 33.5%; Pred. No. 1.3e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transferase.
SEQUENCE 1014 AA; 112721 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :||::| :| |:||::
579 YNEYIVYDVAQVNLKYLLKL 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   512 QSEYLIYQESQCRLRYLLEV 531
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Best Local Similarity 33.59
Matches 186; Conservative
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      14;
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                                           KKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGPVRTVTKRVQ 181
                                                                                                                                                      248 IYEFEGKFHNKTNNHWSDRKNFKCYAKKYTWLEMDYGETEKE----IEKG---SITDQIK 300
                                                                                                                                                                                                                                 357 HIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPH----SGGRVGKG 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   413 IYFASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSLKSPPPGFDSVIAR 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :||| ||||| | : | | ||||| : | 534 VYFADMFSKSANYCYASE--ACRSGVLLLCEVALGDMNELLNADYDANNLPKGKLRSKGV 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   473 GHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYLIYQESQCRLRYLLEVH 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEEALK
                                                                                                                                                                                                                                                                                         242 GPTDGGQSLEELSSHFYTVIPHNFGHSQPPP--INSPELLQAKKDMLLVLADIELAQALQ
                                                                                                                                                                                                                                                                                                              --KADRRHLEQLTGEFYTVIPHDFGFRKMREFIIDTPQKLKAKLEMVEALGEIEJATKL-
                                                                                                                                                                                                                                                                                                                                                                         300 AVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT-GSNHRCPTLQ--
        31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 13; Length 607;
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        Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NAD+:PROTEIN(ADP-RIBOSYL)-TRANSFERASE, ADPRT.
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      93; Mismatches 186;
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InterPrc; IPR001357; BRCT.
InterPrc; IPR001290; PARP.
InterPrc; IPR001290; PARP.
Ffam; PF00533; BRCT; 1.
Ffam; PF00643; PARP; 1.
Ffam; PF02877; PARP; 1.
        Conservative
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        Matches 170;
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121 AKKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGPVRTVTKRV 180
                                                                                                                                                                                                                                                                           353 PTLQ--HIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPH----SG 406
                                                                                                                                                                                                                                                                                                                                                                                                                            GRVGKGIYFASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSLKSPPPGF 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 YEDYNCTLNQTNIENNNNKFYIIQLLQ-DSNRFFTCWNRWGRVGEV-GQSKINHFTRLED 120
PSSGPVAGKSSGKVKEEKGSNKSEKKMKLTVKGGAAIDPDSEL---EDSCHVLETGG--- 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                           | : | :::|| | | :|:|| | :|: | | :|: | | :: | | :|
202 AIEHFLNLYQDKTGNAW-HSPNFTKYPKFYPLEIDYGQE-EDVVKKLSVG-AGTKSKLA
                                                                                                                                                                                                      QAL - - QAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT - GSNHRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481 YMFGKGIYFADMVSKSANYCHAMP--GSPIGLILLGEVALGNMHELKAASQITKL-PKGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       467 DSVIARGHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYLIYQESQCRLR
                                                                                                                                                                                   181 QPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALEEAL
                                                                                                                                                                                                                                                        241 KGPTDGGQSLEE----LSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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"The sequence of C. elegans cosmid Y71F9AL.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases EMBL; AC024200; AAF36011.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 108.0 KDA PROTEIN.
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MEDLINE-99069613; PubMed-9851916;
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"Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BRISTOL N2;
Bradshaw-Cordum H.,
"The sequence of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
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Q9N4H4;
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                                    227 ARGFEALEALEEALKGPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDML 286
                                                                                                                                                                                   OAAYSILSEVQQAVSQGSSESQIL-DLSNRFYTLIPHDFGMKKPPLLNNADSVQAKVEML 765
                                                                                                                                                                                                                                   LVLADIELAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT 346
                                                                                                                                                                                                                                                        -GSNHRCPTLQ--HIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMP 403
                                                                                                                                                                                                                                                                                                                                 H----SGGRVGKGIYFASENSKSAGYVIGMKCGAHH----VGYMFLGEVALGREHHINTDN 456
                                                                                                                                                                                                                                                                                                                                                                                                      457 PSLKSPPPGFDSVIARGHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYL 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GQSKINHFTRLEDAKKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQ-AEDEAQEAVV 166
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                                                                                      KVDRGPVRTVTKRVQPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52;
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Pred. No. 1.1e-41;
2; Mismatches 214; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Interpro; IPR001290; PARP.
Interpro; IPR001402; PARP_reg.
Pfam; PF00533; BRCT; 1.
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Pfam; PF02877; PARP_reg; 1.
PROSITE; PS50172; BRCT; 1.
SEQUENCE 607 AA; 67496 MW.
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991 VYDIAQVNLKYLLKL 1005
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Best Local Si
Matches 177;
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RESULT Q9PS81

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Biochimie 77:444-449(1995)
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             HSSP; P26446; 1A26
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SEQUENCE 1
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Auer B., Flick K., Wang Z.Q., Haidacher D., Jager S., Berghammer H.,
Kofler B., Schweiger M., Wagner E.F.;
"On the biological role of the nuclear polymerizing NAD+: protein(ADP-ribosy) transferase (ADPRT): ADPRT from Dictyostelium discoideum and inactivation of the ADPRT gene in the mouse.";
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                                                                                                                                                                                           184 SLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALEEAL-KG 242
                                                                                                                                                                                                                                                                                                                    PTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIELAQALQAVS 302
                                                                                                                                                                                                                                                                                                                                   66 YNCTLNQTNIENNNNKFYIIQLLQDSNR-FFTCWNRWGRVG-EVGQSKINHFTRLEDAKK 123
                                                                                                                                                                                                                           124 DFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGPVRTVTKRVQPC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                             417 SENSKSAGYVIGMKCGAHHVGYMFLGEVALGR-EHHINTDNPSLKSPPPGFDSVIARG-- 473
                                                                                                                                                                                                                                        DVPASTSLGIDPVDINYQKLKCIMEPLQQGCDDWNMIHQYLKNTHGATHDLKVELIDILK
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                                                                                                                                                                                                                                                                                                                                                                                                                 VNQEGEEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPH----SGGRVGKGIYFA
                                                                                                                              Length 945;
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                                                                                                                                                     Indels
                                 Pfam; PF00644; PARP; 1.
Pfam; PF00645; zf-PARP; 1.
Prodom; PD004675; Znf-PARP; 1.
PROSITE; PS50064; PARP_ZN_FINGER_2; 1.
Hypothetical protein.
SEQUENCE 945 AA; 108006 MW; 1D0A62C954BC6AD9 CRC64;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NAD+:PROTEIN(ADP-RIBOSYL)-TRANSFERASE, ADPRT.
                                                                                                                              Query Match 22.5%; Score 636.5; DB 5; Best Local Similarity 34.0%; Pred. No. 3.9e-40; Matches 167; Conservative 84; Mismatches 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         593 AA
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           InterPro; IPR001290; PARP.
InterPro; IPR001510; Znf-PARP.
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929 IQLKYLVRVKM 939
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          381
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               326 GVQLPTLIETHQQIEDLRQMLDSLAEIEVAYSI----IKSEDVSDACNPLDNHYAQIKTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | || : |: :: |:: | || || || 382 LVALDKNSEEFSILSQYVKNTHASTHKSYDLKIVDVFKVSRQGEARREKPFKKLHNRKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99 KSMPVSRTFKVKDGLAVDPDSGLEDI - - AHVYVDSNNKYSVVLGLTDIQRNKNSYYKVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 GHSQPPPINSPELLQAKKDMLLVLADIELAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      326 LQLLDSGAPEYKVIQTYLEQT-GSNHRCPTLQ--HIWKVNQEGEEDRFQAHSKLGNRKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         383 WHGTNMAVVAAILTSGLRI----MPHSGGRVGKGIYFASENSKSAGYVIGMKCGAHHVGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     439 MFLGEVALG-----REHHIN--TDNPSLKSPPPGFDSVIARGHTEPDPTQDTELELDGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 KAIPAEKRI----IRVDPTCPLSSNPGTQVYED----YNCTLNQTNIENNNNKFYIIQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146 HPGKYTLIEVQAEDEAQEAVKVDRGPVRTVTKRVQPCSLDPATQKLITNIFSKEMFKNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217 RTGRMYPIEIQYDDD--QKLVKHE-----SHFFTSKLEISVQNLIKLIFDIDSMNKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MALMDLDVKKMPLGKLSKQQIARGFEALEALEEALKGPTDGGQSLEELSSHFYTVIPHNF
                                                                                                                                                                                                                                                                                                                                                                          58;
                                                                                                                                                                                                                                                                                                           Length 593;
                                                                                                                                                                                                                                                                                                           Ouery Match 22.3%; Score 629; DB 5; Length 59 Best Local Similarity 32.1%; Pred. No. 7.4e-40; Matches 167; Conservative 100; Mismatches 196; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-CV. LANDSBERG ERECTA;
Doucet-chabeaud G., Kazmaier M.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ131705; CAA10482.1; -
                                                                                                                                                                                                                        D9BA37E38B8E7CCD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1999 (TrEMBLrel. 10, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
POLY(ADP-RIBOSE) POLYMERASE (EC 2.4.2.30).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | :| |: : | |: :|| :: | 549 -VEIPYGETI-TDEHLKSSLLYNEYIVYDVAQVNIQYLFRM 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       491 QVVVVPQGQPVPCPEFSSSTFSQSEYLIYQESQCRLRYLLEV 531
                                                                                                                                                                                                                 68018 MW;
InterPro; IPR001357; BRCT.
InterPro; IPR001290; PARP.
InterPro; IPR004102; PARP_reg.
                                                                                     Pram; PRO0533; BRCT; 1.
Pram; PRO0644; PARP; 1.
Pram; PRO0847; PARP_reg; 1.
PROSTIE: PSS0172; BRR_T; 1.
SEQUENCE S93 AA; 68018 MA
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InterPro; IPR004102; PARP_reg.
InterPro; IPR001510; Znf-PARP.
                                                                                                                                                                                                                         Pfam; PF00644; PARP; 1.
Pfam; PF02877; PARP. -reg; 1.
Pfam; PF00645; zf-PARP; 2.
ProDom; PD004675; znf-PARP; 2.
                                                                                                                 Lin X.;
Submitted (MAR-2000) to the
EMBL; AC006593; AAD20677.1;
HSSP; P26446; 1A26.
                                                                                                                                                             InterPro; IPR001357; BRCT.
InterPro; IPR001290; PARP.
                                                             Nature 402:761-768(1999).
                                                                                                                                                                                                             PF00533; BRCT;
                                                                                     SEQUENCE FROM N.A. STRAIN-CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVKLQFLLKV 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QCRLRYLLEV 531
                                                  thaliana
                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                              Lin X.
                                                                                                                                                                                                                Pfam;
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STRAIN-CV. COLUMBIA;
MEDLINE-200081487; Publed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.Y., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,
                                                                                                                                       237
                                                                                                                                                                                                                                                                                                                           EAL----KGPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIE 293
                                                                                                                                                                                                                                                                                                                                                 689 RLLTESDPQPTMKESLLVDASNRFFTMIP----SIHPHIIRDEDDFKSKVKMLEALQDIE 744
                                                                                                                                                                                                                                                                                                                                                                                                                              401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Sperimatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                         69 TLNQTNIENNNNKFYIIQLLQDSNRFFTCW--NRWGRVG--EVGQSKINHFTRLEDAKKD 124
                                                                                                                                                                                                                        125 FEKKFREKTKN---NWAERDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGPVRTVTKRVQ 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                          68
                                                                                                                                                                                                                                                                                                                                                                                                                                           17 KKGRQAGREEDPFRSTAEALKAIPAEKRIIRVDPTCPLSSNPGTQ----VYED----YNC
                                                                                                                                                                                                                                                                         P----CSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALE
                                                                                                                                                                                                                                                                                                                                                                           LAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQTGSNHRCP
                                                                                                                                                                                                                                                                                                                                                                                                    745 IASRI--VGFDVDSTES----LDDKYKKLHCDISPLPHDSEDYRLIEKYLNTT----HAP
                                                                                                                                                                                                                                                                                                                                                                                                                            T-----LQHIWKVNQEGEEDRFQAH-SKLGNRKLLWHGTNMAVVAAILTSGLRI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MPHSGGRVGKGIYFASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPPGFDSVIARGHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYLIYQES
                                                                                                  79;
                                                                          Length 983;
                                                                       Ouery Match 21.2%; Score 598.5; DB 10; Length Best Local Similarity 31.1%; Pred. No. 3.4e-37; Matches 171; Conservative 101; Mismatches 199; Indels
                        POLY(ADP-RIBOSE) POLYMERASE.; 468E12A8EF1B6F4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE POLY (ADP-RIBOSE) POLYMERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1009 AA.
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           ransferase; Glycosyltransferase; NAD.
                                   983 AA; 111232 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              522 QCRLRYLLEV 531
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OVKLOFLLKV 977
HSSP; P26446; 1A26
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Q9SJW4;
01-MAY-2000
                                   SEQUENCE
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Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; "Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 TLNQINIENNNKFYIIQLLQDSNRFFTCW--NRWGRVG--EVGQSKINHFIRLEDAKKD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEKKFREKTKN----NWAERDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGPVRTVTKRVQ 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | :: | | :: | | :| | EDTECT SENDA PER PETUM SEMPLG PEQTES SENDA PETUM SEMPLE PETUM 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MPHSGGRVGKGIYFASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.2%; Score 598.5; DB 10; Length 1009; 31.1%; Pred. No. 3.5e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00292; BRCT; 1.
PROSITE; PS50172; BRCT; 1.
PROSITE; PS0014; PARP_ZN_FINGER_2; 2.
SEQUENCE 1009 AA; 114133 MW; CDE6E41CC2A3A2DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 31.1%; Pred. No. 3.5e-37;
Matches 171; Conservative 101; Mismatches 199;
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PRT;
                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00533; BRCT; 1.
Pfam; PF00644; BRCT; 1.
Pfam; PF00644; PARP; 1.
Pfam; PF00645; PARP_reg; 1.
ProDom; PD004675; Zf-PARP; 2.
ProDom; PD004675; Zf-PARP; 2.
                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR004102; PARP_reg.
InterPro; IPR003034; SAP.
InterPro; IPR001510; Znf-PARP.
                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001357; BRCT.
InterPro; IPR001290; PARP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 30.6
Matches 166; Conservative
                                                                                                                              PRELIMINARY;
                                              LEV 531
                                                                     LKV 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                       14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92
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                                              529
                                                                     961
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Q9ZSV1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
                                                                                         Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Addropogoneae; Zea.
NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    480 KVKGRSAVHESSGLQDTAHILE---------DGKSI---YNATLNMSDL 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 ENNNNKFYIIQLL-QDSNRFFTCWNRWGRVG--EVGQSKINHFTRLEDAKKDFEKKFREK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 TKNNWAE---RDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGPVRTVTKRVQPCSLDPAT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 QKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALEEALKGPTDGGQS 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250 LEE----LSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIELAQALQAV-SE 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQTGSNHRCPT-----LQ 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GIYFASENSKSAGYVIGMKCGA---HHVGYMFLGEVALGREHHINTDNPSLKSPPPGFDS 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 KKKGRQAGREEDPFRSTAEALKAIPAEKRIIRVDPTCPLSSNPGTQVYEDYNCTLNQTNI 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              357 HIWKVNQEGEEDRFQAH-SKLGNRKLLWHGTNMAVVAAILTSGLRIMPH----SGGRVGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86;
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 969;
                                                                                                                                                 [1] SEQUENCE FROM N.A. Bablychuk E., Cottrill.P., Storozhenko S., Fuangthong M., O'Farrell M., Van Montagu M., Inze D., Kushnir S.; "Higher plants possess two poly(ADP-ribose) polymerases."; Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases. EMBL; AJ222589; CAA10889.1; -...EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       96; Mismatches 195; Indels
                                                                                                                                                                                                                                                                                                                                                            SMART; SM00292; BRCT; 1.
PROSITE; PSS0172; BRCT; 1.
PROSITE; PSS0172; BRCT; 1.
SEQUENCE 969 AA: 109128 MW; BB23AC62EEC14009 CRC64;
                                         01-JAN-1998 (TrEMBLrel. 05, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) POLY(ADP-RIBOSE) POLYMERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 578; DB 10;
Pred. No. 1.2e-35;
            969 AA
                                   Created)
            PRT;
                                                                                                                                                                                                                                          InterPro; IPR001357; BRCT.
InterPro; IPR001290; PARP.
InterPro; IPR004102; PARP_reg.
InterPro; IPR003034; SAP.
InterPro; IPR001510; Znf-PARP.
Pfam; PF00533; BRCT; 1
Pfam; PF00644; PARP; 1.
                                                                                                                                                                                                                                                                                                                           Pfam; PF02877; PARP_reg; 1.
Pfam; PF00645; zf-PARP; 2.
ProDom; PD004675; znf-PARP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                20.5%;
30.6%;
                                 05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 166; Conservative
            PRELIMINARY;
                                 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                 01-JAN-1998
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024570
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SEQUENCE FROM N.A.
MEDLINE-9906291; PubMed-9808734;
Mahajan P.B., Zuo Z.;
"Purification and cDNA cloning of maize Poly(ADP)-ribose polymerase.";
"Purification, and Resp. 905(1998).
EMBL; AF093627; AAC79704.1; -...
EMBL; AF09465, 1A26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zea mays (Maize).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
NCBL_TaxID=4577;
                                   | |:| | CHARAGECKTNFRKQPGRFYPLDVD-----YGVKKAPKRDISEMK-SSLAPQL 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 QKLITUIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALEEALKGPTDGGQS 249
469 VIARGHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYLIYQESQCRLRYL 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENNNNKFYIIQLL-ODSNRFFTCWNRWGRVG--EVGQSKINHFTRLEDAKKDFEKKFREK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TKNNWAE----RDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGPVRTVTKRVQPCSLDPAT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEE----LSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIELAQALQAV-SE 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : | |: |:|:|| : |: |VRESLIVAASNRFFTLIP----SIHPHIIRDEDDLMIKAKMLEALQDIEIASKIVGFDSD 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            491 KVKGRSAVHESSGLQDTAHILE----------DGKSI---YNATLNMSDL 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 KKKGRQAGREEDPFRSTAEALKAIPAEKRIIRVDPTCPLSSNPGTQVYEDYNCTLNQTNI 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.5%; Score 578; DB 10; Length 9 30.6%; Pred. No. 1.3e-35; Live 96; Mismatches 195; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9D8AED26BC37E5C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
POLIX(ADP)-RIBOSE POLYMERASE (EC 2.4.2.30).
                                                                                                                                                                                                                                                                                                                                          980 AA
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20;
304 QEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQTGSNHRCPT-----LQ 356
                                     357 HIWKVNQEGEEDRFQAH-SKLGNRKLLWHGTNMAVVAAILTSGLRIMPH----SGGRVGK 411
                                                                                                                                                                                                                                           GIYFASENSKSAGYVIGMKCGA---HHVGYMFLGEVALGREHHINTDNPSLKSPPPGFDS 468
                                                                                                                                                                                                                                                                                                                                                          469 VIARGHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYLIYQESQCRLRYL 528
                                                                                                                                                                                                                                                                                                                                                                                                   ... | .:.; |: | .:.; | | | .:.| | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.; | .:.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AKKDF------EKKFREKTKNNWAERDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOZ EVFSLDRDGELNKYSRYKNNLHNKMLLWHGSRITNFYGILSQGLRIAPPEAPVIGYMFGK 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 RSTAEALKAIPAEKRIIRVDPTCPLSSNPGTQVYEDYNCTLNQTNIENNNKFYIIQLLQ 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                              18.9%; Score 534; DB 5; Length 727; 28.6%; Pred. No. 1.9e-32; ative 104; Mismatches 211; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEDUTENCE FROM N.A.,
MCMUTRAY A.A.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro; IPR001290; PARP.
Interpro; IPR004102; PARP_reg.
Interpro; IPR001510; Znf-PARP.
Pfam; PF02877; PARP: 1.
Pfam; PF00645; Zf-PARP; 1.
Prodom; PD00465; Zf-PARP; 1.
PROSTIE; PS550064; PARP_ZN.FINGER_2; 1.
SEQUENCE 727 AA; 82884 MW; 530ABABE991FFEFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       727 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [2]
SEQUENCE FROM N.A.
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z83097; CAB05448.1; -.
HSSP; P26446; 1A26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-DEC-2001 (TrEMBLrel. 19,
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173 VRTVT--KRVQPCS---LDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIA 227
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:

		Description	Human uterus type	Human brain PARP3	Human PARP-3 prote	Murine PARP1 (shor	Murine PARP1 (long	Mouse PARP-2 prote	hPARP2. Homo sapi	Human ORFX ORF2673	Human PARP-2 prote	Human PARP-2 prote	Human brain PARP2
	f	TD.		AAY51175	AAU29021	AAY51178	AAY51177	AAU29022	AAB47029	AAB42909	AAU29023	AAU29020	AAY51174
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AAB11480 AAB60693 AAY68835 AAB93513 AAY58043	AAU29019 AAB66296 AAY68834 AAY6939	AAR99642 AAY33699 AAB47032	ABB66431 AAY68833 AAY68839 AAY28464	AAU21687 AAB47030 AAY68840	AAU20129 AAU21810 AAB47031 AAB66301	AAU20130 AAU21811 AAU33242	AAY54373 AAB51022 AAU21688	AAB27212 AAY44402 AAB66279	AAB66286 AAB66285
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ALIGNMENTS

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PARP; poly(ADP-ribose) polymerase; human; murine; detection; sepsis; diagnosis; therapy; necrosis; apoptosis; neurodegenerative illness; ischemic tissue damage; PARP3.
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                   AAY51176 standard; Protein; 540 AA
                                                                                    Human uterus type 2 PARP3 protein.
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99DE-1008837.
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N-PSDB; AAZ44289.
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01-MAR-1999;
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poly(ADP-ribose) polymerase; human; murine; detection;
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                                       This invention describes novel human and murine poly(ADP-ribose)

polymerase (PARP) homologues, which are characterised by an amino acid
sequence with a functional NAD^+-binding site and no zinc finger
sequence motif, of general formula CX_2CX_ZMHX_ZC (I). The nucleic acid
sequences, PARP homologues and antibodies are useful for analytic
detection of PARP homologues and for identifying PARP effectors or
binding partners, as well as for determining their effectiveness.
PARP-binding partners are useful for the diagnosis or therapy of a
disease condition, which as the result of a PARP protein, especially an
energy deficiency, which may comprise tissue damage from cell death
following necrosis or apoptosis. The disease condition may be chosen
from a neurodegenerative illness, or sepsis or ischemic tissue damage,
in particular neurotoxic disturbances, etc. This sequence represents the
human PARP3 protein used in the method of the invention.
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                     Claim 4; Page 62-64; 96pp;
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                                                                                                                                                                                                                                                                  Conservative
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polymerase (PARP) homologues, which are characterised by an amino acid sequence with a functional NAD^+-binding site and no zinc finger sequence motif, of general formula CX_2CX_2MHX_2C (I). The nucleic acid sequences motif, of general formula CX_2CX_2MHX_2C (I). The nucleic acid detection of PARP homologues and antibodies are useful for analytic detection of PARP homologues and for identifying PARP effectors or binding partners, as well as for determining their effectiveness. PARP-binding partners are useful for the diagnosis or therapy of a disease condition, which is the result of a PARP protein, especially an energy deficiency, which may comprise tissue damage from cell death following necrosis or apoptosis. The disease condition may be chosen from a neurodegenerative illness, or sepsis or ischemic tissue damage, in particular neurotoxic disturbances, etc. This sequence represents the human PARP3 protein used in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel genes and proteins, antibodies and binding partners useful in diagnosis and therapy of energy deficiency associated disease
diagnosis; therapy; necrosis; apoptosis; neurodegenerative illness; ischemic tissue damage; PARP3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes novel human and murine poly(ADP-ribose)
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99DE-1008837.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Hoeger T,
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                                                                                 Homo sapiens
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Similarity

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The invention relates to antisense oligonuclectides targeted to human PARP nucleic acid and inhibiting expression of human PARP. PARP PARP nucleic acid and inhibiting expression of human PARP. PARP (Poly (ADP-ribose) polymerase plays an important role in chromatin decondensation, DNA replication, DNA repair, gene expression, malignant transformation, cellular differentiation and apoptosis. The antisense oligonuclectide inhibitors are useful for inhibiting the expression of PARP in human cells or tissues. They are also useful for treating a human with a disease associated with PARP especially hyperproliferative disorders (e.g. cancer), cellular injury resulting from oxidative stress, mentological (e.g. parkinsonism, meningitis-associated intracranial complications and ischaemia), inflammatory and autoimmune disorders (e.g arthritis) and diabetes. The present sequence is a PARP protein,
                                                                                                                                                                                                                                                                                                                                                                                             Human; PARP; Poly (ADP-ribose) polymerase; antisense oligonucleotide; cytostatic; nootropic; neuroprotective; antiinflammatory; antidiabetic; immunosuppressant; hyperproliferative disorder; cancer; cellular injury; oxidative stress; neurological disorder; parkinsonism; apoptosis; meningitis-associated intracranial complication; ischaemia; inflammatory disorder; autoimmune disorder; arthritis; diabetes.
                487
                                                                                     VNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPHSGGRVGKGIYFASENS
                                                                    KSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSLKSPPPGFDSVIARGHTEPDPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bound useful for treating hyperproliferative, inflammatory and autoimmune disorders and diabetes
                                                                                                                                    QDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYLIYQESQCRLRYLLEVHL 540
                                                                                                                                                      Example 13; Page 105-107; 168pp; English.
                                                                                                                                                                                                                                                         AAU29021 standard; Protein; 533
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Query Match

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                                                               QVYEDYNCTLNQTNIENNNNKFYIIQLLQDSNRFFTCWNRWGRVGEVGOSKINHFTRLED 127
         Gaps
                          67
                                      Lemaire H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PARP; poly(ADP-ribose) polymerase; human; murine; detection; sepsis diagnosis; therapy; necrosis; apoptosis; neurodegenerative illness; ischemic tissue damage; PARP1.
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                           MAPKPKPWVQTEGPEKKKGRQAGREEDPFRSTAEALKAIPAEKRIIRVDPTCPLSSNPGT
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         Indels
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No. 1.4e-248;
smatches 2;
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01-MAR-1999;
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Best Local Sim
Matches 531;
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                                                            polymerase (PARP) homologues, which are characterised by an amino acid sequence with a functional NAD^++binding site and no zinc finger sequence with a functional NAD^++binding site and no zinc finger sequences. PARP homologues and antibodies are useful for analytic detection of PARP homologues and for identifying PARP effectors or binding partners as well as for determining their effectiveness. PARP-binding partners are useful for the diagnosis or therapy of a disease condition, which is the result of a PARP protein, especially an energy deficiency, which may comprise tissue damage from cell death following necrosis or apoptosis. The disease condition may be chosen from a neurodegenerative illness, or sepsis or ischemic tissue damage, in particular neurotoxic disturbances, etc. This sequence represents the murine PARPI protein used in the method of the invention.
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diagnosis and therapy of energy deficiency associated disease
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ilarity 80.9%; Pred. No. 1.8e-197;
Conservative 37; Mismatches 58;
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                                4; Page 71-73; 96pp;
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This invention describes novel human and murine poly(ADP-ribose)

polymerase (PARP) homologues, which are characterised by an amino acid
sequence with a functional NAD<sup>+</sup>-binding site and no zinc finger
sequence motif, of general formula CX_2CX_ZMHX_ZC (I). The nucleic acid
sequences, PARP homologues and antibodies are useful for analytic
detection of PARP homologues and for identifying PARP effectors or
binding partners, as well as for determining their effectiveness.
PARP-binding partners are useful for the diagnosis or therapy of a
clisease condition, which is the result of a PARP protein, especially an
energy deficiency, which may comprise tissue damage from cell death
following necrosis or apoptosis. The disease condition may be chosen
from a neurodegenerative illness, or sepsis or ischemic tissue damage,
in particular neurotoxic disturbances, etc. This sequence represents the
murine PARPI protein used in the method of the invention.
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diagnosis; therapy; necrosis; apoptosis; neurodegenerative illness; ischemic tissue damage; PARP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 LEEALKGPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIELA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 2241; DB 21;
; Pred. No. 2.5e-196;
37; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Otterbach B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 67-69; 96pp; German.
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80.1%;
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99DE-1008837.
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Best Local Similarity 80.13
Matches 432; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-087218/07
N-PSDB; AAZ44290.
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01-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                      Human; PARP; Poly (ADP-ribose) polymerase; antisense oligonucleotide; cytostatic; nootropic; neuroprotective; antiinflammatory; antidiabetic; immunosuppressant; hyperproliferative disorder; cancer; cellular injury; oxidative stress; neurological disorder; parkinsonism; apoptosis; meningitis-associated intracranial complication; ischaemia; inflammatory disorder; autoimmune disorder; arthritis; diabetes.
                                421
                                                             414
                                                                                        FASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSLKSPPPGFDSVIARGH 481
                                                                                                         fasensksagyvttmhcgghqvgymflgevalgkehhitiddpslkspppgfdsviargq 474
qtlqaapgeeeekveevphpldrdyqllrcqlqlldsgeseykaiqtylkqtgnsyrcpn 354
                                                                                                                                                 TEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYLIYQESQCRLRYLLEVHL 540
                                                                                                                                                             tepdpaqdieleldggpvvvpggppvqcpsfksssfsqseyllykesqcrlrylleihl 533
                                            LQHIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPHSGGRVGKGIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antisense compound useful for treating hyperproliferative, neurological, inflammatory and autoimmune disorders and diabetes inhibits human PARP -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sxample 13; Page 109-111; 168pp; English.
                                                                                                                                                                                                                                                    AAU29022 standard; Protein; 522 AA.
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 295
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Human; poly(ADP-ribose) polymerase; hPARP2; oxidative stress; ARDS; inflammation; ischaemic stroke; hemorrhagic shock; myocardial ischemia; inflammation; cerebaral vasospasm; rhematoid arthritis; osteoarthritis; wordy arthritis; spondylitis; bencet's disease; sepsis; septic shock; my qouty arthritis; spondylitis; bencet's disease; sepsis; septic shock; we andotoxic shock; gram negative sepsis; gram positive sepsis; trauma; troxic shock syndrome; multiple organ injury syndrome; vasculitis; whemorrhage; conjunctivitis; urbits; thyroid-associated ophthalmopath; chronic obstructive pulmonary disease; sllicosis; reperfusion injury; pulmonary sarcoidosis; pleuris; alvenic bronchiectasis; pleuris; alvenic bronchiectasis; pleuris; alvenic bronchiectasis; pleuris; alvenic bronchiectasis; pleuris; alvenic systemic lupus erythematosus; we autoimmune thyroiditis; multiple sclerosis; Reynaud's syndrome; chronic glomerulonephritis; inflammatory bowel disease; ulcerative collitis; necrotizing enterocolitis; contact dermatitis; atopic dermatitis; we psoriasis; urticaria; fever; myalqia; meningitis; encephalitis;
                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FREKTKNNWAERDHFVSHPGKYTLIEV---QAEDEA---QEAVVKVDRGPVRTVTKRVQ 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | :|||||| :|::| |||| ::::
fldktknnwedrenfekvpgkydmlqmdyaastqdesktkeeetlkpe------ 170
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                                                                                                          64;
                                                                                                          Indels
Query Match 25.9%; Score 738; DB 22;
Best Local Similarity 34.3%; Pred. No. 1.5e-58;
Matches 187; Conservative 103; Mismatches 191;
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510 yllki 514
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This protein causes the covalent addition of polymerase (PRANEZ).

This protein causes the covalent addition of polymerase (PRANEZ).

This protein targets. hPARP2 activity is induced in many instances of coxidative stress or during inflammation where there is direct damage to the DNA. hPARP2 may be used to identify antagonists which may be used to treat a human having a disorder mediated by PARP2 activity, such as, inflammatory, neurological, cardiovascular, or neoplastic tissue growth disorders, e.g. ischemic stroke, hemorrhagic shock, myocardial ischemia or infarction, transplantation, cerebral vasospasm; rheumatoid, osteo- or gouty transplantation, cerebral vasospasm; rheumatoid, osteo- or gouty arthritis, spondyllitis; Behcet's disease; sepsis, septic or endotoxic shock, gram negative or positive sepsis, toxic shock syndrome; multiple organ injury syndrome secondary to septicemia, trauma, or hemorrhage; or allergic or vernal conjunctivitis, useltis, thyroid-associated ophthalmopathy; eosinophilic granuloma; asthma, chronic bronchitis, allergic or hinitis, ARDS, chronic obstructive pulmonary disease, allergic or hinitis, pulmonary sarcoldosis, pleurisy, alveolitis, reperfusion injury of the myocardium, brain or extremities; cystic fibrosis; plumonary sarcoldistis, pleurisy, alveolitis, resonance or sutchamatory bowel disease, contact or attofic dermatitis, peneroalises, inflammatory bowel disease, ulcerative colitis, inflammatory bowel disease, ulcerative colitis, neorotizing enterpoolitis; inflammatory dermatory contact or atopic dermatitis, posicians, and brain and spinal cord injury due to minor trainma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           injury due to minor trauma; Sjogren's syndrome; diseases involving leukocyte diapedesis; alcoholic hepatitis; bacterial pneumonia; antiportyte diapedesis; alcoholic hepatitis; bacterial pneumonia; antiport-antibody complex mediated diseases; hypovolemic shock; Type I diabetes mellitus; acute and delayed hypersensitivity; disease states due to leukocyte dyscrasia and metastasis; thermal injury; granulocyte transfusion associated syndromes; and cytokine-induced toxicity. hPARP2 and antibodies to it, can also be used to diagnose these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurological, cardiovascular, or neoplastic tissue growth disorders, such as, arthritis, encephalitis, myocardial ischemia, and leukocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents human poly(ADP-ribose) polymerase (hPARP2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human poly(ADP-ribose) polymerase for treating inflammatory
                      hypovolemic shock; Type 1 diabetes mellitus; hypersensitivity; leukocyte dyscrasia; thermal injury; cytokine-induced toxicity
Sjogren's syndrome; alcoholic hepatitis; bacterial pneumonia;
                                                                                                                                                                                                                                                                                                                                                                                            Goldman PS, McElligott DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 94-95; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            Demaggio AJ,
                                                                                                                                                                                                                                          16-JUN-2000; 2000WO-US16629.
                                                                                                                                                                                                                                                                                             99US-0139543
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                                                                                                                                                                                                                                                                                                                                                                                            Christenson E,
                                                                                                                                            WO200077179-A2
                                                                                                Homo sapiens.
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hypertension;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antianaemic; gene therapy; cancer; proliferative disorder; hypertension neurodegenerative disorder; osteoarthrits; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection;
                                                                                                                                                                                                                                                                                                                            410
                                                                                                                                                                                                                                                                                                                                                                                                             66 G-TQVY----EDYNCTLNQTNIENNNNKFYIIQLLQ-DSNRFFTCWNRWGRVGEVGQ-SK 118
                                                              119 INHFTRLEDAKKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEV----QAEDEAQEAVVK 174
                                                                                              222
                                                                                                                                                                                               294
                                                                                                                                                                                                                447
                                                                                                                                                                                                                                                                                                                                                                                           411 H----SGGRVGKGIYFASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSL 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---KSPPPGFDSVIARGHTEP-DPTQDTELELDGQQVVVPQGQPVPCPE 511
                                                                                                                                                 175 VDRGPVRTVTKRVQPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIA
                                                                                                                                                                                               RGFEALEALEEALKGPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLL
                                                                                                                                                                                                                                                                                                                            354 GS---NHRCPTLQHIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMP
                                                                                                                                                                                                                                                                                                                                                295 VLADIELAQALQAVSEQEKTVEEVP-HPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        506 egllqgkhstkglgkmapssahfvtlngstvplgpasdt-----gilnpdgy-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiviral; antibacterial; antifungal; antirheumatic; antithyroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human ORFX ORF2673 polypeptide sequence SEQ ID NO:5346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         512 FSSSTFSQSEYLIYQESQCRLRYLLEV 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB42909 standard; Protein; 534 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-2000; 2000WO-US08621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0127607.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     thrombosis; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200058473-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-1999;
02-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-FEB-2001
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22;

Gaps

95; Mismatches 184; Indels 87;

1.1e-57

25.6%; Score 729.5; 35.4%; Pred. No. 1.16

Matches 201; Conservative

Similarity

Query Match

Best Local

8 8

DB 22; Length 583;

22 EKKKGRQAG-----REED-----PFRSTA-----EALKAIPAEKRIIRVDPTCPLSSNP 65

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AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
which represent the human ORFX open reading frames 1 to 3161. The ORFX
sequences have activities such as: cytostatic; hepatotropic; vulnerary;
antiporiatic; antiporklisonian; nootropic; neuroprotective;
costeopathic; anticonvulsant; antiarthritic; immunosuppressant;
costeopathic; anticonvulsant; antiarthritic; immunosuppressive;
antidiabetic; hypotensive; dermatological; immunosuppressive;
antidiabetic; hypotensive; dermatological on of the presence of or predisposition to, or preventing or treating
the presence of or predisposition to, or preventing or treating
the presence of or predisposition to, or preventing or treat cancers,
conciled caids can be used to express ORRX proteins in gene therapy
vectors. The proteins and nucleic acids may be used to treat cancers,
conciled caids can be used to express ORRX proteins in gene therapy
vectors. The proteins and nucleic acids may be used to treat cancers,
fypertension, hypothyroidism, cholesterol ester sicorage, systemic lupus
conciled to fungal infection, malaria, auticimmune disorders, asthma,
allergies, aplastic anemia, burns, wounds, bone and cartilage damage,
coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --EDYNCTLNQTNIENNNNKFYIIQLLQ-DSNRFFTCWNRWGRVGEVGQ-SKINHFTRLE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||: |:||| :|||||||||| :|| ||||| :::: :|| : :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 4522-4524; 5507pp; English.
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35.1%;
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
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Matches 196; Conservative
                                                                                                                                                                                                                     Leach M;
                                                                                                                               (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                           WPI; 2000-602362/57.
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                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAC77118
                                                                                                                                                                                                                         Shimkets RA,
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The invention relates to antisense oligonucleotides targeted to human PARP nucleic acid and inhibiting expression of human PARP. PARP (Poly (ADP-Those) polymerase plays an important role in chromatin decondensation, DNA replication, DNA repair, gene expression, malignant transformation, cellular differentiation and apoptosis. The antisense oligonucleotide inhibitors are useful for inhibiting the expression of PARP in human cells or tissues. They are also useful for treating a human with a disease associated with PARP especially hyperproliferative disorders (e.g. cancer), cellular injury resulting from oxidative stress, neurological (e.g parkinsonism, menhigitis-associated intracranial complications and ischaemia), inflammatory and autoimmune disorders (e.g arthritis) and diabetes. The present sequence is a PARP protein,
                                                                                                                                                                                                                                                                                                                                                                                                                Human; PARP; Poly (ADP-ribose) polymerase; antisense oligonucleotide; cytostatic; nootropic; neuroprotective; antiinflammatory; antidiabetic; immunosuppressant; hyperproliferative disorder; cancer; cellular injury; oxidative stress; neurological disorder; parkinsonism; apoptosis; meningitis-associated intracranial complication; ischaemia;
RVGKGIYFASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSL----- 466
                    465 stkglgkmapssahfvtlngstvplgpasdt-----gilnpdgy-----tlny 507
                                                                       -----KSPPPGFDSVIARGHTEP-DPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antisense compound useful for treating hyperproliferative, neurological, inflammatory and autoimmune disorders and diabetes inhibits human PARP -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inflammatory disorder; autoimmune disorder; arthritis; diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 726.5; DB 2
Pred. No. 1.8e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 16; Page 125-127; 168pp; English.
                                                                                                                                                                                                                                                                      AAU29023 standard; Protein; 534 AA
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508 neyivynpnqvrmryllkv 526
                                                                                                                                          520 SEYLIYQESQCRLRYLLEV 538
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35.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-MAR-2000; 2000US-0517467.
                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                 Human PARP-2 protein #2.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                         AAU29023;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CPTLQHIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPH----SGG 414
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Pred. No. 1.8e-57;
); Mismatches 187; Indels 77;
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467
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21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         294
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Gaps
                                           GPEKKKGRQAGREED-PFRSTA----EALKAIPAEKRIIRVDPTCPLSSNPG-TQVY-- 70
                                                                                         61
                                                                        --EDYNCTLNQTNIENNNNKFYIIQLLQ-DSNRFFTCWNRWGRVGEVGQ-SKINHFTRLE
                                                                                                                                                                                                                                                                                                                         183 VTKRVQPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEA
                                                                                                                                                                                                                                                                                                                                                                     esg-----ldlrvgeliklicnvgameemmmemkyntkkaplgkltvagikagygslkk
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77;
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Indels
Mismatches 187;
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508 neyivynpnqvrmryllkv 526
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Conservative
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Matches 196;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 --EDYNCTLNQTNIENNNNKFYIIQLLQ-DSNRFFTCWNRWGRVGEVGQ-SKINHFTRLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 LEEALKGPTDGGOSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QALQAVSEQEKTVEEVP-HPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQTGS---NHR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DAKKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEV----QAEDEAQEAVVKVDRGPVRT
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                                                                         Antisense compound useful for treating hyperproliferative, neurological, inflammatory and autoimmune disorders and diabetes inhibits human PARP -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         534;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .2e-57;
es 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                          Example 13; Page 102-104; 168pp; English.
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508 neyivynpnqvrmryllkv 526
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WPI; 2001-602570/68.
N-PSDB; AAS45586.
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Matches 19
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416

466

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Human; poly ADP-ribose polymerase; PARP; neuroprotective; nootropic; cerebroprotective; antiparkinsonian; nephrotropic; cardiant; vasotropic; anticonvulsant; cytostatic; antibacterial; immunosuppressive; treatment; antinflammatory; antirheumatic; antiarthritic; antidiabetic; epilepsy; 2H-phthalazin-1-one derivative; neurodegenerative disease; tumor; neuronal damage; Alzheimer's disease; Huntington's disease; metastasis; parkinson's disease; ischemic damage; microinfarction; sepsis; diabetes mellitus.
  274 dcira-gqhgralmeacnefytriphdfglrtpplirtqkelsekiqllealgdieiaik 332
                                                                                                                                     LQAVSEQEKTVEEVP-HPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQTGS---NHRCP 360
                                                                                                                                                            Drugs for inhibiting PARP or especially homologous enzymes comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes novel 4-substituted 2H-phthalazin-1-one derivatives (I) which are used for the treatment or prophylaxis of diseases associated with elevated poly-(ADP-ribose)-polymerase (PARP;
                                                                                                                                                                                                                                                                                                                                                                           ----KSPPPGFDSVIARGHTEP-DPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSE 521
                                                           EALKGPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIELAQA
                                                                                                                                                                                                                                                                                                                                gkgiyfadmssksanycfasr--lkntgllllsevalgqcnelleanpkaegllqgkhst
                                                                                                                                                                                                                                                                                                                                                                                                      4-substituted phthalazinone derivatives, useful e.g. for treating neurodegenerative disease, ischemic damage, tumors or diabetes
                                                                                                                                                                                                                   361 TLQHIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPH----SGGRV
                                                                                                                                                                                                                                                                                               417 GKGIYFASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human brain poly-ADP-ribose-polymerase protein.
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546 yivynpnqvrmryllkv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes novel human and murine poly(ADP-ribose) polymerase (PARP) homologues, which are characterised by an amino acid sequence with a functional NAD<sup>+</sup>+-binding site and no zinc finger sequence motif, of general formula CX_2CX_2NHX_2C (I). The nucleic acid detection of PARP homologues and antibodies are useful for analytic detection of PARP homologues and for identifying pARP effectors or binding partners, as well as for determining their effectiveness. PARP-binding partners are useful for the diagnosis or therapy of a disease condition, which is the result of a PARP protein, especially an energy deficiency, which may comprise tissue damage from cell death following necrosis or apoptosis. The disease condition may be chosen from a neurodegenerative illness, or sepsis or isohemic tissue damage, in particular neurotoxic disturbances, etc. This sequence represents the human PARP2 protein used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDYNCTLNQTNIENNNNKFYIIQLLQ-DSNRFFTCWNRWGRVGEVGQ-SKINHFTRLEDA 128
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                                                                                                                                                                                             poly(ADP-ribose) polymerase; human; murine; detection; sepsis; sis; therapy; necrosis; apoptosis; neurodegenerative illness;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel genes and proteins, antibodies and binding partners useful diagnosis and therapy of energy deficiency associated disease
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                                     AAY51174 standard; Protein; 570
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                                                                                                                                                                                                                                                                                                                                                                                              99WO-EP03889
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                                                                                                                   (first entry)
                                                                                                                                                    Human brain PARP2 protein.
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                                                                                                                                                                                                                                    ischemic tissue damage
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                                                                                                                                                                                                                                                                             Homo sapiens
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Matches 197;
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RESULT 11
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cardiant, vasotropic anticonvulsant, checking in an encorporate control of a cardiant, vasotropic, anticonvulsant, cytostatic, antibacterial, immunosuppressive, antinfonvulsant, cytostatic, antibacterial, immunosuppressive, antinfonvulsant, cytostatic, antibacterial, antidabetic. (I) are especially used for treating or preventing or preventing control decembers. (I) are especially used for treating or preventing neurodegenerative disease or neuronal damage (specifically apoplexy or parkinson's disease), treating or preventing ischemic damage for specifically renal damage after renal ischemia or during and after kidney transplantation or heart damage after cardiac ischemia), treating epilepsy, specifically generalized epileptic attacks (e.g. petit mal and tonic-clonic attacks) or partial epileptic attacks (e.g. temporal lope and complex partial attacks), treating microinfarction (e.g. during and after heart valve replacement, aneuryam resectioning and heart transplantation), revascularization of critically constricted coronary arteries (e.g. leg arteries), treating accountable the term of the procession of the myocardial ischemia and damage during the interties (e.g. leg arteries), treating and treating and treating the procession of the myocardial ischemia and damage during the construction of the moral arteries (e.g. leg arteries), treating and treating and treating the procession of the myocardial ischemia and damage during the construction of the moral and the myocardial ischemia and damage during the metable of the myocardial ischemia and damage during the moral and the myocardial ischemia and damage during the moral and the myocardial ischemia and damage during the moral and the myocardial ischemia and damage during the moral and the myocardial ischemia and damage during the moral and the myocardial and damage during the moral and the myocardial damage during the moral and the myocardial and damage during the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     their metastasis, sepsis and septic shock, inflammatory and rheumatic disease (e.g. rheumatoid arthritis), and diabetes mellitus, although (I) inhibit pARP (i.e. the known form designated PARPI), they especially selectively and strongly inhibit PARP homologs, specifically the homolog ARPR2. In particular (I) have very strong PARP2 inhibitory activity (e.g. with K.i values of 1-20 nM) and high selectivity for PARP2 relative to PARPI (generally by a factor of more than 5).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q-----ldlrvqeliklicnvqameemmmemkyntkkaplgkltvaqikagyqslkkie 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |||||||| :||||| : : | :||||||: : ||
gkgiyfadmssksanycfasr--lkntgllllsevalgqcnelleanpkaegllggkhst 502
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   products of the invention have nootropic
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Matches 197; Conserv
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protein or nuclectide sequence; expression systems and host cells comprising an sbhPaRS2 nucleic acid sequence; the recombinant expression of sbhPaRS2 and an antibody specific for sbhPaRS2; sbhPaRS2 proteins of nuclectides are useful as vaccines for inducing an immunological response in a mammal. The sbhPaRS2 protein is useful for identifying compounds which inhibit or stimulate its activity or expression level. Such agonists and antagonists of sbhPaRS2 are useful for treating human diseases including ischaemia and ischaemic tissue injury (e.g., cerebral and cardiac ischaemia, myocardial infarction, stroke), inflammation, autoimmune disease (e.g., dabbetes, multiple sclerosis) and neurodegenerative disease (e.g., Parkinson's disease and Alzheimer's disease). sbhPaRS2 nucleic acids are useful as-diagnostic reagents for detecting mutations in the associated gene; as hybridisation probes to isolate full-length sbhPaRS2 cDNAs and sbhPaRS2 genomic clones; and for chromosome localisation studies. The sbhPaRS2 protein is also useful as a immunogen to produce antibodies for therapeutic use, sbhPaRS2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteins, nucleotides and antibodies are also useful in screening methods for detecting the effect of added compounds on the production of mRNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human polypeptide of the polyADPribose synthetase family for use in diagnostic assays and for screening modulators used for preventing and treating inflammation, autoimmune disease and Alzheimers disease
                                                                                                                                                                                             drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                               ischaemic disorder; cerebral ischaemia; cardiac ischaemia;
myocardial infarction; stroke; inflammation; autoimmue disease;
diabetes; multiple sclerosis; neurodegenerative disease;
Parkinson's disease; Alzheiner's disease; chromosome localisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a novel human poly(ADP-ribose) synthetase, sbhPARS2. The invention also relates to fragments, variants and sequences with at least 95% identity to the sbhPARS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           zhu Y;
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                                                                                                                                                                                           Human; poly(ADP-ribose) synthetase; sbhPARS2; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McQueney MS,
                                                                                                                                              Human poly(ADP-ribose) synthetase sbhPARS2.
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                 AAB60693 standard; Protein; 521 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kabnick KS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 21; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000WO-US21775.
                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barone F, Field J,
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N-PSDB; AAF59996.
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                                                                                                                                                                                                                                                                                                                                                                  WO200112645-A1.
                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                    11-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                             22-FEB-2001
                                                            AAB60693;
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AAB60693
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----KSPPPGFDSVIARGHTEP-DPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSE

445 467

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503 kglgkmapssahfvtlngstvplgpasdt-----gilnpdgy---

|::| :| |:|||:| 546 yivynpnqvrmryllkv 562 YLIYQESQCRLRYLLEV 538

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NAP; poly(ADP-ribose) polymerase; PARP; poly(ADP-ribose) transferase; programmed cell death; apoptosis; growth rate; stress; cold; pathogen; pest; drought; heat; fungi; nematode; seed-shatter.
                                                                                                                                                                    EKKFREKTKNNWAERDHFVSHPGKYTLIEV----QAEDEAQEAVVKVDRGPVRTVTKRVQ 188
                                                                                                                                                                                                  |::| | : ||| |||:|| || : : | | :| |||:| | a-gqhgralmeacnefytriphdfglrtpplirtgkelsekigllealgdleiaikl--- 284
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5 ggkankdrtedkgd----esvkalllkgk-apvdpec--takvgkahvycegndvyd 54
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400 yfadmssksanycfasr--lkntgllllsevalgqcnelleanpkaegllggkhstkglg
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Location/Qualifiers
Misc-difference 1..138
//note= "these residues are specifically claimed
claim 18"
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The present sequence represents a NAP protein. This protein is a poly(ADP-ribose) polymerase (PARP) protein (also known as poly(ADP-ribose) transferase). The PARP enzyme is involved in programmed cell death or apoptosis, and is a nuclear enzyme. The NAP polymucleotide sequences can be used for modulation of programmed cell death in plants, to induce, or protect against, programmed cell death, depending on the extent to which PARP activity is reduced. Reducing expression of endogenous NAP class PARP only is also used to modulate programmed cell death, to increase growth rate and to produce plant cells that are more tolerant of stress (cold, chemical treatments, pathogens, pests, drought, heat, etc., or during transformation). Particular applications are generation of plants that are resistant to fung or nematedes; are male or female sterile, or have better seed-shatter properties. The methods are also used to improve growth of transformed plant cells (and derived calli or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                  Modulating cell death, growth and stress resistance in eukaryotes, specifically plants, used, e.g. to impart fungus or nematode resistance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.1%; Score 688.5; DB 21; Length 36.2%; Pred. No. 7.2e-54; ive 89; Mismatches 185; Indels
                                                                                                   Claim 18; Page 99-101; 126pp; English.
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Best Local Similarity 36.2
Matches 174; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 637 AA;
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N-PSDB; AAZ60617.
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AAB93513

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Human; primer; detection; diagnosis; antisense therapy; gene therapy
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                                                                                                                                                                                            Saito K, Yo
Otsuki T;
                                                                                                                                                                                                                                                                          Claim 8; SEQ ID 12844; 2537pp + CD ROM; English.
                                                                                                                                                                                           ogai T, Nishikawa T, Hayashi K, S
Sugiyama T, Wakamatsu A, Nagai K,
                              Human protein sequence SEQ ID NO:12844.
                                                                                                                             99JP-0248036.
99JP-0300253.
2000JP-0118776.
                                                                                                              28-JUL-2000; 2000EP-0116126
                                                                                                                                                     02-MAY-2000; 2000JP-0183767
09-JUN-2000; 2000JP-0241899
                (first entry)
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Best Local Similarity 36.99
Matches 184; Conservative
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                                                                                                                                       27-AUG-1999;
11-JAN-2000;
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                                                                Homo sapiens
                26-JUN-2001
                                                                                              07-FEB-2001
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Ishii S,
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119 INHFTRLEDAKKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEV----QAEDEAQEAVVK 174
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18;

QO

22 EKKKGRQAG-----REED-----PFRSTA-----EALKAIPAEKRIIRVDPTCPLSSNP 65

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H----SGGRVGKGIYFASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSL 466
                RGFEALEALEEALKGPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLL
                                                                                                                                                           VLADIELAQALQAVSEQEKTVEEVP-HPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT
                                                                                                                                         354 GS---NHRCPTLQHIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMP
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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:
August 29, 2002, 08:02:15; Search time 36.19 Seconds

(without alignments)
577.744 Million cell updates/sec
Perfect score: 2854
Sequence: 1 MSLEFLAMAPKPKPWVQTEG......EYLIYQESQCRLRYLLEVHL 540

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
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Total number of hits satisfying chosen parameters: 105224

105224 segs, 38719550 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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dP	Query Match	98.5	25.9	25.6	24.1	23.9	23.6	23.6	23.6	23.5	23.3	22.9	22.9	22.4	13.8	0.6	6.7	4.4	4.2	4.0	4.0	4.0	4.0	3.8	æ. œ.	3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.6
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ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                              PPO3_HUMAN STANDARD, PRT; 533 AA.

Q9Y6F1; Q9UG81;

L6-CGT_2001 (Rel. 40, Last sequence update)

16-OCT_2001 (Rel. 40, Last annotation update)

16-OCT_2001 (Rel. 40, Last annotation update)

Poly [ADP-ribose] polymerase-3 (EC 2.4.2.30) (PARP-3) (NAD(+) ADP-ribosyltransferase-3) (Poly[ADP-ribose] synthetase-3)
                                                                                                                                                     Homo sapiens (Human).
Vertebrata; Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                           "A human poly(ADP-ribose) polymerase gene family (ADPRTL): cDNA cloning of two novel poly(ADP-ribose) polymerase homologues."; Genomics 57:442-445(1999).
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InterPro; IPR001290; PARP.
InterPro; IPR04102; PARP.reg.
Pfam; PF00644 ARP; I.
Pfam; PF00877; PARP; I.
Transferase; Glycosyltransferase; NAD; Nuclear protein;
                                                                                                                                                                                                                                         TISSUE-Fetal brain;
MEDLINE-99263509; Pubmed-10329013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF083068; AAD29855.1; -. EMBL; AL050034; CAB43246.1; -.
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SEQUENCE OF 75-533 FROM N.A.
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RESULT 1
PPO3_HUMAN
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MEDLINE=21179160; PubMed=11133988;
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Ame J.-C., Rolli, V., Schreiber V., Niedergang C., Apiou F., Decker
Muller S., Hoger T., Menissier-de Murcia J., de Murcia G.M.;
"PARP-2, A novel mammalian DNA damage-dependent poly(ADP-ribose)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPO2_MOUSE STANDARD; PRT; 559 AA.
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
10-NRT-2002 (Rel. 41, Last annotation update)
10-NRR-2002 (Rel. 41, Last annotation update)
10-NAR-2003 (Rel. 41, Last annotation update)
10-NAR-2003 (Rel. 41, Last annotation update)
11-NAR-2003 (Rel. 41, Last annotation update)
12-NAR-2003 (Rel. 41, Last annotation update)
13-NAR-2003 (Rel. 41, Last annotation update)
14-NAR-2003 (NAD(+) ADP-10-2003 (NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 MAPKPWVQTEGPEKKKGRQAGREEDPFRSTAEALKAIPAEKRIIRVDPTCPLSSNPGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rođentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                       Length 533;
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A -> G (IN REF. 2).

K -> E (IN REF. 2).

7C0AB89E64D1B9FD CRC64;
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                                                                                                                               Score 2811; DB 1;
Pred. No. 1.3e-188;
0; Mismatches 2;
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J. Biol. Chem. 274:17860-17868(1999)
                                                      MM;
                                                                                                                                    Query Match 98.5%;
Best Local Similarity 99.6%;
Matches 531; Conservative
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171
411
533 AA;
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STRAIN=129Sv;
                                                      SEQUENCE
CONFLICT
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Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein;
                                                                                                                                                                           Berghammer H., Ebner M., Marksteiner R., Auer B.; "pADPRT-2: a novel mammalian polymerizing(ADP-ribosyl)transferase generated to truncated pADPRT homologues in plants and Caenorhabditis elegans.";
                                     "A bidirectional promoter connects the poly(ADP-ribose) polymerase (PARP-2) gene to the gene for RNase P RNA."; J. Biol. Chem. 276:11092-11099(2001).
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      de Murcia
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V -> I (IN REF. 2).
R -> Q (IN REF. 2).
EOAEDAEE412C1445 CRC64;
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Ame J.-C., Schreiber V., Fraulob V., Dolle P., Niedergang C.P.;
"A bidirectional promoter connects the poly(ADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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EMBL; AF191547; AAK13253.1; -.
EMBL; AF072521; AAC25415.1; ALT_INIT.
                                                                                                                                              STRAIN=129/Sv X C57BL/6;
MEDLINE=99268466; PubMed=10338144;
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InterPro; IPR004102; PARP_reg.
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                                                                                                                        SEQUENCE OF 9-559 FROM N.A.
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MGD; MGI:1341112; Adprt2.
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177
486
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Pfam; PF02877; PARP_rec
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177
486
559 AA;
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DNA_BIND 1
DOMAIN 66
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"pADPRT-2: a novel mammalian polymerizing(ADP-ribosyl)transferase generelated to truncated pADPRT homologues in plants and Caenorhabditis elegans.";
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208 -SQLDLRVQELLKLICAVQTMEEMMYIEMKYDTKRAPLGKLTVAQIKAGYQSLKKIEDCIR 266
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                                                                              SEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT-GSNHR--CPTLQHI 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 2).
TISSUB-Fetal brain.
MEDLINE-99292755; PubMed-10364231;
Ame J.-C., Rolli V., Schreiber V., Niedergang C., Apiou F., Decker I Muller S., Hoeger T., Menissier-de Murcia J., de Murcia G.M.;
"PARP-2, a novel mammalian DNA damage-dependent poly(ADP-ribose)
                                                                                                                                                                                                                                                                                                                                                 PPO2_HUMAN STANDARD; PRT; 583 AA.
09UGN5; Q9Y6C8; Q9NUV2; Q9UMR4;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
Poly [ADP-ribose] polymerase-2 (EC 2.4.2.30) (PARP-2) (NAD(+) ADP-ribosyltransferase-2) (Poly[ADP-ribose] synthetase-2) (PADPRT-2)
                                               GPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIELAQALQAV
                                                                                          324 KSERQGLE---HPLDQHYRNLHCALRPLDHESNEFKVISQYLQSTHAPTHKDYTWTLLDV
                                                                                                                                                                         FASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSLKSPPPGFDSVIARGH
                                                                                                                          WKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPH----SGGRVGKGIY
                                                                                                                                                                                                                     TEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSS-----TFSQSEYLIYQESQCRLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE-Placenta;
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A human poly(ADP-ribose) polymerase gene family (ADPRTL): cDNA cloning of two novel poly(ADP-ribose) polymerase homologues."; Genomics 57:442-445(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 22-583 FROM N.A. (ISOFORM 1).
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MEDLINE-99263509; PubMed-10329013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Fibroblast;
MEDLINE=99268466; PubMed=10338144;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ADPRTL2 OR PARP2 OR ADPRT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
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547 YLLKI 551
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                                                                                                                                                                                                    similarity).
-!-CATALYTIC ACTIVITY: NAD(+) + {ADP-D-ribosyl}(N)-acceptor -
nicotinamide + {ADP-D-ribosyl}(N+1)-acceptor.
-!-SUBCELLULAR LOCATION: NUCLEAR (By similarity).
-!-ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be produced by alternative splicing.
-!-TISSUE SPECIFICITY: WIDELY EXPRESSED. THE HIGHEST LEVELS ARE IN TISSUE SPECIFICITY: PANCREAS, SKELETAL MUSCLE AND TESTIS: ALSO DETECTED IN KIDNEY, LIVER, LUNG, PLACERTA, OVARY AND SPLEEN.
LEVELS ARE LOW IN LEUKOCYTES, COLON, SMALL INTESTINE, PROSTATE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 ESKKMPVÄGGKANKDRTEDKQDGMPGRSWASKRVSESVKÄLLLKGK-APVDPEC--TAKV 102
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Pfam; PF02877; PARP_reg; 1.
Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein; ANP-ribosylation; Alternative splicing.
DNA_BIND 1 88 POTENTIAL.
Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Kanehori K., "NEDO human CDNA sequencing project."; Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
-: FUNCTION: HAS DNA -DEPENDENT POLY (ADP-RIBOSE) POLYMERASE ACTIVISEEMS TO PLAY A ROLE IN THE RESPONSE TO DNA DAWAGE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EKKKGRQAG-----REED-----PFRSTA-----EALKAIPAEKRIIRVDPTCPLSSNP
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NUCLEAR LOCALIZATION SIGNAL 2ND PART
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-> H (IN REF. 4).
5B7AE8AE531836AF CRC64;
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MISSING (IN ISOFORM 2)
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EMBL; AJ236876; CAB41505.2; ALT_INIT.
EMBL; AK001980; BAA92017.1; ALT_TERM.
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InterPro; IPR001290; PARP.
InterPro; IPR004102; PARP_reg.
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583 AA;
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RA Lepiniec L., Babiychuk E., Kushnir S., van Montagu M., Inze D.;

CC CON DNA AND IS INVOLVED IN THE REGULATION OF VARIOUS IMPORTANT ON PRANSFORMATION AND ALGO IN THE REGULATION OF THE MOLECULAR EVENTS INVOLVED IN THE RECOVERY OF CELL FROM DNA DAMAGE.

CC TOTAL TRANSFORMATION AND ALGO IN THE REGULATION OF THE MOLECULAR EVENTS INVOLVED IN THE RECOVERY OF CELL FROM DNA DAMAGE.

CC TOTAL TRANSFORMATION NAD(+) + [ADP-D-TIDOSY] (N)-acceptor = nicotinamide + [ADP-D-TIDOSY] (N+1)-acceptor = nicotinamide + [ADP-D-TIDOSY] (N+1)-acceptor = nicotinamide + [ADP-D-TIDOSY] (N+1)-acceptor = SIMILARITY: BELONGS TO THE PARP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Poly [ADP-ribose] polymerase (EC 2.4.2.30) (PARP) (ADPRT) (NAD(+) ADP-ribosyltransferase) (Poly[ADP-ribose] synthetase).
447
                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                 336 ALGDIEIAIKL-----VKTELQSPEHPLDQHYRNLHCALRPLDHESYEFKVISQYLOST 389
                                                                                                                                         H----SGGRVGKGIYFASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSL
                                                                                                                  GS---NHRCPTLQHIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMP
                                                                                                                                                                                                                                                        --KSPPPGFDSVIARGHTEP-DPTQDTELELDGQQVVVPQGQPVPCPE
                                                                                                                                                                                                                                                                            VLADIELAQALQAVSEQEKTVEEVP-HPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT
                                                                                                                                                                                                                                                                                                                                                                                                                                             637 AA.
                                                                                                                                                                                                                                                                                                                        512 FSSSTFSQSEYLIYQESQCRLRYLLEV 538
                                                                                                                                                                                                                                                                                                                                                      ----TLNYNEYIVYNPNQVRMRYLLKV 575
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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Pfam; PF00644; PARP; 1.
Pfam; PF02877; PARP_reg; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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NCBI_TaxID=3702;
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Q11207;
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P18493; Q9TS00;
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Poly [ADP-ribose] polymerase-1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+)
ADP-ribosyltransferase-1) (Poly[ADP-ribose] synthetase-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 YNCTLNQTNIENNNNKFYIIQLLQ-DSNRFFTCWNRWGRVGEVGQSKIN-HFTRLEDAKK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                        NAD-BILLONG (BY SIMILARITY).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
527A8F464605D127 CRC64;
Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein;
ADP-Tibosylation.
1 POTENTIAL.
DOMA_BIND 140 637 NAD-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDIALIPE-9038267; MEDIAINE-90382673; PubMed=2119324; MEDIAINE-90382673; PubMed=2119324; Saito I., Hatakeyama K., Kido T., Ohkubo H., Nakanishi S., Ueda K.; "Cloning of a full-length cDNA encoding bovine thymus polyfAbP-tibose) synthetase: evolutionarily conserved segments and their potential functions."; dene 90:249-254(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 IFTNKFNDKTKNYWSDRKEFIPHPKSYTWLEMDYGKEENDSPVNND---IPSSSSEVKPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -CSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALEEALK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT-GSNHRCPTLQ--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GHTEPDPTQDTELELDGQQVVVPQGQPV - - PCPEFSSSTFSQSEYLIYQESQCRLRYLLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   286 QSKLDTRVAKFISLICNVSMMAQHMMEIGYNANKLPLGKISKSTISKGYEVLKRISEVI-
                                                                                                                                                                                                                                                                                                                                                                                                         Length 637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
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36.2%; Pred. No. 1.5e-40;
live 89; Mismatches 185
                                                                                                                                                                                                  62 NI
72175 MW;
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Matches 174;
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                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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PPOL_BOVIN
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                MEDLINE-88151954; PubMed-2450019; Taniguchi T., Yamauchi K., Yamamoto T., Toyoshima K., Harada N., Taniguchi T., Takahashi S., Yamamoto H., Fujimoto S.; "Depression in gene expression for poly(ADP-ribose) synthetase during the interferon-gamma-induced activation process of murine macrophage tumor cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02877; PARP_reg; 1.
Pfam; PF00645; 2f-PARP; 2.
Pr0064075; Znf-PARP; 2.
Pr006475; Znf-PARP; 2.
PR051TE; P550172; BRCT; 1.
PR05ITE; P550147; PARP_ZN_FINGER_1; 2.
PR05ITE; P550064; PARP_ZN_FINGER_2; 2.
Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein; ADP-ribosylation; Zinc-finger; Zinc.
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NUCLEAR LOCALIZATION SIGNAL 2ND PA
ADP-RIBOSYL[N] (POTENTIAL).
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SIMILARITY: BELONGS TO THE PARP FAMILY.
SIMILARITY: CONTAINS 1 BRCT DOMAIN.
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         647-714 AND 838-903 FROM N.A.
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                                                                            Biochem. 171:571-575(1988)
                                                                                                                                                                                                                                                                                                                                                      EMBL; D90073; BAA14114.1; -.
EMBL; X06886; CAA30046.1; -.
EMBL; X06887; CAA30047.1; -.
PIR; JS0428; JS0428.
PIR; S00328; S00328.
HSSP; P26446; LAG.
InterPro; IPR001357; BRCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR004102; PARP_reg.
InterPro; IPR001510; Znf PARP.
Pfam; PF00633; BRCT; 1.
Pfam; PF00644; PARP; 1.
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386
386
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DNA_BIND
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01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Poly (Apprince)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
17-OCT-2001 (Rel. 40, L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                657 TVNP-GTKSKLPKP-----VQNLIKMIFDVESMKKAMVEYEIDLQKMPLGKLSKRQIQA 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 DRGPVRTVTKRVQPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 GFEALEALEEAL-KGPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           542 HN--AHVLEKGGKVFSATLGLVDIVKGTNSYYKLQLLEDDKESRYWIFRSWGRVGTVIGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLKSPPPGFDSVIARGHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62;
                                                                                                                                                                                                                                                                                                                                                                                                              Length 1015;
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                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 681; DB 1; Length 10; Pred. No. 9.4e-40; 99; Mismatches 205; Indels
ADP-RIBOSYL[N] (POTENTIAL).
AMW; OASFE9D9F04F5B04 CRC64;
                                              (POTENTIAL).
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MEDLINE-94170813; Pubmed-8125121;
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33.9%;
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YDIAQVHLKYLLKL 1006
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Q11208;
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NCBI_TaxID=9031;
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16-OCT-2001
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PPOL_CHICK
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                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESKSSKSKSIYTKSVPKSMTLKIKDGLAVDPDSGLED--VAHVYVSRNKEKYNVVLGITD 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IENNNNKFYIIQLLQD--SNRFFTCWNRWGRVG-EVGQSKINHFTRLEDAKKDFEKKFRE 138
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                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50172; BRCT; 1.
PROSITE; PS00347; PRRP_ZN_FINGER_1; FALSE_NEG.
PROSITE; PS50064; PARP_ZN_FINGER_2; 2.
Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein;
                 cDNA from Sarcophaga peregrina.";
Eur. J. Biochem. 220:607-614(1994).
-!- FUNCTION: POLY[ADP-RIBOSE] POLYMERASE MODIFIES VARIOUS NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEAR LOCALIZATION SIGNAL 1ST PART.
NUCLEAR LOCALIZATION SIGNAL 2ND PART.
1; 690DDD36E7487298 CRC64;
de Prati A.C., Kurata S., Natori S., Sugimura T., Esumi H.; "Cloning and functional expression of poly(ADP-ribose) polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
AUTOMODIFICATION DOMAIN.
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BY SIMILARITY.
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M
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Pfam; PF02877; PARP_reg; 1.
Pfam; PF00645; Zf-PARP; 2.
ProDom; PD004675; Znf-PARP; 2.
SWART; SM00292; BRCT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                    nc-finger;
                                                                                                                                                                                                                                                                                                           InterPro; IPR001290; PARP.
InterPro; IPR004102; PARP_reg.
InterPro; IPR001510; Znf-PARP.
Ffam; PF00533; BRCT; 1.
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996
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996 AA;
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                                                                                                                                                                                                                                                                                         P26446; 1A26
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Matches 179;
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DOMAIN
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Best Local 8
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ZN_FING
ZN_FING
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Poly [ADP-ribose] polymerase-1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+)
ADP-ribosyltransferase-1) (Poly[ADP-ribose] synthetase-1).
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"Inhibitor and NAD+ binding to poly(ADP-ribose) polymerase as derived
from crystal structures and homology modeling.";
Blochemistry 37:3893-3900(1998).
                                  428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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-!- FUNCTION: POLY(ADP-RIBOSE) POLYMERASE MODIFIES VARIOUS NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 659-1011.
MEDLINE-696358441, PubMed-e4755499;
Ruf A., Mennissier de Murcia J., de Murcia G.M., Schulz G.E.;
"Structure of the catalytic fragment of poly(AD-ribose) polymerase
                                                                                                                                                                   KFIDATNRFYTLIPHNFGTQSPPLLDTTEQVEQLRQMLDSLIEIECAYSLLQTEDSKADI
                                                                                                                                                                                                                                                                                                     Ittel M.-E., Garnier J.-M., Jeltsch J.-M., Niedergang C.;
"Chicken poly(ADP-ribose) synthetase: complete deduced amino acid
KLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALEALKGPTDGGQSL
                                                                                                                              E--ELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIELAQALQAVSEQEKTV
                                                                                                                                                                                                                                                            EEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT-GSNHRCPTLQ--HIWKVNQEG
                                                                                                                                                                                                                                                                                                                                                                                          EEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPH----SGGRVGKGIYFASENSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SANYC----CTSHHNSTGLMLLSEVALGDMMECTAAKYVTKLPNDK-HSCFGRGRTMPNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          487 TQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYLIYQESQCRLRYLLEVH 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of p
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Gene 102:157-164(1991).
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MEDLINE=98239716; PubMed=9571033;
Ruf A., Rolli V., de Murcia G.M., Schulz G.E.;
"The mechanism of the elongation and branching reaction ribose) polymerase as derived from crystal structures an mutagenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Natl. Acad. Sci. U.S.A. 93:7481-7485(1996).
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(Rel. 36, Last sequence update)
(Rel. 40, Last annotation update
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MEDLINE=91340148; PubMed=1840535;
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PROSITE; PS50172; BRCT; 1.
PROSITE; PS00347; PARP_ZN_FINGER_1; 2.
PROSITE; PS50064; PARP_ZN_FINGER_2; 2.
Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein;
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NUCLEAR LOCALIZATION SIGNAL 2ND
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DNA_BIND 1 370
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ADP-RIBOSYL[N]
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                                                                                                                                                                                                                                                   EMBL; X52690; CAA36917.1; -
PIR; JH0581; JH0581.
PDB; 2PAW; 27-MAY-98.
PDB; 1PAX; 15-MAY-98.
PDB; 2PAX; 27-MAY-98.
PDB; 3PAX; 27-MAY-98.
PDB; 3PAX; 27-MAY-98.
PDB; 1A26; 27-MAY-98.
InterPro; IPR001230; PARP_reg.
InterPro; IPR001357; BRCT.
InterPro; IPR001357; BRCT.
InterPro; IPR001331; BRCT.
InterPro; IPR001331; BRCT.
Pfam; PF00543; BRCT; 1.
Pfam; PF00543; BRCP; 1.
Pfam; PF00644; ZaF-PARP; 2.
ProDom; PP00645; ZaF-PARP; 2.
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Ganesh A., Phillips E., Thacker J., Meuth M.;
"Suppression of the radiation-sensitive phenotype of hamster irsl and irs2 strains selected for resistance to 3-aminobenzamide.";
Int. J. Radiat. Biol. 77:609-616(2001).
-I- FUNCTION: POLY[ADP-RIBOSE] POLYMERASE MODIFIES VARIOUS NUCLEAR
                                                                                                                                                                                                                             59 CPLSSNPGTQVYED----YNCTLNQTNIENNNNKFYIIQLLQD--SNRFFTCWNRWGRVG 112
                                                                                                                                                                                                                                                                                                   EV-GOSKINHFTRLEDAKKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQ-AEDEAQE 170
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16-OCT-2001 (Rel. 40, Last sequence update)
01-WAR-2002 (Rel. 41, Last annotation update)
Poly [ADP-ribose] polymerase-1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+)
                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            289 KKDMLLVLADIELAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 AVVKVDRGPVRTVTKRVQPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSK
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                        69
                                                                                       Length 1011;
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                                                                                                                        Indels
                  -> R (IN REF. 1).
261AED9383139144 CRC64;
 ADP-RIBOSYL[N] (POTENTIAL)
                                                                                       DB 1;
                                                                                                                        204;
                                                                                      Score 674.5; DB 1
Pred. No. 2.7e-39;
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                                                                                                        Best Local Similarity 33.4%; Pred. No. 2.7e
Matches 187; Conservative 100; Mismatches
517 517 ADP
895 895 A -
1011 AA; 113520 MW;
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                                                                                      23.68;
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09R152;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mes by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                     similarity).
CATALYTIC ACTIVITY: NAD(+) + {ADP-D-ribosyl}(N)-acceptor =
nicotinamide + {ADP-D-ribosyl}(N+1)-acceptor.
COFACTOR: ZINC, CONTAINS TWO WOLES OF ZINC PER MOLE OF PROTEIN (BY
                                                                                                                          SIMILARITY).
SUBUNIT: HOMODIMER (Potential).
SUBCELLUALAR LOCATION: Nuclear.
MISCELLANEOUS: THE ADP-D-RIBOSYL GROUP OF NAD(+) IS TRANSFERRED TO
AN ACCEPTOR CARBOXYL GROUPO ON A HISTONE OR THE ENZYME ITSELE, AND
FURTHER ADP-RIBOSYL GROUPS ARE TRANSFERRED TO THE 2'-POSITION OF
FURTHER ADP-RIBOSYL GROUPS ARE TRANSFERRED TO THE 2'-POSITION OF
AVERAGE CHAIN LENGTH OF 20-30 UNITS.
SIMILARITY: BELONGS TO THE PARP FAMILY.
PROTEINS BY POLY(ADP-RIBOSYL)ATION. THE MODIFICATION IS DEPENDENT ON DNA AND IS INVOLVED IN THE RECULATION OF VARIOUS IMPORTANY CELLULAR PROCESSES SUCH AS DIFFERENTIATION, PROLIFERATION, AND TUMOR TRANSFORMATION AND ALSO IN THE REGULATION OF THE MOLECULAR EVENTS INVOLVED IN THE RECOVERY OF CELL FROM DNA DAMAGE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY)
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PROSITE; PS00347; PARP_ZN_FINGER_1; 2.
PROSITE; PS50064; PARP_ZN_FINGER_2; 2.
Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein; ADP-ribosylation; Zinc-finger; Zinc.
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AUTOMODIFICATION DOMAIN (BY
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InterPro; IRR001357; BRRCT.
InterPro; IPR001510; Znf-PARP.
Pfam; PF0053; BRCT; 1.
Pfam; PF00545; PARP_reg; 1.
Pfam; PF00545; Zf-PARP; 2.
ProDom; PD004675; Znf-PARP; 2.
SMART; SM00292; BRCT; 1.
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Length 1012;

Score 673.5; DB 1; Pred. No. 3.1e-39;

23.6%; 33.8%;

Query Match Best Local Similarity

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01-DEC-1992 (Rel. 24, Last Sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Poly (ADP-ribose) polymerase-1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+)
ADP-ribosyltransferase-1) (Poly[ADP-ribose] synthetase-1).
ADPRT OR PPOL OR PARP1.
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                                                               493 APKGKSAAPSKKSKGLYKEEG--VNKSEKRMKLTLKGGAA------VDPDSGLEHS- 540
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Uchida K., Morita T., Sato T., Ogura T., Yamashita R., Noguchi S., Suzuki H., Nyunoya H., Miwa M., Sugimura T.;
"Nucleotide sequence of a full-length cDNA for human fibroblast poly(ADP-ribose) polymerase.";
Biochem. Biophys. Res. Commun. 148:617-622(1987).
                                                                                                                    654 TVKPGTK----SKLPKAVQELVGMIFDVESMKKALVEYEIDLQKMPLGKLSKRQIQAAYS
                                                                                                                                                                                                                                                                                                                   SHE TGYMFGKGIYFADMVSKSANY----CHTSQGDPIGLILLGEVALGNMYELKHAS-HISK
                                  APKPK - - - PWVQTEGPEKKKGRQAGREEDPFRSTAEALKAIPAEKRIIRVDPTCPLSSNP
                                                                                                 66 GTQVYED----YNCTLNQTNIENNNNKFYIIQLLQDSNRF-FTCWNRWGRVGEV-GQSKI
                                                                                                                                                                  120 NHFTRLEDAKKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQ-AEDEAQEAVVKVDRG
                                                                                                                                                                                                                                 179 PVRTVTKRVQPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFE
                                                                                                                                                                                                                                                                                                239 ALEALEEALKGPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLAD
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 59;
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MEDLINE=90091744; PubMed=2513174;
Auer B., Nagl U., Herzog H., Schneider R., Schweiger M.;
Alman nuclear NAD+ ADP-ribosyltransferase(polymerizing):
Organization of the gene.";
DNA 8:575-580(1989).
Conservative 100; Mismatches 205; Indels
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01-MAR-2002 (
Matches 186;
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P09874;
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  "Molecular cloning of cDNA for human poly(ADP-ribose) polymerase and expression of its gene during HL-60 cell differentiation."; Blochem. Biophys. Res. Commun. 146:403-409(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The zinc fingers of human poly(ADP-ribose) polymerase are differentially required for the recognition of DNA breaks and nicks and the consequent enzyme activation. Other structures recognize
                     TISSUE-Fibroblast;
MEDLINE-88058958; PubMed=2824474;
Kurosaki T., Ushiro H., Mitsuuchi Y., Suzuki S., Matsuda M.,
Matsuda Y., Ratunma N., Kangawa K., Matsuo H., Hirose T.,
Inayama S., Shizuta Y.;
Primary structure of human poly(ADP-ribose) synthetase as deduced
from CDNA sequence.";
J. Biol. Chem. 262:15990-15997(1987).
                                                                                                                                                                                  "cDNA sequence, protein structure, and chromosomal location of the human gene for poly(ADP-ribose) polymerase."; Proc. Natl. Acad. Sci. U.S.A. 84:8370-8374(1987).
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-94 FROM N.A.
MEDLINE-91099327: PubMed-2125269;
MCDLINE-91099327: PubMed-2125269;
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Ushiro H., Terashima M., Sumimoto H., Kuribayashi I., Yamamoto Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-39 FROM N.A.
MEDLINE-90211250; PubMed-2108670;
Ogura T., Nyunoya H., Takahashi-Masutani M., Miwa M., Sugimura T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        that of
                                                                                                                                                                                                                                SEQUENCE OF 440-1013 FROM N.A.
MEDLINE-87298455; PubMed-3113420;
Suzuki H., Uchida K., Shima H., Sato T., Okamoto T., Kimura T.,
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Proc. Natl. Acad. Sci. U.S.A. 87:2990-2994(1990).
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MEDLINE-88068596; PubMed-2891139;
Cherney B.W., McBride O.W., Chen D., Alkhatib H., Bhatia K.,
Hensley P., Smulson M.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Characterization of a putative promoter region of the human poly(ADP-ribose) polymerase gene: structural similarity to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANALYSIS OF ZINC FINGERS.
MEDILINE-91072398; PubMed=2123876;
IRelima M., Noguchi S., Yamashita R., Ogura T., Sugimura T.,
Gill D.M., Miwa M.;
                                                                                                                                                                                                                                                                                                                                               Suzuki H., Uchida K., Shima H., Sato T., Okamoto T., Kimura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Herzog H., Schneider R., Hirsch-Kauffmann M., Schnitzer D., Schweiger M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (JUL-1991) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                        Biochem. Biophys. Res. Commun. 148:1549-1550(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the DNA polymerase beta gene.";
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MEDLINE-90222155; Pubmed-2109322;
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           SEQUENCE FROM N.A.
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MEDLINE-91035460; PubMed-2121735;
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Molinete M., Penning C., Keith G., de Murcia G.M.;
"Expression and site-directed mutagenesis of the catalytic domain of human poly(ADP-ribose)polymerase in Escherichia coli. Lysine 893 is MEDLINE-92371433; PubMed-1505517; Schreiber V., Molinete M., Boeuf H., de Murcia G.M., Menissier de Murcia J.; Biol. Chem. 265:19249-19256(1990) M17081; AAA51599.1; ALT_SEQ. M32721; AAA60155.1; -. JOINED. JOINED. JOINED. JOINED. JOINED. JOINED. JOINED. JOINED. JOINED. JOINED JOINED JOINED JOINED MUTAGENESIS OF CATALYTIC DOMAIN. EMBL; X16674; CAA34663.1; -. NUCLEAR LOCALIZATION SIGNAL. AAA51663.1; AAA51663.1; AAB59447.1; AAA51663.1; AAA51663.1 AAA51663.1 AAA51663.1 AAA51663.1 critical for activity. M18112; M29786; M29774; M29778; M29545; M29768: M29769; M29770; M29772: M29776; M29777 M29767 M29773 EMBL;
AAA51663.1;

M29780;

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                                                                     ; AAAS1663.1; JOINED.
; CAA39606.1; -.
; CAA39606.1; JOINED.
; AAA60000.1; -.
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                                           JOINED.
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Znf-PARP.
Jud.1)

Jud.1563.1;

AAA51663.1;

AAA51663.1;

Jud.1 M29544; AAA51663.1;

Jud.1 M29544; AAA51663.1;

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                                                                   EMBL; M29782; AAA51663
EMBL; X56140; CAA39606
EMBL; X56141; CAA39606
EMBL; M60436; AA60000
PIR; A26901; A26901.
PIR; A28498; A28498.
PIR; A28498; A28498.
PIR; A35635; A3321.
PIR; A33321; A33321.
PIR; B33321; B33321.
PIR; B33321; B33321.
PIR; S39376; S14010; S14010.
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InterPro; IPR004102;
InterPro; IPR001510;
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Pfam; PF00644; PARP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thodeau J., Cradwoll G., Dumas C., Clairoux-Moreau S., Brunet G.;

MEDLINE-90027702; PubMed-2508731;

MIDDGeduu J., Gradwoll G., Dumas C., Clairoux-Moreau S., Brunet G.;

Tibodeau J., Gradwoll G., Dumas C., Clairoux-Moreau S., Brunet G.;

Tibodeau J., Gradwoll G., Dumas C., Clairoux-Moreau S., Brunet G.;

RT "cloning of rodent cDNA coding the poly(ADP-ribose) polymerase

RT "cloning of rodent cDNA coding the poly(ADP-ribose) polymerase

RT "cloning of rodent CDNA coding the poly(ADP-ribose) polymerase

RT Estochem. Cell Biol. 67:653-660(1999). As Biochem. Cell Biol.

C. I. FUNCTION: POLY(ADP-RIBOSE) POLYMERASE MODIFIES VARIOUS INFORTANT

CELLULAR PROCESSES SUCH AS DIFFERREWIATION OF VARIOUS IMPORTANT

CELLULAR PROCESSES SUCH AS DIFFERREWIATION OF VARIOUS INPORTANT

CELLULAR PROCESSES SUCH AS DIFFERREWIATION OF VARIOUS INPORTANT

CELLULAR PROCESSES SUCH AS DIFFERREWIATION OF VARIOUS INPORTANT

CELLULAR PROCESSES SUCH AS DIFFERREWIATION OF PREDECTION

C. CAPALYTIC ACTIVITY: NAD(+) + (ADP-D-ribosyl)(N) - acceptor

INCOCTIONALING LOCATION NUCLES OF ZINC PER MOLE OF PROTEIN

C. I. SUBCELLUREDOST THE ADP-D-RIBOSYL GROUP OF NAD(+) IS TRANSFERRED TO

THE TERMINAL ADENOSINE MOIEST.

C. I. SUMILARITY: BELONGS TO THE PARP FRAMILY.

C. I. SIMILARITY: CONTAINS I BRCT DOMAIN.
                                                                                 16-OCT-2001 (Rel. 40, Last annotation update)
Poly [ADP-ribose] polymerase-1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+)
ADP-ribosyltransferase-1) (Poly[ADP-ribose] synthetase-1).
                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                     STRAIN=SPRAGUE-DAWLEY; TISSUE-Monocytes;
MEDLINE=98046546; Pubbled=9385436;
Beneke S., Meyer R., Buerkle A.;
"Isolation of cDNA encoding full-length rat (Rattus norvegicus) poly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Potvin F., Thibodeau J., Kirkland J.B., Dandenault B., Duchaine C., Poirier G.G.; Extractural analysis of the putative regulatory region of the sending poly(ADP-ribose) polymerase."; FEBS Lett. 302:269-273(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beneke S., Meyer R., Buerkle A.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases
1013 AA
                                                                 Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                             (ADP-ribose) polymerase.";
Biochem. Mol. Biol. Int. 43:755-761(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-11 FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-Prostate;
MEDLINE-92290013; PubMed-1601134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U94340; AAC53544.1; -.
EMBL; X65496; CAA46477.1; -.
EMBL; X65497; CAA46478.1; ALT_INIT.
HSSP; P26446; 1A26.
InterPro; IPR001357; BRCT.
                  15-JUL-1992 (Rel. 23, Created)
15-JUL-1998 (Rel. 36, Last sem
16-OCT-2001 (Rel 46)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 514-1013 FROM N.A.
  STANDARD;
                                                                                                                                                                           (Rat)
                                                                                                                                                                             Rattus norvegicus
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Poly (ADP-ribose) polymerase (EC 2.4.2.30) (PARP) (ADPRT) (NAD(+) ADP-ribosel) polymerase (EC 2.4.2.30) (PARP) (Ragment).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
 HATTHNAYDLEVIDIFKIEREGESQRYKPFRQLHNRRLLWHGSRTTNFAGILSQGLRIAP 880
                                                                                    411 H----SGGRVGKGIYFASENSKSAGYVIGMKCGAHH---VGYMFLGEVALGREHHINTDN
                                             881 PEAPVIGYMFGKGIYFADMVSKSANY -----CHTSQGDPIGLILLGEVALGNMYELKHAS
                                                                     PSLKSPPPGFDSVIARGHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYL
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 742-876 FROM N.A.
MEDLINE-93277538; Pubmed-8503897;
Ozawa Y., Uchida K., Uchida M., Ami Y., Kushida S., Okada N.,
                                                                                                                                                                                                                                                                                                                                                                                                Thesis (1992), University of Rennes, France.
                                                                                                                                                                                                    998 AA.
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990 VYDIAQVNLKYLLKL 1004
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NCBI_TaxID=8355;
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SMART; SM00292; BRCT; 1.
PROSITE; PS00172; BRCT; 1.
PROSITE; PS00047; PARP_ZN_FINGER_1; 2.
PROSITE; PS50064; PARP_ZN_FINGER_2; 2.
PROSITE; PS50064; PARP_ZN_FINGER_2; 2.
Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein;
Transferase; Glycosyltransferase; Zinc.
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NUCLEAR LOCALIZATION SIGNAL 2ND
                                                                                                                                                                                                                                                                                 DDC-RIBOSYL (N) (POTENTIAL).
ADP-RIBOSYL (N) (POTENTIAL).
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-> D (IN REF. 4).
AA566F2B29BE97C0 CRC64;
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                                                       Pfam; PF02877; PARP_reg; 1.
Pfam; PF00645; zf-PARP; 2.
ProDom; PD004675; Znf-PARP; 2.
            IPR004102; PARP_reg. IPR001510; Znf-PARP.
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                                 Pfam; PF00533; BRCT; 1.
Pfam; PF00644; PARP; 1.
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456
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752 75
1013 AA;
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ADP-ribosylation, Z
INIT_MET 0
DNA_BIND 1
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437
444
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SUBCELLULAR LOCATION: Nuclear.
ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a short form/SPARP-1; may be produced by alternative initiation.
MISCELLANEOUS: THE ADP-D-RIBOSYL GROUP OF NAD(+) IS TRANSFERRED TO AN ACCEPTOR CARBOXYL GROUP ON A HISTONE OR THE BUZNE ITSELF, AND FURTHER ADP-RIBOSYL GROUP ON A HISTONE OR THE BUZNE ITSELF, AND THE TERMINAL ADENOSINE MOIETY, BUILDING UP A POLYMER WITH AN
                                                                                                                                                                                                                                                                                                                    PPOL_MOUSE STANDARD; PRT; 1012 AA.
P1103; 095174; 09003;
01-JUL-1989 (Rel. 11, cateded)
01-CT-1989 (Rel. 12, Last sequence update)
16-CT-2001 (Rel. 40, Last annotation update)
16-CT-2001 (Rel. 40, Last annotation update)
ADP-riboss| polymerase-1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+)
ADP-ribosyltransferase-1) (Poly[ADP-ribose] synthetase-1) (mspARP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEINS BY POLY (ADP-RIBOSYL) ATION. THE MODIFICATION IS DEPENDENT ON DRA AND IS INVOLVED IN THE REGULATION OF VARIOUS IMPORTANY CHELLULAR PROCESSES SUCH AS DIFFERENTIATION, PROLIFERATION, AND TUMOR TRANSFORMATION AND ALSO IN THE REGULATION OF THE MOLECULAR EVENTS INVOLVED IN THE RECOVERY OF CELL FROM DNA DAMAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 with poly(ADP-ribose) polymerase activity independent of DNA strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COFACTOR: ZINC, CONTAINS TWO MOLES OF ZINC PER MOLE OF PROTEIN SUBUNIT: HOMODIMER (Potential).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                   872 YMFGKGIYFADMVSKSANYCHAMP--GSPIGLILLGEVALGNMHELKAASQITKL-PKGK
                                                   414 GRVGKGIYFASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSLKSPPPGF
                                                                                                                        474 DSVIARGHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYLIYQESQCRLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salimann F.R., Vodenicharov M.D., Wang Z.-Q., Poirier G.G.; "Characterization of SPARP-1. An alternative product of PARP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: NAD(+) + (ADP-D-ribosyl)(N)-acceptor nicotinamide + (ADP-D-ribosyl)(N+1)-acceptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Huppi K., Bhatia K., Siwarski D., Klinman D., Cherney B.,
"Sequence and organization of the mouse poly (ADP-ribose)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION.
STRAIN=129/Sv X C57BL/6; TISSUE-Fibroblast;
MEDLINE-20270268; PubMed=10809783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic Acids Res. 17:3387-3401(1989)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YEDYNCTLNQTHIENNNNKFYIIQLLQ-DSNRFFTCWNRWGRVGEV-GQSKINHFTRLED 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AKKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGPVRTVTKRV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KP-----VQELIKLIFDVESMKKAMVEFEIDLQKMPLGKLSKRQIQSAYSILSQVQQAV 703
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                                                                                                                                                                                                                                                                  DNA-binding; Nuclear protein;
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PART.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               303 QAL--QAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT-GSNHRC
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PROSITE; PS50172; BRCT; 1.
PROSITE; PS00347; PARP_ZN_FINGER_1; 2.
PROSITE; PS50064; PARP_ZN_FINGER_2; 2.
Transferase; Glycosyltransferase; NAD; 1
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                                                              InterPro; IPR001519; PARP_reg. Pfam; PF00533; BRCT; 1. Pfam; PF00644; PARP: 1
                                                                                                                         Pfam; PPO2877; PARP.reg; 1.
Pfam; PPO0645; zf-PARP; 2.
ProDom; PD004675; znf-PARP; 2.
SMART; SM00292: въст.
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                HSSP; P26446; 1A26.
InterPro; IPR001357;
                                                 InterPro; IPR001290;
InterPro; IPR004102;
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998 AA;
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Smulson M. polymerase

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                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50172; BRCT; 1.
PROSITE; PS50172; BARP_ZN_FINGER_1; 2.
PROSITE; PS50064; PARP_ZN_FINGER_2; 2.
Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein;
ADP-ribosylation; Zinc-finger; Zinc; Alternative initiation.
                                                                                                                                                                                                                                                                                                                                                                                                                               POLY [ADP-RIBOSE] POLYMERASE-1,
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4354C3E5F01B9439 CRC64;
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AVERAGE CHAIN LENGTH OF 20-30 UNITS. SIMILARITY: BELONGS TO THE PARP FAMILY. SIMILARITY: CONTAINS 1 BRCT DOMAIN.
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PIR; S04200; S04200.
HSSP; P26446; 1A26.
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InterPro; IPR004102; Daf-PARP.
Pfam; PF00533; BRCT; 1.
Pfam; PF00644; PARP; 1.
Pfam; PF00847; PARP_reg; 1.
Pfam; PF00645; Zf-PARP; 2.
ProDom; PD004675; Zf-PARP; 2.
SMART; SM00292; BRCT; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
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23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                685 VEXEIDLQKMPLGKLSRRQIQAAYSILSEVQQPVSQGSSESQIL-DLSNRFYTLIPHDFG 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ADPRT) (NAD(+) ADP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GKYTLIEVQ-AEDEAQEAVVKVDRGPVRTVTKRVQPCSLDPATQKLITNIFSKEMFKNTM 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSQPPPINSPELLQAKKDMLLVLADIELAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQL 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QLLDSGAPEYKVIQTYLEQT-GSNHRCPTLQ--HIWKVNQEGEEDRFQAHSKLGNRKLLM 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    391 HGTNMAVVAAILTSGLRIMPH----SGGRVGKGIYFASENSKSAGYVIGMKCGAHH---V 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GYMFLGEVALGREHHINTDNPSLKSPPPGFDSVIARGHTEPDPTQDTELELDGQQVVVPQ 503
                                                                                                                                                                                                                                           SLQDLLSAHSLSPWGAEVKAEPGEVVAPRGKSAAPSKKSKGCFKEEGVNKS----- 517
                                                                                                                                                                                                                                                                                                                                                                                                  518 -EKRMKLTLKGGAAVDPDSGLEHS--AHVLEKGGKVFSATLGLVDIVKGTNSYYKLÖLLE 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSNRF-FTCWNRWGRVGEV-GQSKINHFTRLEDAKKDFEKKFREKTKNNWAERDHFVSHP 154
                                                                                    Gaps
                                                                                                                                                           SLLFLAMAPKPKPW---VQTEGPE-----KKKGRQAGREEDPFRSTAEALKAIP 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., ALTERNATIVE SPLICING, DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY.
STRAIN-CANTON-S;
                                                                                                                                                                                                                                                                                                                           AEKRI-----IRVDPTCPLSSNPGTQVYED----YNCTLNQTNIENNNKFYIIQLLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214 ALMDLDVKKMPLGKLSKQQIARGFEALEALEEALKGPTDGGQSLEELSSHFYTVIPHNFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HGSRTTNFAGILSQGLRIAPPEAPVTGYMFGKGIYFADMVSKSANY -----CHTSQGDPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE-23234521; PubMed-8475096;
Uchida K., Hanai S., Ishikawa K.-I., Ozawa Y.-I., Uchida M.,
Sugimura T., Miwa M.;
Cloning of cDNa encoding Drosophila poly(ADP-ribose) polymerase:
leucine zipper in the auto-modification domain.";
Proc. Natl. Acad. Sci. U.S.A. 90:3481-3485(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Length 1012;
                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPOL__DROME STANDARD; PRT; 994 AA. P354875; 09W5S1; 09W5S1; 09W5S1; 00W5S1; 00
    ; DB 1;
8.4e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GQPVPCPEFSSSTFSQSEYLIYQESQCRLRYLLEV 538
                                                                                    Mismatches
22.9%; Score 653;
                                          Pred. No.
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                                                                               Conservative 102;
                                          32.3%;
                                              Similarity
                                                                                    186;
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D13806; BAA02964.1;

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RA Adams W.D., Celnis Fudnace-10/3113;

RA Adams W.D., Celnis Fudnace-10/3113;

RA Adams W.D., Celnis Fudnace-10/3113;

RA Adams W.D., Celnis Fudnace S.E., Li P.W., Hoskins R.A., Galle R.F.,

Sutton G.G., Worthan J.R., Yandell W.D., Zhang Q., Chen L.X.,

RA Sutton G.G., Worthan J.R., Yandell W.D., Zhang Q., Chen L.X.,

RA Bandon R.C., Rogers Y.-H.C., Blazef R.G., Champe M., Pfelifer B.D.,

RA Adams D.D., Baxter E.G., Helt G., Champe M., Pfelifer B.D.,

RA Ballew R.M., Doyle C., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Ballew R.M., Cawley S., Dahlke C., Davenport L.B., Davies P., R.

Burtis R.C., Busam D.A., Deller H., Cadleu E., Center A., Chandra I.,

RA Burtis R.C., Busam D.A., Dahlke C., Davenport L.B., Davies P., A

Burtis R.C., Busam D.A., Deller C., Perraz C., Ferraz C., Perriser S., Pleischman W.,

RA Burtis N.L., Harvey D., Heiman T.J., Hernadez J.R., Glodek A., Gong F., Gorrell J.H., Gu Z., Gana P., Harris M.,

RA Hostin D., Harvey D., Heiman T.J., Hernadez J.R., Retchum K.A.,

RA Hostin D., Harvey D., Heiman T.J., Hernadez J.R., Retchum K.A.,

RA Hostin D., Houston K.A., Woland T.J., Wei M.-H., Ibeywan C.,

RA Jazzolo M., Pittman G.S., Changer J.R., Moshrefi A.,

Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Bazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Jiews R., Woong F.N., Walsher E., Wang A.H., Wang A.H.,

Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

Mullams S.M., Woodeger T., Worley K.C., Wu D., Yang S., Yan Q.A.,

RA Jiews R., Yangen G. W., Weissenbach J.,

Mang Z.-Y., Wassarman D.A., Weinstock G.W., Weissenbach J.,

RA Jiems R., Jane R., Subin M., Pang G., Sun E.,

RA Jeng C., Stapleton M., Shung G., Zhu X., Smith H.O.,

Ra Jeng C., Shong F.N., Woodege T., Worley K., Wall R., Shung S., Shung G., Shung S., Shung S., Shung S., Shung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- CATALYTIC ACTIVITY: NAME (+) + {ADP-D-TIDOSY1]{N}-acceptor = nicotinamide + {ADP-D-TIDOSY1]{N+1}-acceptor.

-i- COFACTOR: ZING, CONTAINS TWO MOLES OF ZINC PER MOLE OF PROTEIN.

-i- SUBCELLULAR LOCATION: Nuclear.

-i- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.

-i- STAGE 12 EMBRYOS AND IN CELLS AROUND THE CENTRAL NERVOUS SYSTEM IN LATER EMBRYOS.

-i- DEVELOPMENTIAL STAGE: EXPRESSED BOTH MATERNALLY AND ZYGOTICALLY IN EMBRYOS.

-i- BEMBRYOS, PUPPAE AND ADULTS. EXPRESSION IS HIGHEST IN EMBRYOS.

-i- MISCELLANEOUS: THE ADP-D-RIBOSYL GROUP OF NAD(+) IS TRANSFERRED TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLY(ADP-RIBOSYL)ATION. THE MODIFICATION IS DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TUMOR TRANSFORMATION AND ALSO IN THE REGULATION OF THE MOLECULAR EVENTS INVOLVED IN THE RECOVERY OF CELL FROM DNA DAMAGE.
                  "Genomic organization of Drosophila poly(ADP-ribose) polymerase and distribution of its mRNA during development."; J. Biol. Chem. 273:11881-11886(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- FUNCTION: POLY[ADP-RIBOSE] POLYMERASE MODIFIES VARIOUS NUCLEAR PROTEINS BY POLY(ADP-RIBOSYL)ATION. THE MODIFICATION IS DEPENDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ON DNA AND IS INVOLVED IN THE REGULATION OF VARIOUS IMPORTANT CELLULAR PROCESSES SUCH AS DIFFERENTIATION, PROLIFERATION, AND
Uchida M., Kobayashi S., Miwa M., Uchida K.;
                                                                                                                                                    STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
                                                                                                                             SEQUENCE FROM N.A. (LONG ISOFORM).
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726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 LQ-DSNRFFTCWNRWGRVG-EVGQSKINHFTRLEDAKKDFEKKFREKTKNNWAERDHFVS 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   617
                                                                                                                                                                                                                                                                                       Pfam; PF00644; PARP; 1.
Pfam; PF00847; PARP; 1.
Pfam; PF00847; PARP; 2.
SMART; SM00292; BRCT; 1.
PROSITE; PS50172; BRCT; 1.
PROSITE; PS50172; BRCT; 1.
TROSITE; PS500847; PARP_ZN_FINGER_1; 1.
TROSITE; PS500847; PARP_ZN_FINGER_2; 2.
Transferase; Glycosyltransferase; NAD; DNA-binding; Nuclear protein; ADP-ribosylation; 2inc-finger; Zinc; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |: ||:| :| || :| 618 RTGRMYPIEIQYDDD--QKLVKHE-----SHFFTSKLEISVQNLIKLIFDIDSMNKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LQLLDSGAPEYKVIQTYLEQT-GSNHRCPTLQ--HIWKVNQEGEEDRFQAHSKLGNRKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 KAIPAEKRI----IRVDPTCPLSSNPGTQVYED----YNCTLNQTNIENNNKFYIIQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153 HPGKYTLIEVQAEDEAQEAVVKVDRGPVRTVTKRVQPCSLDPATQKLITNIFSKEMFKNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             213 MALMDLDVKKMPLGKLSKQQIARGFEALEALEEALKGPTDGGQSLEELSSHFYTVIPHNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GHSQPPPINSPELLQAKKDMLLVLADIELAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEAR LOCALIZATION SIGNAL 1ST
NUCLEAR LOCALIZATION SIGNAL 2ND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 32.2%; Pred. No. 9.1e-37;
Matches 168; Conservative 100; Mismatches 195; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MISSING (IN SHORT ISOFORM).
MW; ACA85A270DD29E08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                AUTOMODIFICATION DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; DB 1;
9.1e-37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PARP-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PARP-TYPE
                                                                                                                                                              EMBL; AE002666; -; NOT_ANNOTATED_CDS
EMBL; AE002892; AAF45445.2; ALT_SEQ.
                                                                                   EMBL, AF051548; AAC24518.1; -...
EMBL, AF051544; AAC24518.1; JOINED.
EMBL, AF051545; AAC24518.1; JOINED.
EMBL, AF051546; AAC24518.1; JOINED.
EMBL, AF051547; AAC24518.1; JOINED.
EMBL, AE002935; AAF45400.1; -...
                                                                                                                                                                                                                            InterPro; IPR001357; BRCT.
InterPro; IPR001290; PARP.
InterPro; IPR004102; PARP_reg.
InterPro; IPR001510; Znf-PARP.
Pfam; PF00533; BRCT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.4%;
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994
54
161
210
228
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FlyBase; FBgn0010247;
                                                                                                                                                                                        PIR; A47474; A47474.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            380
508
19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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EMBL;
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19;

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -

AN ACCEPTOR CARBOXYL GROUP ON A HISTONE OR THE ENZYME ITSELF, AND FURTHER ADP-RIBOSYL GROUPS ARE TRANSFERRED TO THE 2'-POSITION OF THE TERMINAL ADENOSINE MOIETY, BUILDING UP A POLYMER WITH AN AVERAGE CHAIN LENGTH OF 20-30 UNITS.
SIMILARITY: BELONGS TO THE PARP FAMILY.
SIMILARITY: CONTAINS I BRCT DOMAIN.

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PPOV_HUMAN STANDARD; PRT; 1724 AA.
O9UKK3; 075903; O9HM6; 014682;
16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
vault poly(AbP-ribose) polymerase (EC 2.4.2.30) (VPARP) (193-kDa vault protein) (PARP-related/Ialphal-related H5/proline-rich) (PHSP).
                                                                                                                                                                                                                                          :||: : | | |:|||: :||| | MGLQFPVGDRCGLMFGNGVYFANVPTKSANYC----CPEASKRVFMLLCEVETANPLVL 453
                                                                                                                                                                                                                                                                                                              -----IYORLYERLPCHLEPVSE------EIAGKIGDCLAMRGPTHCYKLSLI 337
                                                                                                                                                                                                                  TSGLR--IMPHSGGRVGKGIYFASENSKSAGYVIGMKC-GAHHVGYMFLGEVALGR---- 455
   LSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVL----ADIELAQALQAVSEQEKT 314
                                                                                                                                                                   239 INK-YYSLIPHSFGFCVPPKIDSHAKIQAERELLDALKGSIEASLELKDLKKTASSKD--
                                                                                                                                              -QEGEEDRFQAHSKLG-----NRKLLWHGTNMAVVAAIL
                                                                                                                                                                                                                                                                                         - EHHINTDNPSLKSPPPGFDSVIARGHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND SEQUENCE OF 306-319.
MEDLINE=99408776; PubMed=10477748;
Kickhoefer V.A., Siva A.C., Kedersha N.L., Inman E.M., Ruland C.,
Streuli M., Rome L.H.;
"The 193 kpa vault protein, VPARP, is a novel poly(ADP-ribose)
polymerase.";
                                                                         315 VEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQTGSNHRCPTLQ---HIWKVN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nagase T., Seki N., Ishikawa K.-I., Tanaka A., Nomura N.; "Prediction of the coding sequences of unidentified human genes. The coding sequences of 40 new genes (KIAA0161-KIAA0200) deduced analysis of cDNA clones from human cell line KG-1."; DNA Res. 3:17-24(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Thymus;
MEDLINE-20112770; PubMed-10644454;
MEDLINE-20112770; PubMed-10644454;
MEDLINE-20112770; PubMed-1064454;
MEDLINE-20112770; PubMed-1064454;
MIGHITIAGATION OF a novel gene (ADPRTLL) encoding a potential poly(ADP-ribosyl)transferase protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISCUSSION OF SEQUENCE.
MEDLINE-99198702; PubMed=10100603;
Jean L., Risler J.-L., Nagase T., Coulouarn C., Nomura N.,
Saller J.-P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                   538
                                                                                                                                                                                                                                                                                                                                                                                      | : ::|::||
497 ETIEEETRLLYDEYVMFNKEHFKIKYVVEV 526
                                                                                                                                                                                                                                                                                                                                                                 STFSQ-----SEYLIYQESQCRLRYLLEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Bone marrow;
MEDLINE=96281124; PubMed=8724849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell Biol. 146:917-928(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 94-1724 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomics 62:533-536(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27;
390 WHGTNMAVVAAILTSGLRI----MPHSGGRVGKGIYFASENSKSAGYVIGMKCGAHHVGY 445
                      EKKFREKTKNNWAERDHFVSHPGKYTLIEV-----QAEDEAQEAVVKVD----- 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | || || || :| || || || || || ::|:
ESKFYEKTHLHWEERDD-EPVPNKYAVVELATNARQTEKEVKKEEPEPEPKVDEKNTRGR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 YNCTLNQTNIENNNNKFYIIQLLQDSNRFFTCWNRWGRVGEVGQSKINHFTRLEDAKKDF 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --RGPV----RTVTKRVQPCSLDPATQKLITNIFSKEMFKNTMALMDLDV-----KKM--- 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----DGGQSLEE 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 YKVHLCKTNIAQNNNKFYDWELLDEGGDFIVKLIN-GRIGYRGYTQLKDFDDLDRAKKFF 70
                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                     446 MFLGEVALG -----REHHIN--TDNPSLKSPPPGFDSVIARGHTEPDPTQDTELELDGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hitted (JAN-1995) to the EMBL/GenBank/DDBJ databases. SIMILARITY: SOME, TO THE MIDDLE PART OF NAD(+) ADPRIBOSYLTRANSFERASE (EC 2.4.2.30).
                                                                                                                                                                                                                                                                                                         01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Hypothetical 61.3 kDa protein E02H1.4 in chromosome II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         il protein.
538 AA; 61268 MW; 3144E25465FC7341 CRC64;
                                                                                                                                                               -VEIPYGETI-TDEHLKSSLLYNEYIVYDVAQVNIQYLFRM 988
                                                                                                                                           498 QVVVPQGQPVPCPEFSSSTFSQSEYLIYQESQCRLRYLLEV 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 393.5; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 4.3e-20;
; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----PLGKLSKQQIARGFEALEALEEALKGPT-----
                                                                                                                                                                                                                                                                         538 AA.
                                                                                                                                                                                                                                                                          PRT;
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Best Local Similarity 26.1%; Pro
Matches 149; Conservative 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; 247075; CAA87379.1; -. HSSP; P26446; 1A26. wormpep; E02411.4; CE01539. InterPro; IPR001290; PARP. InterPro; IPR004102; PARP_reg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00644; PARP; 1.
Pfam; PF02877; PARP_reg; 1.
                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
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SEQUENCE 5:
                                                                                                                                                                                                                                                                   YON4_CAEEL
Q09525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith A.;
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                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERACTION WITH THE MAJOR VAULT PROTEIN.
NUCLEAR LOCALIZATION SIGNAL 1ST PART
"The nuclear protein PH5P of the inter-alpha-inhibitor superfamily: a
           missing link between poly(ADP-ribose)polymerase and the inter-alpha-inhibitor family and a novel actor of DNA repair?"; FEBS Lett. 446:6-8(1999).
-!- CATALYTIC ASTIVITY: NAD(+) + {ADP-D-ribosyl}(N)-acceptor = nicotinamide + {ADP-D-ribosyl}(N+1)-acceptor.
-!- SUBUNIT: BINDS TO THE MAJOR VAULT PROTEIN (MPV). THE VAULT, A LARGE RIBONUCLEOPROTEIN COMPLEX, CONTAINS THE 100-kDA MPV AND
                                                                                                          PROTEINS OF 193 AND 240 KDA.

-1 SUBCELLULAR LOCATION: CYTOPLASMIC, BUT IS ALSO FOUND IN THE NUCLEUS, ASSOCIATED WITH MITOTIC SPINDLES.

-1 TISSUE SPECIFICITY: WIDELY EXPRESSED: THE HIGHEST LEVELS ARE THE KIDNEY; ALSO DETECTED IN HEART, PLACENTA, LUNG, LIVER, SKELETAL MUSCLE, SPLEEN, LEUKCYTES AND PANCREAS.
-1 SIMILARITY: BOLONGS TO THE PRAPP FAMILY.
-1 SIMILARITY: CONTAINS 1 BRCT DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
NUCLEAR LOCALIZATION SIGNAL 2ND PART
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fransferase; Glycosyltransferase; NAD; Nuclear protein;
ADP-ribosylation; Ribonucleoprotein.
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EMBL, AA1359763; CAC21562.1; --
EMBL, D79999; BAA11494.1; --
HSSP; P26446; 1A26.
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Interpro; IPR001290; PARP.
Interpro; IPR002035; vWFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00533; BRCT; 1.
Pfam; PF00644; PARP; 1.
Pfam; PF00092; wwa; 1.
SMART; SW00292; BRCT; 1.
SMART; SW00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50172; BRCT; 1.
PROSITE; PS50234; VWFA; 1.
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25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298 EGILLLVKAALKNGET--AEQLQKMMTEFYRLIPHK--GTWPKEVNL-GLLAKKADLCQL 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              353 IRDM------VNVCETNLSKPNPPSLAKYRALRCKIEHVEQNTEEFLRVRKEVLQNHH 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               405 SKSPVDVLQ-IFRVGRVNETTEFL--SKLGNVRPLLHGSPVQNIVGILCRGLLLPKVVED 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SG-----GRVGKGIYFASENSKSAGYVIGMKCGAHHVG-----YMFLGEVALGREHHI 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          460 NTDNPSLKSPPPGFDSVIARGHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQ 519
                                                                                                                                                                      83 EKRLLDVKNYDPYKPLDITPPPDQKASSSEVKTEGLCPDSATEEEDTVELTEFGMQNVEI 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               250 -----LEEVMNSSTLSQEVSDLVEMIWAE-----ALGHLEHMLLKPVNRISLNDVSKA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNHRCPTLQHIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGL---RIMPH 411
                                                                                                                   49 EKRIIRV---DPTCPLSSNP-----GTQVYEDYNCTLNQTNIEN-----NNNKFYI 91
                                                                                                                                                                                                                                                                                                                                                                                  201 QFAIKKTSEDASEYFENYIEELKKQGFLLREHF-----TPEATQLASEQLQALL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 GPVRTVTKRVQPCSLDPATQKLITNIFSKEMFKNTMALMDLD-VKKMPLGKLSKQQIARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237 FEALEALEEALK-GPTDGGOSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             296 LADIELAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEY-KVIQTYLEQTG
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9.0%; Score 258; DB 1; Length 1724;
22.8%; Pred. No. 5.9e-10;
ive 92; Mismatches 193; Indels 146;
                                                                                                                                                                                                                                 92 IQLLQDSNRFFTCWNRWGRVG-EVGQSKI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               514 HEKDFSLTEAPPGYDSVHGVSQTASVTTD----
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DEFVVYKTNQVKMKYIIK 563
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                             Best Local Similarity 22.8 Matches 127; Conservative
     Query Match
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Search completed: August 29, 2002, 08:02:19 Job time: 296 sec

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095271 homo saplen
095271 homo saplen
066878 aquifex aeo
0688 aquifex aeo
06878 aquifex aeo
095273 drosophila
092473 drosophila
09246 homo saplen
09152 aequipecten
09152 aequipecten
09172 aequipecten
09173 asculu
091x4 mus musculu
091x4 mus musculu
091x1 mus musculu
091x1 mus musculu
091x1 mus musculu
091x1 am saculu
091x1 mus musculu
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091x1 mus musculu
091x1 aeccharomyc
03391 saccharomyc
03391 saccharomyc
03663 mus musculu
095xy9 homo saplen
003291 saccharomyc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 QVYEDYNCTLNQTUIENNNNKFYIIQLLQDSNRFFTCWNRWGRVGEVGQSKINHFTRLED 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AKKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGPVRTVTKRV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 QPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALEEAL 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 HAPKPKPWYQTEGPEKKKGRQAGREEDPFRSTAEALKAIPAEKRIIRVDPTCPLSSNPGT
                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL 60.1 KDA PROTEIN.
HOMO SAPJORA; MACAZOA; Chaniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidee; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.9%; Score 2823; DB 4; Length 533; 100.0%; Pred. No. 1.4e-208; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE-PRIMARY B-CELLS FROM TONSILS;
Strausberg M.N.
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC014260; AAH14260.1; -.
Hypothetical protein.
SEQUENCE 533 As; 60089 MW; 6296A0E439CC7767 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            09-6063;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                    533 AA
                                                                      09XZ37
09VBP3
0924M2
09Y2K0
                                                                                                               09H9X9
09NJ23
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09NJ21
09IX18
091XT8
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091XT7
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Best Local Similarity 100.0
Matches 533; Conservative
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                     NCBI_TaxID=9606;
Q96CG2
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                                                                                  (without alignments)
795.853 Million cell updates/sec
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                                                                      August 29, 2002, 08:01:31 ; Search time 117.38 Seconds
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                                                                                                                          2854
1 MSLLFLAMAPKPKPWVQTEG.....EYLIYQESQCRLRYLLEVHL
           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                            Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                        562222 segs, 172994929 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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09TNC6
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Gapop 10.0 , Gapext 0.5
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sp_bactoria:*
sp_fung1:*
sp_fung1:*
sp_human:*
sp_morertebrate:*
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sp_organelle:*
sp_organelle:*
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sp_vertebrate:*
sp_unclassified:*
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sp_bacteriap:*
sp_archeap:*
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Maximum DB
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                                      KGPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIELAQALQA
MAPKPKPWVQTEGPEKKKGRQAGREEDPFRSTAEALKA I PAEKR I IRVDPTCPLSSNPGT
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                                                                   VSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQTGSNHRCPTLQHIWK
                                                                                                         VNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPHSGGRVGKGIYFASENS
                                                                                                                                               KSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSLKSPPPGFDSVIARGHTEPDPT
                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; MusinCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                    540
                                                                                                                                                                                                                                                                                                                                                                                                                                      78.8%; Score 2249.5; DB 11; Length 80.7%; Pred. No. 1.6e-164; ive 37; Mismatches 59; Indels
                                                                                                                                                                                    QDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYLIYQESQCRLRYLLEVHL
                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
SEQUENCE R.;
Strausberg R.;
Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC014870; AAH14870.1; -
Hypothetical protein.

From Figure 528 AA; 59413 MW; 82EFB0C498EB5F74 CRC64;
                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                    HYPOTHETICAL 59.4 KDA PROTEIN. Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 80.7 Matches 431; Conservative
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Q91YR6;
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MEDLINE-96007847; PubMed-7578427;

Auer B., Filer K., Wang Z.Q., Haidacher D., Jager S., Berghammer H.,

Auer B., Filer K., Wang Z.Q., Haidacher D., Jager S., Berghammer H.,

Kofler B., Schweiger M., Wagner E.F.;

On the biological role of the nuclear polymerizing NAD+: protein(ADP-
ribosyl) transferase (ADPRT): ADPRT from Dictyostellum discoideum and
inactivation of the ADPRT gene in the mouse.";

Biochimie 77:444 449(1995).

HSSP; P26446; 1A26.

InterPro; IPR001290; PARP.

InterPro; IPR001201; PARP_reg.

Pfam; PF00644; PARP; 1.

Pfam; PF00644; PARP_reg; 1.
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                                                 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 EVGQSKINHFTR--LEDAKKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQAEDEAQE 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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KVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPHSGGRVGKGIYFASEN
                           --- KPKNGASTTATTTTKKVVEHKKECSLDERVQELVKLIFDVKMMERTMTEAKYDLKK
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                                                                                                     SKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSLKSPPPGFDSVIARGHTEPDP
                                                                                                                                171 AVVKVDRG----PVRTVTKRV----QPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKK
                                                                                                                                                                                                          487 TQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYLIYQESQCRLRYLLEVHL 540
                                                                                                                                                                                                                               475 AQDIELELDGQPVVVPQGPPVQCPSFKSSSFSQSEXLIYKESQCRLRYLLEIHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 612;
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AA; 69241 MW; CB340F7A88FF2364 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NAD+-PROTEIN(ADP-INBOSYL)-TRANSFERASE (EC 2.4.2.30).
Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
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                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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Matches 218; Conserv
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Zea mays (Maize).
Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                       364 HIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPH----SGGRVGKG 419
                                                                                                                                                                                                                                                                                                                                                                                                           420 IYFASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSLKSPPPGFDSVIAR 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YNCTLNQTNIENNNNKFYIIQLLQ-DSNRFFTCWNRWGRVGEVGQSKIN-HFTRLEDAKK 130
                                                                                                                                                                                                                                                                                                              SVDPGLQ-----DDPLYYHYQQLNCGLTPVGNDSEEFSMVANYMENTHAKTHSGYTVEIA 456
                                                                                                                                                                                                                                                                                                                                                                                                                              SNAPVKSSNDEAEDDNNGFEEEKKEEKIVTATKKGAAVLDQWIPDEIKSQYHVLQRGDDV 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        480 GHTEPDPTQDTELELDGQQVVVPQGQPV--PCPEFSSSTFSQSEYLIYQESQCRLRYLLE 537
                                                                                                              227 IFTUKENDKTKNYWSDRKEFIPHPKSYTWLEMDYGKEENDSPVNND---IPSSSSEVKPE
                                                                                                                                                                        GPTDGGQSLEELSSHFYTVIPHNFGHSQPPP -- INSPELLQAKKDMLLVLADIELAQALQ
                                                                                                                                                                                                                                                                                   307 AVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT-GSNHRCPTLQ--
                                                                                                                                                         -CSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEEALK
                                                                                            DFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGPVRTVTKRVQP-
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Babylchuk E., Cottrill P., Storozhenko S., Fuangthong M.,
O'Farrell M., Van Montagu M., Inze D., Kushnir S.;
"Higher plants possess two poly(ADP-ribose) polymerases.";
"Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ222588; CAA10888.1; -.
HSSP; PS6446; 1A26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SFD01923C4ABCD1D CRC64;
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Last annotation update)
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Pfam; PF02877; PARP_reg; 1.
Pfam; PF02037; SAP; 2.
SMART; SM00513; SAP; 2.
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InterPro; IPR004102; PARP
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                                                                                                                                                                                                                            081294 PRELIMINARY; PRT; 635 AA.
081294;
081294;
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 09, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
T14P8.19 PROTEIN (NAD+ ADP-RIBOSYLITRANSFERASE).
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Erassicales; Brassicaceae; Arabidopsis.
                   SQGLRIAPPEAPVSGYRFGKGVYFADCMSLSANY -----CRTVGFLIDFCMLLGDVAL 530
                                                             GREHHINTDNPSLKSPPPGFDSVIARGHTEPDPT---QDTELELDGQQVVVPQGQPVPCP 510
                                                                               403 TSGLRIMPH----SGGRVGKGIYFASENSKSAGYVIGMKCGAHHVGY-----MFLGEVAL 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lamar B., Stoneking T., Stumpf J., Mewes H.W., Lemcke K.,
Mayer K.F.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECULENCE FROM N.A.
STRAIN-CV. COLUMBIA;
KAILCH, J., Ellind, G., Cloud J.;
"The sequence of A. thaliana T14P8.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing Project.";
the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF065298; AAC19283.1;
EMBL; AI161494; CAB80732.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                         584 HKGVSCY-EHQYVVYDVAQVHLKYLLQL 610
                                                                                                                         511 EFSSSTFSQSEYLIYQESQCRLRYLLEV 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR004102; PARP_reg.
InterPro; IPR003034; SAP.
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Pfam; PF02877; PARP_reg; 1.
Pfam; PF02037; SAP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P26446; 1A26.
InterPro; IPR001290; PARP.
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Submitted (JUN-1998) to
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                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=CV. COLUMBIA; WASHU;
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STRAIN-CV. COLUMBIA;
Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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Best Local S
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Length 653;
DB 10;
Score 670.5; DB 1
Pred. No. 4.9e-43;
 23.5%;
 Query Match
Best Local Similarity
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296 288 348 409 405 469 458 524

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113 EV-GOSKINHFTRLEDAKKDFEKKFREKTKNNWAERDHFVSHPCKYTLIEVQ-AEDEAQE 170
                                                      246 RKLTVSAG---TKSKLAKP-----IQDLIKMIFDVESMKKAMVEFEIDLQKMPLGKLSK
                                                                                                                                                                                               231 QQIARGFEALEALEEALKGPTDGGQSLE--ELSSHFYTVIPHNFGHSQPPPINSPELLQA
                                                                                                                                                                                                                                                                                                   349 YLEQT-GSNHRCPTLQ--HIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSG
                                                                                                                                                                                                                                                                                                                                                       406 LRIMPH----SGGRVGKGIYFASENSKSAGYVIGMKC---GAHHVGYMFLGEVALGREHH
                                                                                                                                                                                                                                                                                                                                                                                                         459 INTDNPSLKSPPPGFDSVIARGHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFS
                                     59 CPLSSNPGTQVYED----YNCTLNQTNIENNNKFYIIQLLQD--SNRFFTCWNRWGRVG
                                                                                                                                           171 AVVKVDRGPVRTVTKRVQPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSK
                                                                                                                                                                                                                                                 KKDMLLVLADIELAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1014 AA; 112721 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          519 QSEYLIYQESQCRLRYLLEV 538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (JUL-2001) to the
EMBL; BC012041; AAH12041.1;
Transferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Auer B., Flick K., Wang Z.Q., Haidacher D., Jager S., Berghammer H.,
Kofler B., Schweiger M., Wagner E.F.;
On the biological rolle of the nuclear polymerizing NAD+: protein(ADP-ribosyl) transferase (ADPRT): ADPRT from Dictyostelium discoideum and inactivation of the ADPRT gene in the mouse.";
                                                                                         248 IYEFEGKFHNKTNNHWSDRKNFKCYAKKYTWLEMDYGETEKE----IEKG---SITDQIK 300
                                                                                                                               248
                                                                                                                                              419
                                                                                                                                                                                GPTDGGQSLEELSSHFYTVIPHNFGHSQPPP--INSPELLQAKKDMLLVLADIELAQALQ 306
                                                                                                                                                                                                                                   AVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT-GSNHRCPTLQ-- 363
                                                                                                                                                                                                                                                                                                                                         IYFASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSLKSPPPGFDSVIAR 479
                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
NaD+:PROTEIN(ADP-RIBOSYL)-TRANSFERASE, ADPRT.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                         EDYNCTLNQTNIENNNNKFYIIQLLQ-DSNRFFTCWNRWGRVGEVGQSKINHFTRLED-A 128
                                     KKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGPVRTVTKRVQ 188
                                                                                                                                                                                                                                                                                                                                                                   591
 Gaps
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                                                                                                                                                                                                                                                                                                                                                        PCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALEALK
                                                                                                                                                                                                                                                                                       HIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPH----SGGRVGKG
                                                                                                                                                                                                                                                                                                    480 GHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYLIYQESQCRLRYLLEVH
                                                                                                                                                                                                --KADRRHLEQLTGEFYTVIPHDFGFRKMREFIIDTPQKLKARLEMVEALGEIEIATKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PW----VQTEGPE------KKKGRQAGREEDPFRSTAEALKAIPAEKRIIRVDPT
31;
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 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75F6EE1D30D8F402 CRC64;
Mismatches 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 23.5%; Score 669.5; DB 13; Best Local Similarity 33.2%; Pred. No. 5.3e-43; Matches 186; Conservative 100; Mismatches 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   607 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
93;
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InterPro; IPR001357; BRCT.
InterPro; IPR001390; PARP.
InterPro; IPR004102; PARP_reg.
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Pfam; PF00644; PARP; 1.
Pfam; PF02877; PARP_reg; 1.
PROSITE; PS50172; BRCT; 1.
 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9031;
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01-MAY-2000 (
01-MAY-2000 (
01-DEC-2001 (
Matches 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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61 LSSNPGTQVYED----YNCTLNQTNIENNNNKFYIIQLLQDSNRF-FTCWNRWGRVGEV- 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 494 VAPKGK----SAAPSKKSKGAVKEEGVNKS------EKRMKLTLKGGAAVDPDSG
                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67;
                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO ADP-RIBOSYLTRANSFERASE (NAD+, POLY (ADP-RIBOSE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 23.5%; Score 669.5; DB 11; Length Best Local Similarity 33.5%; Pred. No. 1.1e-42; Matches 186; Conservative 99; Mismatches 203; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDCE68E4CB3F46EB CRC64;
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PSSGPVAGKSSGKVKEEKGSNKSEKKMKLTVKGGAAIDPDSEL---EDSCHVLETGG--- 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                             128 AKKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGPVRTVTKRV
                                                                                                                                                                                                             | : | :::|| | | :| :| | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
                                                                                                                                                                                                                                                                                                                          248 KGPTDGGQSLEE----LSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIELA
                                                                                                                                                                                                                                                                                                                                                                                                                                             QAL - - QAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT - GSNHRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            474 DSVIARGHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYLIYQESQCRLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 YEDYNCTLNQTNIENNNNKFYIIQLLQ-DSNRFFTCWNRWGRVGEV-GQSKINHFTRLED
                                                                                                                                                                                                                                                                                           OPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          360 PTLQ--HIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPH----SG
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The C. elegans Sequencing Consortium.";
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"Direct Submission.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases
EMBL, AC02400; AAF36011.1; -
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"The sequence of C. elegans cosmid Y71F9AL.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
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01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
11FPOTHETICAL 108.0 KDA PROTEIN.
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Science 282:2012-2018(1998).
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Bradshaw-Cordum H.,
"The sequence of C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Q9N4H4;
                                                                                                                                                                                                                                                                                           188
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"On the biological role of the nuclear polymerizing NAD+: protein(ADP-ribosyl) transferase (ADPRT): ADPRT from Dictyostellum discoideum and inactivation of the ADPRT gene in the mouse.";
Blochimia 77:4444449(1995).
InterPro; IPR001357; BRCT.
InterPro; IPR001357; BRCT.
InterPro; IPR001290; PARP.
                        GOSKINHFTRLEDAKKDFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQ-AEDEAQEAVV 173
                                                    234 ARGFEALEALEEALKGPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDML 293
                                                                                                                                                                                                                                                                                           CANAYSILSEVQQAVSQGSSESQIL-DLSNRFYTLIPHDFGMKKPPLLNNADSVQAKVEML 765
                                                                                                                                                                                                                                                                                                                                                                               LVLADIELAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT 353
                                                                                                                                                                                                                                                                                                                                                                                                              -GSNHRCPTLQ--HIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMP 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       411 H----SGGRVGKGIYFASENSKSAGYVIGMKCGAHH----VGYMFLGEVALGREHHINTDN 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          464 PSLKSPPPGFDSVIARGHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYL 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                     KVDRGPVRTVTKRVQPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 607;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam: PF00533; BRCT: 1.
Pfam: PF00544; PARP: 1.
Pfam: PF02847: PARP_res; 1.
SEQUENCE 607 AA: 67496 MW; 54CDEBBE22079886 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAD+:PROTEIN(ADP-RIBOSYL)-TRANSFERASE, ADPRT.
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VYDIAQVNLKYLLKL 1005
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RESULT Q9PS81

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Matches
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MEDLINE=96007847; PubMed=7578427;
Auer B., Flick K., Wang Z.Q., Haidacher D., Jager S., Berghammer H.,
Kofler B., Schweiger M., Wagner E.F.;
"On the biological role of the nuclear polymerizing NAD+: protein(ADP-
ribosyl) transferase (ADPRT): ADPRT from Dictyostelium discoideum and
inactivation of the ADPRT gene in the mouse.";
                                                                                                                                                                                                             DFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGPVRTVTKRVQPC 190
                                                                                                                                                                                                                                                       SLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALEEAL-KG 249
                                                                                                                                                                                                                                                                                                               529
                                                                                                                                                                   73 YNCTLNQTNIENNNNKFYIIQLLQDSNR-FFTCWNRWGRVG-EVGQSKINHFTRLEDAKK 130
                                                                                                                                                                              647
                                                                                                                                                                                                                                                                                                   PTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIELAQALQAVS 309
                                                                                                                                                                                                                                                                                                                                              367
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                                                                                                                                                                                                                                                                                                                                                                                                                                   424 SENSKSAGYVIGMKCGAHHVGYMFLGEVALGR-EHHINTDNPSLKSPPPGFDSVIARG-- 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila sp. (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7242;
                                                                                                                                                                                                                           VNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPH----SGGRVGKGIYFA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                       881
                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                              EQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT-GSNHRCPT-LQHIWK
                                                                                                                                             51;
                                                                                                                       Length 945;
                                                                                                                                              Indels
                            Pfam; PF00644; PARP; 1.
Pfam; PF00645; zf-PARP; 1.
Prodom; PD00465; znf-PARP; 1.
PROSTE; PS50064; PARP_zN_FINGER_2; 1.
Hypothetical protein.
SEQUENCE 945 AA; 108006 MW; 1D0A62C954BC6AD9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NAD+:PROTEIN(ADP-RIBOSYL)-TRANSFERASE, ADPRI.
                                                                                                                        DB 5;
                                                                                                                                            84; Mismatches 189;
                                                                                                                       22.3%; Score 636.5; DB 5 34.0%; Pred. No. 3.5e-40;
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         InterPro; IPR001290; PARP.
InterPro; IPR001510; Znf-PARP.
                                                                                                                                 Best Local Similarity 34.08 Matches 167; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        530 CRLRYLLEVHL 540
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929 IQLKYLVRVKM 939
HSSP; P26446;
                                                                                                                        Query Match
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Q9TX05;
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID-3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   326 GVQLPTLIETHQQIEDLRQMLDSLAEIEVAXSI----IKSEDVSDACNPLDNHYAQIKTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153 HPGKYTLIEVQAEDEAQEAVVKVDRGPVRTVTKRVQPCSLDPATQKLITNIFSKEMFKNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       213 MALMDLDVKKMPLGKLSKQQIARGFEALEALEEALKGPTDGGQSLEELSSHFYTVIPHNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 22.0%; Score 629; DB 5; Length 595 Local Similarity 32.1%; Pred. No. 6.6e-40; Local 167; Conservative 100; Mismatches 196; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-CV. LANDSBERG ERECTA;
Doucet-chabeaud G., Kazmaier M.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ131705; CAA10482.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D9BA37E38B8E7CCD CRC64;
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Last annotation update)
(EC 2.4.2.30).
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Biochimie 77:444-449(1995).
HSSP; P26446; 1A26.
InterPro; IPR001357; BRCT.
InterPro; IPR001290; PARP.
InterPro; IPR004102; PARP.
Fram; PF00533; BRCT; 1.
Pfam; PF00644; PARP; 1.
Pfam; PF00847; PARP; 1.
Pfam; PF02877; PARP; 1.
PROSITE; PS50172; BRCT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                    SRCT; 1.
68018 MW;
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InterPro; IPR001357; BRCT.
InterPro; IPR001290; PARP.
InterPro; IPR004102; PARP_reg.
InterPro; IPR001510; Znf-PARP.
Pfam; PF00533; BRCT.
Pfam; PF00644; PARP; 1.
                                                                                                                                                                                                                                         Pfam; PF02877; PARP_reg; 1.
Pfam; PF00645; zf-PARP; 2.
ProDom; PD004675; Znf-PARP; 2.
                                                                                                             Lin X.;
Submitted (MAR-2000) to the
EMBL; AC006593; AAD20677.1;
HSSP; P26446; 1A26.
                                                            Nature 402:761-768(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | :|::||:|
QVKLQFLLKV 1003
                                                                                    SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
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STRAIN-CV. COLUMBIA;
MEDLINE=20083487; Pubbed=10617187;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Roo H., Moffat K.S.,
Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,
                                                                                                                                                                                                                                          |::||||| :| :| :: :| |||: :: FKRLFLEKTGNTWESWEQKTNFQXQPGKFLPLD-------IDYGVNKQVAKK-E 628
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                             FEKKFREKTKN---NWAERDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGFVRTVTKRVQ 188
                                                                                                                                                                                                                                                                                                                                EAL----KGPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIE 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                         854
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                                                                                                                                        PPRGKHSTKGLGKKVP---QDSEFAKWRGDVTVPCGKPV-SSKVKASELMYNEYIVYDTA 967
                                                                                                                           75
                                                                                                                                                                          TLNQTNIENNNNKFYIIQLLQDSNRFFTCW--NRWGRVG--EVGQSKINHFTRLEDAKKD 131
                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                               KKGRQAGREEDPFRSTAEALKAIPAEKRIIRVDPTCPLSSNPGTQ----VYED----YNC
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                                                                                                  79;
                                                                        Length 983
                         POLY(ADP-RIBOSE) POLYMERASE.; 468E12A8EF1B6F4F CRC64;
                                                                                                  Indels
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Last sequence update)
Last annotation update)
                                                                       DB 10;
                                                                       Query Match 21.0%; Score 598.5; DB 10; Best Local Similarity 31.1%; Pred. No. 3.1e-37; Matches 171; Conservative 101; Mismatches 199;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seque
01-DEC-2001 (TrEMBLrel. 19, Last annot
PUTATIVE POLY (ADP-RIBOSE) POLYMERASE.
           Transferase; Glycosyltransferase; NAD
                                  983 AA; 111232 MW;
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QVKLQFLLKV 977
                                  SEQUENCE
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360 408 FEKKFREKTKN---NWAERDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGPVRTVTKRVQ 188 C.R., 76 TLNQTNIENNNKFYIIQLLQDSNRFFTCW--NRWGRVG--EVGQSKINHFTRLEDAKKD 131 Gaps 24 KKGRQAGREEDPFRSTAEALKAIPAEKRIIRVDPTCPLSSNPGTQ----VYED----YNC 75 EAL----KGPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIE T-----LQHIWKVNQEGEEDRFQAH-SKLGNRKLLWHGTNMAVVAAILTSGLRI----P----CSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALE PFQTSSNLAPSLIELMKMLFDVETYRSAMMEFEINMSEMPLGKLSKHNIQKGFEALTEIQ LAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQTGSNHRCP MPHSGGRVGKGIYFASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSLKS PPPGFDSVIARGHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYLIYQES Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville (Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana."; 79; Length 1009; Query Match 21.0%; Score 598.5; DB 10; Length Best Local Similarity 31.1%; Pred. No. 3.2e-37; Matches 171; Conservative 101; Mismatches 199; Indels SMART; SM00292; BRCT; 1.
PROSITE; PS50172; BRCT; 1.
PROSITE; PS50104; PARP_XN FINGER_2; 2.
SEQUENCE 1009 AA: 114133 MW; CDE6E41CC2A3A2DB CRC64; databases the EMBL/GenBank/DDBJ

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Pfam; PF00533; BRCT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM00292; BRCT
                                                     536 LEV 538
                                                                          961 LKV 963
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                                                                                                                               09ZSV1
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                                                                                                        RESULT 14
Q9ZSV1
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                                                                                            Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              480 KVKGRSAVHESSGLQDTAHILE-------DGKSI---YNATLNMSDL 516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 TKNNWAE---RDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGPVRTVTKRVQPCSLDPAT 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 KKKGRQAGREEDPFRSTAEALKAIPAEKRIIRVDPTCPLSSNPGTQVYEDYNCTLNQTNI 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | :|::|: | | ::|:: | | 517 ALGVNSYYVLQIIEQDDGSECYVFRKWGRYGSEKIGGQKLEEMSKTE-AIKEFKRLFLEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          576 TGNSWEAWECKTNFRKOPGRFYPLDVD-----YGVKKAPKRKDISEMK-SSLAPQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            364 HIWKVNQEGEEDRFQAH-SKLGNRKLLWHGTNMAVVAAILTSGLRIMPH----SGGRVGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 969;
                                                                                                                                                                     20.3%; Score 578; DB 10; Length 9 ilarity 30.6%; Pred. No. 1.1e-35; Conservative 96; Mismatches 195; Indels
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Pfam; PF0045; 2.
ProDom; PF004675; 2n-PARP; 2.
SMART; SM00292; BRCT; 1.
PROSITE; PS50172; BRCT; 1.
PROSITE; PS50172; BRCT; 1.
SROUGENCE 969 AA: 109128 MW; EB23AC62EEC14009 CRC64;
                                         01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                     969 AA
                      PRT;
                                                                                                                                                                                                                                             InterPro; IPR001290; PARP.reg.
InterPro; IPR0004102; PARP_reg.
InterPro; IPR000344; SAP.
InterPro; IPR001510; Znf-PARP.
                                                                          POLY (ADP-RIBOSE) POLYMERASE
                                                                                                                                                                                                                                    InterPro; IPR001357; BRCT.
                      PRELIMINARY;
                                                                                                                                                                                                                                                                                       Pfam; PF00533; BRCT; 1.
Pfam; PF00644; PARP; 1.
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Best Local Similarity
Matches 166; Conserva
                                                                                                                                                             SEQUENCE FROM N.A.
                     024570
RESULT 13
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           024570
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SEQUENCE FROM N.A.
MEDILINE-99026291; PubMed-9808734;
MEDILINE-99026291; PubMed-9808734;
Mahajan P.B., Zuo Z.;
"Purification and cDNA cloning of maize Poly(ADP)-ribose polymerase.";
"Purification 118:895-905(1998).
EMBL; AF093627; AAC79704.1; -.
HSSP; P26446; 1A26.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukary,raines):
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
                           905 TKGLGKTVP---LESEFVKWRDDVVVPCGKPVP-SSIRSSELMYNEYIVYNTSQVKMQFL 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               476 VIARGHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYLIYQESQCRLRYL 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENNNNKFYIIQLL-QDSNRFFTCWNRWGRVG--EVGQSKINHFTRLEDAKKDFEKKFREK 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TKNNWAE----RDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGPVRTVTKRVQPCSLDPAT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEE----LSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIELAQALQAV-SE 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 KKKGRQAGREEDPFRSTAEALKAIPAEKRIIRVDPTCPLSSNPGTQVYEDYNCTLNQTNI 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALEEALKGPTDGGQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            528 ALGVNSYYVLQIIEQDDGSECYVPRKWGRVGSEKIGGQKLEEMSKTE-AIKEFKRLFLEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 980;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50172; BRCT; 1.
PROSITE; PS50064; PARP_ZN_FINGER_2; 2.
Transferase: Glycosyltransferase.
SEQUENCE 980 As: 110475 MW; 9D8AED26BC37ESC1 CRC64;
                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
(EC 2.4.2.30).
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                                                                                                                                                                                                                                                                                            980 AA
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                                                                                                                                                                                                                                                                                            PRT;
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Pfam; PF00645; zf-PARP; 2.
ProDom; PD004675; znf-PARP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001290; PARP.
InterPro; IPR004102; PARP_reg.
InterPro; IPR00334; SAP
InterPro; IPR001510; Znf-PARP.
                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-DEC-2001 (TrEMBLrel. 19, POLY(ADP)-RIBOSE POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001357; BRCT
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Matches 166; Conservative
                                                                                                                                                                                                                                                                                            PRELIMINARY;
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311 QEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQTGSNHRCPT-----LQ 363
                                                                                                                 364 HIWKVNQEGEEDRFQAH-SKLGNRKLLWHGTNMAVVAAILTSGLRIMPH----SGGRVGK 418
                                                                                                                                                      239 IDGEGNPDENDFAKKRRAKKEARLMEVQKKRMKKQSDLLWEYRQIFERMPYTDNISILRE 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AKKDF-----EKKFREKTKNNWAERDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDES-----LDDKYMKLHCDITPLAHDSEDYKLIEQYL----LNTHAPTHKDWSLELE 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSTAEALKAIPAEKRIIRVDPTCPLSSNPGTQVYEDYNCTLNQTNIENNNNKFYIIQLLQ 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aron...
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                        476 VIARGHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYLIYQESQCRLRYL
                                                                                                                                                                                                                                      GIYFASENSKSAGYVIGMKCGA---HHVGYMFLGEVALGREHHINTDNPSLKSPPPGFDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Genome sequence of the nematode C.elegans: A platform for
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Pfam; PF00847; PARP_reg; 1.
Prodom; PF00645; zf-PARP; 1.
PROSTIE; PS50064; PARP; 1.
PROSTIE; PS50064; PARP_ZN-FINGER_2; 1.
SEQUENCE 727 AA; 82884 MW; 530ABA8E99IFFEFD CRC64;
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Last annotation update)
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Science 282:2012-2018(1998).
EMBL: 283097; CAB05448.1; -.
HSSP; P26446; 1A26.
InterPro; IPR001290; PARP.
InterPro; IPR004102; PARP.
InterPro; IPR001510; Znf-PARP.
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Submitted (NOV-1996)
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SEQUENCE FROM N.A.
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Best Local Similarity
Matches 162; Conserv
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SEQUENCE FROM N.A.
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LKV 974
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Q9XUA5
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                                                                                                                                                                                                                                                                                                                                           467 KSPPPGFDSVIARG------HTEPD----PTQDTELELDGQQVVVPQGQPVPCPEFS 513
                                                                                                                                                                                                                                                                                                                                                                             694
180 VRTVT--KRVQPCS---LDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIA 234
                                                                RGFEALEALEEL-KGPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDML
                                                                                                                                    LVLADIELAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT
                                                                                                                                                                                                      -GSNHRCPT-LQHIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPH
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                                                   Sednence Sed
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APPLICANT: Weinfeld, Michael
APPLICANT: Weinfeld, Michael
APPLICANT: Wing, James Z.
TITLE OF INVENTION: Methods for Quantitating Low Level
TITLE OF INVENTION: Medifications of Nucleotide Sequences
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: USA
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Best Local Similarity 33.6%; Pred. No. 1.1e-59;
Matches 187; Conservative 100; Mismatches 192; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/078,347A
FILING DATE: 13-MAY-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CATTOL PEET G.
FREERRACTON NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 32,837
TELECOMMUNICATION INFORMATION:
TELEPRAX: (415) 705-8410
TELEPRAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHRRACTERISTICS:
TENNEYAL 1014 amino acids
                   US-08-973-462-8

US-08-353-700-1

US-08-310-1167A-1

US-08-144-618-6

US-08-144-618-6

US-08-146-855A-2

US-08-150-741-8

US-08-121-601-8

US-08-021-601-8

US-08-021-601-6

US-08-021-601-6

US-08-021-601-6

US-08-031-601-6

US-08-031-601-6

US-08-031-601-6

US-08-031-601-6

US-08-031-601-6

US-08-031-601-6

US-08-031-529-6

US-09-231-529-6
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281.894 Million cell updates/sec
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Sequence 6, A
Sequence 3, A
Sequence 1, P
Sequence 1, P
Sequence 1, P
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                                                                                                                                                               August 29, 2002, 07:58:13 ; Search time 46.79 Seconds
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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Compugen Ltd.
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US-08-9196-387-2

US-08-910-925-1

US-08-910-925-1

US-08-913-992A-6

US-08-910-925-3

US-08-910-925-3

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US-08-910-925-3

US-09-349-546-1

US-09-349-546-1

US-09-349-546-1

US-08-923-992A-10

US-08-923-992A-10

US-08-923-992A-10

US-08-923-992A-10

US-08-923-992A-4

US-08-923-992A-4

US-08-923-992A-4

US-08-923-92A-4

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US-08-185-432-2
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Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                             RGFEALEALEEALKGPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLL
                                                                                                                                                                                                                                                                        295 VLADIELAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQT-
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502 ALSKKSKGQVKEEGINKSEKRMKLTLKGGAAVDPDSGLEHSAHVLE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IDEM COMPATIBLE
OFBRATING SYSTEM: Windows
SOFTWARE: FASTEEQ for Windows Version 2.0b
CURREW APPLICATION DATA:
FILLING DATE: 03-0CT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Burkle, Alexander
APPLICANT: Zur Hausen, Harald
APPLICANT: Zur Hausen, Harald
APPLICANT: Jan-Heiner, Kupper
TITLE OF INVENTION: VECTORS AND VIRUSES FOR UTITLE OF INVENTION: IN GENE THERAPY
NUMBER OF SEQUENCES: 2
ADDRESSEE: Pennie & Edmonds, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A
REGISTRENON NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8484-0028-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08860886
Patent No. 6335009
GENERAL INFORMATION:
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989 YIVYDIAQVNLKYLLKL 1005
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: NY
COUNTRY: USA
ZIP: 10036-2811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-860-886-2
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501 ALSKKSKGQVKEEGINKSEKRMKLTLKGGAAVDPDSGLEHSAHVLE-------546
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                                                                                                                                                                                                                                                                                                                                                                                                                      7 AMAPKPWWQTEGPEKKKGR----QAGREEDP---FRSTAEALKAIPAEKRIIRVDPT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          336 HISKLPKGKHSVKGLGKTTPDPS--ANISLDG--VDVPLGTGI-SSGVNDTSLINEYIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               465 SLKSPPPGFDSVIARGHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS TITLE OF INVENTION: OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                   ; DB 4; Length 1013;
1.7e-59;
                                                                                                                                                                                                                                                                                                                                                                               Matches 186; Conservative 101; Mismatches 195;
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                                                                                                                                                                                                                                                                                                                                   23.5%; Score 670; 33.6%; Pred. No. 1
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Patent No. 6277613
GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klauber & Jackson
TELECOMMUNICATION INFORMATION:
                                    TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1013 amino acids
                                                                                                                                                                                                                      MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | :| |:|||::
991 YDIAQVNLKYLLKL 1004
                                                                                                                                                                      STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                525 YQESQCRLRYLLEV 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
US-09-196-387-2
                                                                                                                                                                                                                                                                  US-08-860-886-2
                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116
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TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1222 NOYVYGIGGGTGCPTHKDRSCYICHRQMLFC-RVTLGKS-FLQFSTMKMAHAPPGHHSVI 1279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   335 ---LLDSGAP---EYKVIQTYLEQTGSNHRCP-----TLLQHIWKVNQEGEEDRF- 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              378 -----QAHSKLGNRKLLWHGTNMAVVAAILTSGL-RIMPHSGGRVGKGIYFASENSKS 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       430 AGYVIGM----KCGAH-----HVGYMFLGEVALGREHHINTDNPSLKSPPPGFDSVI 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284 ELLQAKKDMLLVLADI---ELAQ-ALQAVSEQEKTVEEVPHPL----DRDYQLLKCQLQ 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Tai, Joseph Y.
APPLICANT: Blake, Milan S.
TITLE OF INVENTION: No. 6280738-1gA Fc Binding Forms of the Group TITLE OF INVENTION: Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 1327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                  PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
4.9%; Score 138.5; DB 4;
Best Local Similarity 24.4%; Pred. No. 0.00012;
Matches 73; Conservative 41; Mismatches 102;
                                                                                                                                                                                                                                                                                                                 NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPANE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/196,387
                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08923992A Patent No. 6280738
                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 133521
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1327 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
               STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: PI
HYPOTHETICAL: NO
                                                                                                                                                                                                     FILING DATE
                                                       07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-923-992A-2
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309 QATQVKNQFLENAQKLKEIQ------PLIKETNVKLYKAMSESLEQVEKELKHN 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        417 TPKKRVKRDLAANENNQQKIELTVS-PENITVYE--GEDVKFTVTAKSDSKTTLDFSDLL 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 QAGREEDPFRSTAEALKAIPAEKRIIRVDPTCPLSSNPGTQVYEDYNCTLNQTNIE-NNN 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 -----TKNNWAERDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGPV---RTVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 KRVQPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 EALKGPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIELAQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   363 QHIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPHSGGRVGKGIYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          590 ------MEQPEIPSNPEYGIQKSIWESQKEPIQEAI-TSFRKIIGDSSSKYYTEHYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       540 NKYKSDFMNYQL-----HAQMEMLTRKVV-----QYMNKYPDNAEIKKI---FESDMKRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----SKTEEKVPQEPKSND----KNQLQELIKSAQQELEKLEKAIKEL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----GHTEPD------PTQDTELELDGQQVVVPQGQPVPCPEFS 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                687 KEDNYGSLENDALKGYFEKYFLTPFNKIKQIVDDLDKKVEQDQPAPIPENS 737
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COUNTRY:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION UNMER: US/08/923,992A

FILING DATE: 05-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 4.0%; Score 113.5; DB 4; Best Local Similarity 20.2%; Pred. No. 0.034; Matches 107; Conservative 72; Mismatches 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1438.0140001/RWE
                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,707
FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: ESEMONG, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1438.01400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1164 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-923-992A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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299 IELAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQTGSNHR 358
                                                                                                                             359 CPTLQHIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPHSGGRVGK 418
                                                                                                                                                                                                                                                                  419 GIYFASENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSLKSPPPGFDSVIA 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  272 QATQVKNQFLENAQKLKEIQ------PLIKETNVKLYKAMSESLEQVEKELKHN 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87 NKFYIIQLLQDSNRFFTCW----NRWGRVGEVGQSKINHFTRLEDAKKDFEKKFREK--- 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/08923992A
Patent No. 6280738
GENERAL INFORMATION:
APPLICANT: Tai, Joseph Y.
APPLICANT: Blake, Milan S.
TITLE OF INVENTION: No. 6280738-IgA Fc Binding Forms of the Group I TITLE OF INVENTION: Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.9%; Score 112.5; DB 4; Length 1098; 20.0%; Pred. No. 0.039; ive 75; Mismatches 199; Indels 153;
                                                           349 AEKEQ-----EEEEQKQEMEVKMEEETEVRESEKQ-QDSQPEEVMDVLEMVE---
                                                                                                                                                                                               --ASKELEPE--
                                                                                                                                                                                                                                                                                                                                    429 -MEFEIEPDK-----ECKSLSPGKENVSALDMEKESEEKEEKESEPOPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        473 --VAQPQPQSQPQLQLQSQSQPVLQSQPPSQPEDLSLAVLQPTPQVTQE 519
                                                                                                                                                                                                                                                                                                                                                                                                      479 RGHTEPDPTQDTELELDGQQVVVPQGQPVPCPEFSSSTFSQSEYLIYQE 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Sterne, Kessler, Goldstein & Fox P.L.L.C.
1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPUTER: TEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/923,992A .
FILING DATE: 05-SEP-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 05.5EP-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATE: 05.60/024,707
FILING DATE: 06.5EP-1996
ATTORNEY/AGENT INFORMATION:
NAME: ESMONT, ROBERT W.
REFERENCE/DOCKET NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1438.0140001/RWE
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                              ::|: : | ::| :: | ::| :: | ::| :: | ::| :: | ::| :: | ::| :: | ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2610
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1098 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 3.9%
Best Local Similarity 20.0%
Matches 107; Conservative
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                                                                                                                   GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN PININ SPLICE VARIANT
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,925
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET UNDBER: PF-O:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                           Sequence 1, Application US/08910925
Patent No. 6162601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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SEQUENCE CHARACTERISTICS:
LENGTH: 717 amino acids
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LIBRARY:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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; CLONE: 53219
US-08-910-925-1
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380 TPKKRLKRDLAANENNQQKIELTVS-PENITVYE--GEDVKFTVTAKSDSKTTLDFSDLL 436
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                                                                                                                                                                                                                                                                                           305 LQAVSEQEKTVEEVP-HPLDRDYQLLKCQLQ-LLDSGAPEYKVIQTYLEQTGSNHRCPTL 362
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-----TKNNWAERDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGPV---RTVT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Tal, JOSEPh Y.
APPLICANT: Black, Milan S.
TITLE OF INVENTION: No. 6280738-1gA FC Binding Forms of the Group
TITLE OF INVENTION: Streptococcal Beta Antigens
CORRESPONDENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                              185 KRVQPCSLDPATQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALE
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                                                                                                                                                                                                                           -TLKAKDDSGNVVEKT----FTITYQKKEEKQVP--KTPE----QKD----
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MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPATIBLE PATENTIN Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,992A
FILING DATE: 05-SEP-1997
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: US 60/024,707
FILING DATE: 06-SEP-1996
ATTONINIVAGENT INFORMATION:
MANE: FORMATION:
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TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 6:
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LENGTH: 1128 amino acids
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US-08-923-992A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 LQAVSEQEKTVEEVP-HPLDRDYQLLKCQLQ-LLDSGAPEYKVIQTYLEQTGSNHRCPTL 362
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                                                                                                 Gaps
                                                                                                                                                                                    28 QAGREEDPFRSTAEALKAIPAEKRIIRVDPTCPLSSNPGTQVYEDYNCTLNQTNIE-NNN 86
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                                                                                                 Indels
    DB 4;
                                                                                            205;
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APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN PININ SPLICE VARIANT
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
3.9%; Score 110.5; DE 20.0%; Pred. No. 0.066; Live 73; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 3, Application US/08910925; Patent No. 6162601; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
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                                                                                            Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Herewith
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                  Similarity
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         Query Match
                                                       Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140
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Torbert, K.
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                                                                                                                                                                                  COUNTRY: US
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      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 TLNQTNIENNNNKFYII----QLLQDSNRFFTCWNRWGRVGEVGQSKINHFTRLEDAKK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 DFEKKFREKTKNNWAERDHFVSHPGKYTLIEVQAE-DEAQEAVVKVDRGPVRTVTKR--- 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 QVENERRELFEERRAKQTELRLLEQKVELAQLQEEWNEHNAKIIKY----IRTKTKPHLF 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 VQPCSLDPATQKLITNIFSKEMFKNTMALMD------LDVKKMPLG-----KLSKQQI 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 ARGFEALEALEEALKGPTDGGQSLEEL----SSHFYTVIPHNFGHSQPPPINSPELLQA- 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 GPEKKKGRQAGREEDP----FRSTAEALKAIPAEKRIIRVDPTCPLSSNPGTQVYEDYNC 75
                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.8%; Score 109; DB 4; Length 743; Best Local Similarity 20.0%; Pred. No. 0.046; Matches 115; Conservative 79; Mismatches 190; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           507 VPC-PEFSSSTFSQSEYLIYQESQCRLRYLLEVH 539
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                                           PF-0365 US
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/POCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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Patent No. 5994123
GENERAL INFORMATION:
APPLICANT: OISZEWSKI, N.
                                                                                                                                     : INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 743 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear IMMEDIATE SOURCE: LIMEATY: GenBank CLOME: 1684847
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Tzafrir, I.
Somers, D. A.
Lockhart, B.
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APPLICANT:
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100 RFFTCWNRWGR-----VGEVGQSKINHFTRLEDAKKDFEKKFREKTKNNWA------145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  272 FGHSQPPPINSPELLQAKKDMLLVLADIELAQALQAVSEQE------KTVEEVPH 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222 ----KMPL---GKL---SKQQIARGFEALEEALKGPTDGGQSLEELSSHFYTVIPHN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 177;
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                                                                                              ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A. STREET: P.O. Box 2938 CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.8%; Score 108.5; DB 2; 21.0%; Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64; Mismatches 135;
TITLE OF INVENTION: SUGARCANE BACILLIFORM VIRUS
TITLE OF INVENTION: PROMOTER
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/694,869
FILING DATE: 09-AUG-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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LENGTH: 1871 amino acids
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Best Local Similarity 21.09
Matches 100; Conservative
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                                               NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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TOPOLOGY: linear
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us-09-701-586b-6.rai

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US-09-172-422-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40 AEALKAIPAEKRIIRVDPTCPLSSNPGTQVYEDYNCTLNQTNIENNNNKFYIIQLLQDSN 99
                    187 VQPCSLDP-----ATQKLITNIFSKEMF------KNTMALMDLDVK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           370 QEGEEDRFQAH-SKLGNRKLLW----HGTNMAVVAAILTSGLRIMPHSGGRV-GK 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1871;
370 QEGEEDRFQAH-SKLGNRKLLW----HGTNMAVVAAILTSGLRIMPHSGGRV-GK
                                                                                                                                      GENERAL INFORMATION:
APPLICANT: 01szewski, N.
APPLICANT: 1zafrir, I.
APPLICANT: Somers, D.A.
APPLICANT: Somers, D.A.
APPLICANT: Lockhart, B.
APPLICANT: Lockhart, B.
APPLICANT: Lockhart, B.
TITLE OF INVENTION: Sugarcane bacilliform virus promoter;
FILE REFERENCE: 600.369152
CURRENT APPLICATION NUMBER: US/09/349,546
CURRENT FILING DATE: 1999-07-08
EARLIER APPLICATION NUMBER: PCT/1B97/01338
EARLIER FILING DATE: 1996-09-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastsEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.8%; Score 108.5; DB 3; Best Local Similarity 21.0%; Pred. No. 0.25; Matches 100; Conservative 64; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: sugarcane bacilliform virus US-09-349-546-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09172422A Patent No. 6300485
                                                                                                             Sequence 1, Application US/09349546
Patent No. 6093569
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APPLICANT: Adams, Arwen E.
APPLICANT: Adams, Arwen E.
APPLICANT: Duli, David
APPLICANT: Duli, David
APPLICANT: Buli, David
APPLICANT: Gorman, Susan W.
APPLICANT: Sheffield, Val
APPLICANT: Sheffield, Val
APPLICANT: Sheffield, Val
APPLICANT: Welch, Juliet
TITLE OF INVENTION: COMPOSITIONS, METHODS, AND USES THEREOF
TITLE OF INVENTION: COMPOSITIONS, METHODS, AND USES THEREOF
FILE REFERENCE: 200130, 442
CURRENT APPLICATION NUMBER: US/09/172,422A
CURRENT FILIKO DATE: 1998-10-14
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
US-08-923-992A-10
US-08-923-992A-10
Sequence 10, Application US/08923992A
Fatent No. 6280738
GENERAL INFORMATION:
APPLICANT: Tai, Joseph Y.
APPLICANT: Tai, Joseph Y.
TILLE OF INVENTION: No. 6280738-1gA FC Binding Forms of the Group B
TITLE OF INVENTION: Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1003 ---LKEQERQHLQDLLHQEVLRRIILLQRWFRVLLCRQHFL------HLRQAS- 1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHPG--KYTLIEVQA-----EDEAQEAVVKVDRGPVRTVTKRVQPCSLDPATQ--- 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -KLITNIFSKEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALE--EALKGPTDGG 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255 QSLEELSSHFYTVIPHNFGHSQPPPIN-----SPELLQAKKDMLLVLADIELAQA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 RFFTCWNRWGRVGEVGOSKINHFTRLEDAKKDFEKKFREKTKNNWAERDH-----FV 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 EALKAIPAEK-RIIRVDPTCPLSSNPGTQVYEDYNCTLNQTNIENNNNKFYIIQLLQDSN 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            305 LQAVSEQEKT-VEEVPHP-----LDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    356 NHRCPTLQHIWK--VNQEG-----EEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 3.8%; Score 108.5; DB 4; Best Local Similarity 21.0%; Pred. No. 0.42; Matches 88; Conservative 63; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20005
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APPLICANT: Jens Kossmann
APPLICANT: Jens Kossmann
APPLICANT: Ruth Lorberth
TITLE OF INVENTION: PLANTS WHICH SYNTHESIZE A MODIFIED STARCH,
TITLE OF INVENTION: PROCESS FOR THE PRODUCTION THEREOF AND MODIFIED STARCH
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: FISH & NEAL A.
                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 (EPA) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/045,360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FP96/04109
FILING DATE: 19-5EP-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 19547733.2
FILING DATE: 20-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 19534759.5
FILING DATE: 19-5EP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Haley Jr., James F. REGISTRATION NUMBER: 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1464 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 3.7%
Best Local Similarity 20.8%
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 212-596-9090 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-045-360-2
                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                  New York
GENERAL INFORMATION:
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                                                                                                                                                                                                          New York
                                                                                                                                                                                                                                                       USA
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87 NKFYIIQLLQDSNRFFTCW----NRWGRVGEVGQSKINHFTRLEDAKKDFEKKFR---EK 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140 TKNNWAERDHFVSHPGKYTLIEVQAEDEAQEAVVKVDRGPVRTVTKRVQPCSLDPATQKL 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246 ALKGPTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIELAQAL 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   425 ENSKSAGYVIGMKCGAHHVGYMFLGEVALGREHHIN--TDNPSLKSPPPGFDSVIAR--- 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 QAGREEDPFRSTAEALKAIPAEKRIIRVDPTCPLSSNPGTQVYEDYNCTLNQTNIE-NNN 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.8%; Score 107.5; DB 4; Length 1164; 20.4%; Pred. No. 0.14; tive 68; Mismatches 210; Indels 143;
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              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,992A
FILING DATE: 05-SEP-1997
                                                                                                                                                                                              CLASSIFICATION: 330
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,707
FILING DATE: 06.5EP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REGISTRATION NUMBER: 1438.0140001/RWE
                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1164 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 20.4%
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-923-992A-10
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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US-09-045-360-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 KKIPMEKKRAFSSSPHAVLTTDTSSELAEKFSLGGNIELQVDVRPPTSGDVSFVDFQVTN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 DSNRFFTCWNRWGRVGEVGQSKINHFT-RLEDAKKDFEKKFREKTKNNWAERDHFVSHPG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204 FS------KEMFKNTMALMDLDVKKMPLGKLSKQQIARGFEALEALEEALKGPTDGGQ 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226 OSYLRWERKGKONYPPEKEKEEYEAARTVL----QEEIARG-ASIQDIRARLTKTNDKSQ 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            256 SLEELSSHFYTVIPHNFGHSQ-------PPPINSPELLQAKKDMLLVL-ADIEL 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----APEYKVIQTYLEQT 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 KAIPAE-KRIIRVDPTCPLSSNPGTQVYEDYNCTLN---QTNIE---NNNNKFYIIQLLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 KYTLIEVQAEDEAQEAV------VKVDRGPVRTVTKRVQPCSLDPATOKLITNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                 81;
                                                                                                                                                                                                                                                                                                                                                                                            Length 1464;
                                                                                                                                                                                                                                                                                                                                                                                         3.7%; Score 105.5; DB 4; Length 1
20.8%; Pred. No. 0.34;
Live 73; Mismatches 193; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    302 AQALQAVSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSG----
REFERENCE/DOCKET NUMBER: GF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
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; Sequence 2, Application US/09045360 ; Patent No. 6207880

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--ALAKKEVEAKELEIEKLQYEISTLEQEVATAQHQVDNLKKLLAG 215
                                                                                                                               308 VSEQEKTVEEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQTGSNHRCPTLQHIWK 367
                                                                                                                                                              257 LDPEGKTQDE----LDKEAEERE-----LDKKADELQNKVADLEKEISN-----LEILL 301
                                                                                                                                                                                                                427
                                                                                                                                                                                                                                                                                               487
                                                                                                                                                                                                                                                                                                                                         -------GDEEETPAPAPOPEOPAPA------PKPE 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 PGTQVYEDYN------CTLNQTNIENNNNKFYIIQLLQDSNRFFTCWNRWGRVGE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 PGMQQYM-FNVRVDGQSLVAGVSLAIVNIDDNAP---IIQ------NFEPC-----RVPE 186
                                              250 --PTDGGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVLADIELAQALQA 307
                                                                                     216 ADPDDGTEVIEAKLKK-----GEAE---LNAKQAELAKK-----QTELEKLLDS
                                                                                                                                                                                                                368 VNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPHSGGRVGKGIYFASENS
                                                                                                                                                                                                                                                                                                 428 KSAGYVIGMKCGAHHVGYMFLGEVALGREHHINTDNPSLKSPPPGFDSVIARGHTEPDPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RECEPTOR FOR A BACILLUS THURINGIENSIS TOXIN
                                                                                                                                                                                                                                                          302 GGADXEDDTAALQNKLATKKAELEKTQKELDAALNELG----PD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CUBRENT APPLICATION DATE: US/08/326,117B FILING DATE: 19-0CT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.6%; Score 103.5; DB 1;
20.3%; Pred. No. 0.58;
.1ve 67; Mismatches 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7112-0037.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                          365 ОРАРАРКРЕОРАРАРКРЕОРАРАРК 389
                                                                                                                                                                                                                                                                                                                                                                                   488 QDTELELDGQQVVVPQ-GQPVPCPE 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08326117B Patent No. 5693491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 7112
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELERAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: MILLMAN, ROBERT A REGISTRATION NUMBER: 36,217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1528 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: BULLA, LEE A.
APPLICANT: JI, TAE
TITLE OF INVENTION: FECEPT
TITLE OF INVENTION: TOXIN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 20.3
Matches 120; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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                                                                                                                                                                                                                                                                                                                                         342 -----
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    168 TLKV-
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                                                                    341 DELRKTITKGEIKTKVEKHLKRSSFAVERIQRKKRDFGHLINKYTSSPAVQV-QKVLEEP 399
                                           354 GSNHRCPTLQHIWKVNQEGEEDRFQAHSKLGNRKLLWHGTNMAVVAAILTSGLRIMPHSG 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 NIENNNNKFYIIQLLQDSNRFFTCWNRWGRVGEVGQSKINHF-TRLEDAKK---DFEKKF 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 REKTKNNWAERDHFVSHPGKYTLIEVQAED-EAQEAVVKVDRGPVRTVTKRVQPCSLDPA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TQKLITNIFSKEMFKNTMALMDLDVKKMPLGKLS-----KQQIARGFEALEALEBALKG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 KKKGRQAGR--EEDPFRSTAEALKAIPAEKRIIRVDPTCPLSSNPGTQVYEDYNCTLNQT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43 KKKAEDAQKKYEDDQKRTEEKARKEAEASQKLNDVALVV-----QNAYKEYREVQNQR 95
                                                                                                                                                                                                                                                                         Sequence 160, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.7%; Score 105; DB 4; Length 641;
19.0%; Pred. No. 0.093;
Live 67; Mismatches 168; Indels 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

WEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB34(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 160:
SEQUENCE CHARACTERISTICS:
LENGTH: 641 amino acids
                                                                                                                             414 GRVGKGIYFASENSKSAG 431
                                                                                                                                                                      450 TDLNQPITLHWALSKSPG 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 19.0%
Matches 96; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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148	246	205	294	252	354	296	414	336	472	378	532	427	576	470	627		
VGQSKINHFTRLEDAKKDEEKKFREKTKNNWAERD	LGEPGLIECTYQVSDADGRISTEFWIFRIDSVRGDEETFYIERTNIPNQWMWLNMTIGVN		TSLNFVTSPLHIFSVTALDSLPNTHTVTMMVQVANVNSRPPRWL-EIFA		· VQQFEEKSYQNFTVRAIDGDTEINMPINYRLITNEEDTFFSIEALPGGKSGAVFLVSPID	GGQSLEELSSHFYTVIPHNFGHSQPPPINSPELLQAKKDMLLVL	RDTLQREVFPLTIVAYKYDEEAFSTSTNVVIIVTDINDQRPEPIHKEYRLAIMEETPLTL	/ADIELAQALQAVSEQEKTVEEVPHPLDRDYQLLKCQLQLL	NFDKE		DYEVPERQSITIRVVATDNNDTRHVGVALVHIDLINWNDEQPIFEHAVQTVTFDETEGEG	AHSK-LGNRKLLWHGTNMAVVAAILTSGLRIMPHSGGRVGKGIYFASENS	FEVAKAVAHDRDIGDVVEHTLIGNAVNFLTIDK-LTGDIRVSAND	KSAGYVIGM	-SFNYHRESELFVQVRATDTLGEPFHTATSQLVIRLNDINNTPPTLRLPRGS		POVEENVPDGHVITQE
114	187	149	247	206	295	253	355	297	415	337	473	379	533	428	577	471	628
δλ	qq	οy	QQ	Οy	qq	0y ,	qq	Qy	q	٥y	QQ	δy	qq	οy	qq	δy	QΩ

Search completed: August 29, 2002, 07:58:18 Job time: 295 sec